

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: November 22, 2002, 12:21:10 : Search time 27.804 Seconds  
(without alignments)  
3433.372 Million cell updates/sec

Title: US-09-686-346A-4

Perfect score: 5140  
Sequence: 1 MPAGRAGSLKDPVALLELF.....LLPLPLLRMRWLAGSTAGP 993

Scoring table: BLOSUM62  
Gapop 10.0 , Gapept 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3530	68.7	1062	T46444	hypothetical prote
2	2803.5	54.6	1001	T17365	serine/threonine p
3	1416.5	27.6	982	T18576	serine/threonine k
4	663	12.9	1231	T18532	serine/threonine k
5	662.5	12.9	836	B96716	probable serine/pr
6	651.5	12.7	1233	T30989	serine/threonine p
7	643	12.5	1233	T14157	serine/threonine p
8	625.5	12.2	1206	T34021	serine/threonine p
9	592	11.5	426	S71886	protein kinase SK2
10	591.5	11.5	1102	JC6316	Ste20-like protein
11	585	11.4	690	C96572	probable protein k
12	566.5	11.0	829	T29372	protein fl2M16.4 l
13	565	11.0	653	T34356	hypothetical prote
14	561.5	10.9	819	A53714	hypothetical prote
15	520.5	10.1	1228	T18897	protein kinase (EC
16	510	9.9	544	S40482	serine/threonine-s
17	508	9.9	545	G01773	p21-activated prot
18	505	9.8	544	A57597	beta-p21-activated
19	500	9.7	544	T49376	p21 activated kina
20	499	9.7	490	S47946	protein kinase hom
21	498.5	9.7	1080	T27622	hypothetical prote
22	498	9.7	1075	T27623	hypothetical prote
23	497.5	9.5	1080	S48944	hypothetical prote
24	490.5	9.5	525	S58682	hypothetical prote
25	489.5	9.5	312	T38525	serine/threonine p
26	477	9.3	471	T39232	probable serine th
27	474	9.2	693	B85112	hypothetical prote
28	472	9.2	652	T39722	serine/threonine p
29	471.5	9.2	561	T51417	protein kinase-lik

30	463	9.0	378	2	T26684	hypothetical prote
31	463	9.0	622	2	T15467	hypothetical prote
32	463	9.0	1062	2	S45367	protein kinase CDC
33	459.5	8.9	710	2	T13458	hypothetical prote
34	450.5	8.8	1230	2	T18256	probable serine/th
35	450.5	8.8	1230	2	T18259	serine/threonine p
36	449	8.7	1230	2	T39500	serine/threonine-s
37	447	8.7	939	2	S28394	probable serine/th
38	439.5	8.6	607	2	T01904	hypothetical prote
39	438	8.5	589	2	T38086	serine/threonine-p
40	435	8.5	651	2	A96591	NPX1-related prote
41	431	8.4	658	2	S60170	protein kinase Pak
42	429.5	8.4	553	2	T01479	hypothetical prote
43	429.5	8.4	608	2	G96575	probable MEK kins
44	426.5	8.3	487	2	A71407	probable Ste20-lik
45	424.5	8.3	883	2	A96662	hypothetical prote

## ALIGNMENTS

RESULT 1  
T46444

hypothetical protein DKFp434N1427.1 - human

C:Species: Homo sapiens (man)

C:Date: 04-Feb-2000 #sequence-revision 04-Feb-2000 #text\_change 04-Feb-2000

C:Accession: T46444

R:Bioecker, H.; Boeher, M.; Brandt, P.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.

Submitted to the Protein Sequence Database, January 2000

A:Reference number: 223032

A:Accession: T46444

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-1062 <AA>

A:Cross-references: EMBL:AL137701

A:Experimental source: adult testis; clone DKFp434N1427

A:Genetics:

A:Note: DKFp434N1427.1

Query Match	68.7%	Score 3530;	DB 2;	Length 1062;
Best Local Similarity	90.8%	Pred. No. 1.4e-97;		
Matches 695;	Conservative 24;	Mismatches 40;	Indels 6;	Gaps 3;
QY	218	LARKRPPLRNMAASLYHQAQNEPALOSGHWSEYFRNFVDSCLQIKIDRPTSEVLK	277	
DB	45	VAERKPELFNMNMAALYHQAQNEPVLQSGHSEYFRNFVDSCLQIKIDRPTSEVLK	104	
QY	278	HRVLERPPTVIMDLIORTKDAVRELDNIQYKMKKILFOEAPNGPAGAEPEEEAEP	337	
DB	105	HRVLERPPTVIMDLIORTKDAVRELDNIQYKMKKILFOEAPNGPAGAEPEEEAEP	164	
QY	338	YHRACTLSLESSHSVPKMSISASSQSSVNSLADASDNEEEEEEDEEEDEE	397	
DB	165	YHRACTLSLESSHSVPKMSISASSQSSVNSLADASDNEEEEEEDEEEDEE	222	
QY	398	SRPMAMQGEHVTSHSSTIHLRPGSDNLYDDPYQPEMPTGLQPPAPPTSSSSAR	457	
DB	223	ARMAMQGEHVTSHSSTIHLRPGSDNLYDDPYQPEMPTGLQPPAPPTSSSSAR	282	
QY	458	RRAYCNRDHFATIRPASLVSRQIQEHEDSALREQLSGYRRRROHOKOLALESLRG	517	
DB	283	RRAYCNRDHFATIRPASLVSRQIQEHEDSALREQLSGYRRRROHOKOLALESLRG	342	
QY	518	EREHSGRLQRELEAQRAGGTAEKRLARRHQAIGEKARMAQAEEERKFTQOHTLGOOKE	577	
DB	343	EREHSGRLQRELEAQRAGGTAEKRLARRHQAIGEKARMAQAEEERKFTQOHTLGOOKE	402	
QY	578	LAALLAOKRTYTLRKEQLKEELQENPSTPKRKAWLRLQKQLODQCAEEAGLLRRQ	637	
DB	403	LAALLAOKRTYTLRKEQLKEELQENPSTPKRKAWLRLQKQLODQCAEEAGLLRRQ	462	
QY	638	ROYFELOQYKRRKMLARSLDQDLREDLNRKQTKQDECALLRQHEATRELELROL	697	

Db 463 KQYFELQKQYRKMLLAHNSLDQDLREDLNKKQOTQKDECALLRQHEATRELELROL 522  
 QY 698 QAVORTRAELTRLOHOTELIGNOLEYKRRREOELROKHAQVROQPSKSLYVRAGOLPMG-- 755  
 Db 523 QAVORTRAELTRLOHOTELIGNOLEYKRRREOELROKHAQVROQPSKSLYVRAGOLPMG 582  
 QY 756 LPATGALGPLSTGTLSEEPCCSSGGOBAILGQRMIGEBAVBERMILLEGTTLEPEEOR 815  
 Db 583 LPIPGALGPPNMGTPLEEQPCSPGQAVLADQRMIGEBAVBERMILLEGTTLEPEEOR 642  
 QY 816 ILQEEGTSSSSROKRSILVNEEDMISKEMKESRPSLASQERNITIGEEAGANMLMK 875  
 Db 643 ILGEEGAPSPQKHSLVDEEWGLPEIEELRPSLVPEQERSTIVGQEEAGTSLMGK 702  
 QY 876 EHGNIIVMEFKLGWVGPLYTPVPEEEEEEBCAPIGTPRDPGDCSPDIPEPPPS 935  
 Db 703 EDESILDEEFELGWVGPRALTPVPEEEEEE--GAPIGTPRDPGDCSPDIPEPPPT 760  
 QY 936 HLQYRPASQLPGFLSHGLTGLSPAVSSSGLPLLLLLPLLA 980  
 Db 761 HLRCPRASQLPGLSHGLTGLSPAVSSSGLPLLLLLPLLA 805

## RESULT 2

T17365  
 serine/threonine protein kinase TA01 - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C:Accession: T17365  
 R:Hutchinson, M.; Berman, K.S.; Cobb, M.H.  
 J. Biol. Chem. 273, 28625-28632, 1998  
 A:Title: Isolation of TA01, a protein kinase that activates MEKs in stress-activated pro  
 A:Reference number: 218730; MUID:99003202; PMID:9786855  
 A:Accession: T17365  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-1001 <HUT>  
 A:Cross-references: EMBL:AF084205; NID:g3452472; PID:g3452473; PIDN:AACT1014.1  
 C:Function:  
 A:Description: probably implicated in the regulation of the p38-containing stress-respon

Query Match 54.6%; Score 2805.5; DB 2; Length 1001;  
 Best Local Similarity 57.8%; Pred. No. 27e-76;  
 Matches 596; Conservative 108; Mismatches 225; Indels 103; Gaps 16;

QY 1 MPAGGAGSLKPDVAELFFKDDPEKLFSDLEIGHSGFAYFARVNSEVVAIKKMS 60  
 Db 1 MPSTNRAGSLKPEIAELFFKDDPEKLFSDLEIGHSGFAYFARVNSEVVAIKKMS 60  
 QY 61 YSGKSNKEMODIIEKVRFLQKLRHPTNTIYNGCYLREHTAMLVMEYCLGSASDLEVRK 120  
 Db 61 YSGKSTKEMODIIEKVRFLQKLRHPTNTIYNGCYLREHTAMLVMEYCLGSASDLEVRK 120  
 QY 121 KLOVEETAAVTHGALOGIAYLHSHNMHRDVKAGNIIISLSEGVLYKLGPGFSASIMAPN 180  
 Db 121 KLOVEETAAVTHGALOGIAYLHSHNMHRDVKAGNIIISLSEGVLYKLGPGFSASIMAPN 180  
 QY 181 SFVGTPTWMAPEVILAMDEGOYDKVWVSLGTCIETLAERKPPLENNMAMALVHIAON 240  
 Db 181 SFVGTPTWMAPEVILAMDEGOYDKVWVSLGTCIETLAERKPPLENNMAMALVHIAON 240  
 QY 241 ESPALQSGHWSYEFNPNVDSCLQKIPQDRPTSEVLKHRFLVLRPPVIMDLQRTKDA 300  
 Db 241 ESPALQSGHWSYEFNPNVDSCLQKIPQDRPTSEVLKHRFLVLRPPVIMDLQRTKDA 300  
 QY 301 VVELDNLQYRKMKKLLTFQAPNGPAGAEAPDEEAPRYHRRAGTILTSLESSISVSMIS 360  
 Db 301 VVELDNLQYRKMKKLLTFQAPNGPAGAEAPDEEAPRYHRRAGTILTSLESSISVSMIS 360  
 QY 361 ASSQSSSVNSLADSDNEEEEEEDEEPEEESREEMAMOGEGHTVYSHSIIHR 420  
 Db 361 ASSQSSSVNSLADSDNEEEEEEDEEPEEESREEMAMOGEGHTVYSHSIIHR 420

QY 421 LPESDNLVDDPYQPEMTGCP-LQPPAAPPTSTSSSARRRAYCRNDRPATIRTSLSYR 479  
 Db 400 KPEEEN-----YQEGEDPRTASAPSP-----QVSRKSHYRNREHPATIRTSLSYR 449  
 QY 480 QIQEHEODSALAEQSLSGYRMRROKOLLAEISRLRGREHSGRLQELAEQRAFGFT 539  
 Db 450 QIQEHEODSALAEQSLSGYRMRROKOLLAEISRLRGREHSGRLQELAEQRAFGFT 509  
 QY 540 EAEKLARRQALGEEKPARAAQAEERKFOOHILGQOKKELALAEOKRTYKLRKDLKEE 599  
 Db 510 EMEKLIRKQAAEMERKAKMANDEKKFQOHLQAQOKKELNSLDESQKRYKLRKDLKEE 569  
 QY 600 LGQNPSTPKREKAEMLLRQKQDLQOCQAEEBAGLLRRQRYFELQCRQYRKMLLAHNSL 659  
 Db 570 LNEQSTPKREKQEWMLSKQENIQHQAEEBANLLRRQRYLELQCRQYRKMLLAHNSL 629  
 QY 660 DDDLREDLNKQOTQKDECALLRQHEATRELELROLQAVORTRAELTRLOHOTELIGN 719  
 Db 630 EDDLREELNKRQOTQKDECALLRQHEATRELELROLQAVORTRAELTRLOHOTELIGN 689  
 QY 720 LEYKRRREOELROKHAQVROQPSKLYVRAGOLPGLPATGALP-----LSTGT 769  
 Db 690 LEYKRRREOELROKHAQVROQPSKLYVRAGOLPGLPATGALP-----LSTGT 749  
 QY 770 LSE-----EQPCSSGOBAILGQRM-IGEEBAVPE--RMILGKRG 806  
 Db 750 KSEHFAVLRLKEEQTRLALIAEYDHSINMLSTQALRLDEAQEBQVLMKQLOQEL 809  
 QY 807 TLEPEEORILQD-----ENGTFSSSQKRSVLNEDMDISKEM-----KESRVP 853  
 Db 810 ELLINAYQSKIKKQAAQAHNDRELEQRYVSLRALLEOK---IEEMALQNERTERINS 866  
 QY 854 LASQENITIGQEEAGAMNLMKEH--GNLVDMFK-----LGWVGPP-----L 895  
 Db 867 LLEQARQETLEAPDSESMRLGFSNMVLSNLSPAFHSISYGAASWSKINPGSGGPPHGM 926  
 QY 896 TPVPEEEEEEBCAPIGTPRDPGDCP-SPDIPEPPPSHLQYRPASQLPGLSHGLT 954  
 Db 927 GGTPOAMGHPMGGPQPMGHPGPGVGRSSIGVRNPSQALRRTAGS---GRTEQGS 983  
 QY 955 TGLSFAVSSSG 966  
 Db 984 RSTSVTSQISNG 995

## RESULT 3

T18576  
 serine/threonine kinase - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C:Accession: T18576  
 R:Cope, M.J.T.V.; Kendrick-Jones, A.  
 submitted to the EMBL Data Library, July 1995  
 A:Reference number: Z18984  
 A:Accession: T18576  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-982 <BAR>  
 A:Cross-references: EMBL:U32275; PIDN:AAA75370.1; GSPDB:GNO0021; CESP:SUlu  
 A:Experimental source: strain N2 Bristol  
 C:Genetics:  
 A:Gene: CESP:SUlu  
 A:Map position: 3

Query Match 27.6%; Score 1416.5; DB 2; Length 982;  
 Best Local Similarity 34.8%; Pred. No. 2e-35;  
 Matches 333; Conservative 162; Mismatches 346; Indels 115; Gaps 17;

QY 6 RAGSLKPDVAELFFKDDPEKLFSDLEIGHSGFAYFARVNSEVVAIKKMSYSGK 65  
 Db 8 KPGVTKDPSIALFSSNKPDEQRYDRLREIGHSGFAYFARVNSEVVAIKKMSYSGK 67  
 QY 66 SNEKMODIIEKVRFLQKLRHPTNTIYNGCYLREHTAMLVMEYCLGSASDLEVRKPLQD 125

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      : ||| ||| ||| : ||| : ||| : ||| ||| ||| ||| : ||| : |||
68 AVEKMDIIEVSEFLTVVPHIVDVKACFLKDTCTMVLWEYICGASADIVDLRGMRE 127
126 VETAAVTHGALQGLAYLHSHNMTHRDYKAGNILLSEGLVKLDDPSASIMAPNVG 185
128 VETAAVTHGALQGLAYLHSHNMTHRDYKAGNILLSEGLVKLDDPSASIMAPNVG 187
186 PYMAPEVILLAMDEGQYDGVWSLGTICIELAEKRPPLFNMMASALYHIAQNSPAL 245
188 PYMAPEVILLAMDEGQYDGVWSLGTICIELAEKRPPLFNMMASALYHIAQNSPAL 247
246 -----QSGHWESEYFNVDSCLOKIPDRPTSEVLLKHFVLRERPPYIMDLORTKD 299
248 SPIDTSEGEFMSLEFVOFLDKCRKPAEERMSAECEFRHPIORSRPSDTIQELIORTKN 307
300 AYVELDNLQYRKKKILF-----QAPNPGCA-----EAPPEEAEYEMHRACT 344
308 MYVELDNLQYRKKKILF-----QAPNPGCA-----EAPPEEAEYEMHRACT 344
345 LMSLESHSVPSMSIASOSSVNSLADASDNEEEEEEDEEEDEEEDEEPEPSREMA 404
368 LTFEFSMOSSGGGLVSTVTTCAMDNVHSSGSGSSSTTSARRRPPISQMLSTS 427
405 QEGEHTVTSHTIIRLPGSDNLDDPYOPEMPGLOP-PAAPPTSSSSA-----456
428 TSGVTGMPSHGV-----CASITALAVNP--TPSPSEPIPTSQPTKSSSSSILETAHD 479
457 -----RRAYCRNDHATIRITASLVSRQIOEHODSALRQLS 495
480 DPLDTSIRAPVKDLMHRAVYKRIATLQNHKFKATLSQRIINOEEYENKEMNEMOMS 539
496 GYKMRROHOKOLLESRLGEREESHGRLQRELEAQRGFGTEAEKRLARRQALGEKE 555
540 KYHLLQAHKKEIQOEERKALDRQALRYKMDLEQLTTY--SKEMVYKCSQNNELD 597
556 ARAQAE--ERKFOHILGOQKKEALALEAQRKYKLRKEQLELOENPSTPKREKAE 613
598 KRKDIJEDGKKKKTKTNSQNOQOMKLYSAQOLKEKYKYNNEAOKTRLR-SLNNPRSYEN 656
614 WILRQEQLOQCOAEBAEAGLRQYFELQCOYKRYKMLLHNSLDODLLREDLUNKQT 673
657 AMEYVADLNRVADARENDEDEKLRLEDEIVYRQQLSNLHOEEQDDDEDVYQER 716
674 QKLECALLRHAEARELEBOLQAVQRTARELTRIOHTELGNOLENYKRRQELROK 733
717 QMPTRHGLSKOHEMTKDEIQHNLHANKKRLHETQHAESASONEYTOQROODELRK 776
734 HAAVQOQPSKLVYRAGOL-----PMGLPATGALPLS-----TGTLSSE 773
777 HAMQSRQPRDLKIQEQAIRKQYRQYKQTRQFKLYLTQMVQVPRDEQKELTSRLKQD 836
774 Q-----PSSGQEAIIQORMLGEEBAVPERMILGREGT--807
837 QOKQVALLASQYESQIKKMWQDKTVKLESQED--EQRVSEKLEKELEELLIAVOKKTRA 894
808 TLERPE--EORIOEMGTFFSSPOKHRSLVNFBEDMDSKEMESRPSLASQERN 860
895 TLERQIKKERTALEKIGT-RRAMLEOKIIEERQMGEMRLKKEQIORDHQSQRH 949

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A:Molecule type: mRNA
A:Residues: 1-1231 <IIT>
A:Cross-references: EMBL:D88425; NID:G2911113; PIDN:BAA24930.1; PID:G2911114
A:Experimental source: strain Hartley; liver

Query Match      12.9%; Score 663; DB 2; Length 1231;
Best Local Similarity 22.3%; Pred. No. 3.7e-13;
Matches 277; Conservative 166; Mismatches 372; Indels 428; Gaps 39;

6 RAGSLNDPVAELFFRD-DPEKFLSDRLGHSFGAVYFARVYRSEVVAIKKMSYSGK 64
11 KLGSEKKKKQYEHVKRDLNDEEFMERITGELGDGAFKQYKAKQNKENVLAALAAVID--T 67
65 QSNKEMODIKEYEYFQKLRHPTIYRGCYLREHMAVMEVCLGSASD--LLEVHKRP 122
68 KSEELLEDVYVEIDILLASCDHPYIVKLDAPFYENMLWILTEGACAGADAVAYLEL-ERP 126
123 LQVEIAAVTHGALQGLAYLHSHNMTHRDYKAGNILLSEGLVKLDDFG--SASIMAP 178
127 LTFESQIQVQCKQTLLEALNYLHDKKIIRDLKAGNILLFTLDGDIKLADFGYSAKNTFRQ 186
179 ANSFVGTPTMAPEVILL--AMDEGQYDGVWSLGTICIELAEKRPPLFNMMASALYH 236
187 RDSFEGTPYMAPEVYVWCETSKDRPYDYKADVWSLGTILEMAEIEPPHHELMPMRVLTK 246
237 IAQNSPAL-QSGHWESEYFNVDSCLOKIPDRPTSEVLLKHFV-----LRRRPT 288
247 IAKSEPTLQAQPSRWSNENFDFLCKCLEKWDARMTTSOLLQHPFYITDSNKPRLIELAE 306
289 VINDLIORTDAVARELDNLQYRKMKRI-----LFOEA-----320
307 AKAEVYEEVDGKEEDDEDEIENSLLPIPTKRASSDLSIASSEDLQSQACLESYSEK 366
321 -----PNGP-----GAEPDE-EEAEPIYMHRA 342
367 TEHNASGDKFSTKVLNEKPCGPENAVELVGAVALPDRATELPESEGEERPKLDR-425
343 GTLTSLESHSVPSMSIASOSSVNSLADASDNEEEEEEDEEE-----EEEE 394
426 --LPDTEQEMADINSVSEGEDHVAVSTETNIEHNLKPEKERQEQVYLENKLVASEDT 483
395 GPSREMAHQEGEHTVTSH--SSIIH-----419
484 TITQTVLVSQETKEVDIHLIDSEVYHVAEDTHEKLRKDDTQOKVYISDTSVGERDE 543
420 -----419
544 IGAVPKTAESSAGAGQGGKETDEGAQILISKATGPKASGTEAPVYTEITENDTQ 603
420 -----RLP-----GS-----424
604 KLVNTHKQPLISSETTIDTSEGLASGSEGEVTEGSTEVEVEGAVSETDEEDVQSET 663
425 -----DNLVDDPYQPEK--TPGPLOPAPAPPTSSSSARRARVACRNRDH 468
664 RGAAPVATQMDTKENETPHAPQAVEYQVYPPQPSPPAPPIPSININSEALNKGEMG 723
469 ATIRTASLV--SRQIOEHQDSA-----MRQOKOLLALESRLRGEREE 521
724 ASLNTETILPESESQKENDTDSGTADNSSIDLNLSSISFLSKTKONGSTISLOETRR 783
493 QLSGYR-----MRQOKOLLALESRLRGEREE 521
784 QKTLTKTRKFIYDGEVSVYTSKIVTSDSKTEELRFLRQELRELFLQKEQORAOQ 843
522 HSGRLRELEAQRAGGTEAKLARH-QAIGKEARAQAERKROOH-----I 570
844 LNKRLDQQRQIIRREFQEMSKKROTDQETENLEKQOKTITRLEDEHTNRLRDEAKRI 903
571 LGOQKELALALAEOKRTYKLRKEQLELOENPSTPKREKAMVLROKQOLOQCOAE 630
904 KGEQEKLS-----KFGNILLNRKKEVLENEVKAAPKDKRLMKRKKELALQSQHVE 956

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RESULT 4  
T18532  
serine/threonine protein kinase - guinea pig  
N:Alternate names: STE20-like kinase  
C:Species: Cavia porcellus (guinea pig)  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 21-Jul-2000  
C:Accession: T18532  
R:Toth, S.; Kamada, Y.; Yamada, E.; Tsujikawa, K.; Mimura, T.; Kohama, Y.  
Arch. Biochem. Biophys. 340, 201-207, 1997  
A:Title: Molecular cloning and characterization of a novel putative STE20-like kinase in  
A:Reference number: Z18952; M01D:97288344; PMID:9143322  
A:Accession: T18532  
A:status: preliminary; translated from GB/EMBL/DBJ

[illegible]

RESULT 5  
B96716  
Probable serine/threonine kinase F23010.20 [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
C:Accession: B96716  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,  
Chiu, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Stilm, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719; PMID:11130712  
A:Accession: B96716  
A:Status: preliminary  
A:Molecule-type: DNA  
A:Residues: 1-836 <STO>  
A:Cross-references: GB:AE005173; NID:g7705100; PID:AA667779.1; GSPDB:GN00141  
C:Genetics:  
A:Gene: F23010.20  
A:Map position: 1

	Query Match	12.9%	Score 662.5;	DB: 2;	Length 836;
	Best Local Similarity	34.4%	Pred. No. 2,8e-13;		
	Matches 159;	Conservative 83;	Mismatches 163;	Indels 57;	Gaps 11;
OY	21	KDPEKLESDLRREIGHSGFAGVAFARDVRNSEVAIKKMSTSGSKOSNMKMODITKEVFLL 80			
Dd	242	KEDPTTKTEFLNEIGKGSGYSGVAKARDLKTSEIVAANKISLT--EGEGBYEIGEIEIML 299			
OY	81	OKLRHPNTIOYRGCCYLRRHTAMLVMEYC-LGSASDILFEVHKPLQEOEVIAATVGALGL 139			
Dd	300	QQCHNPANVKRLGSYQGEDIYIWEYICGGGSVADLMNVTFEALFEIQAIDICBDAKGL 359			
OY	140	AYLHSHNMIHRDVKAGNILLSEPGLVKLGDFGSA---IWAPANSFPQTYYMAAPEYL 195			
Dd	360	AYLHSIYKVHNDINGGNILLDEGEVKKLDGCVAAQLTRMSKNRTFLGTTHMAAPEYL 418			
OY	196	AMDESQYDGKVDVWSLGITCIELAEKRPPLENMNAAMSALYHIHAONESPALOSGH-WSEYF 254			
Dd	419	--QENRYDGKVDVWALGSAIEMAEGLPBRSSVHPMRVLFIISTLEPAMLDEKKMWLYF 476			
OY	255	RNFVDSCLQKITPDORPPISEVULLKHREFULRKERPPTYIMDLIORTDVAERLDNIQRKKK 314			
Dd	477	HDPFAKCTLKPERPRIRPYTAEMLEKHKFY-----ERCKTGASAM-SPIKEKSQ 522			
OY	315	ILPDEARNGPAEAEPDEFEEELPYMHNRAGTITLSLESSHSIVSASISASSOSSVNSL--- 371			

```

Db 523 IRAHMAQAQSVAPSLSDTS-----ILGRSSSEILITVPSKRPQNSTAPLSTLNRO 577
Qy 372 -----AASNDNEEEEEEDEEEDEEEDEEGFSKEMAMOGCEITVSHSIIH 419
Db 578 HITGNTVLAGCGDGFMTIVNGEETESDSRSO-----LVKKESSSSQFEGVPR 628
Qy 420 RLPGS---DNLDDPYOEPMTGGFLQPPAPPTSTSSSARR 458
Db 629 EPPGEELPDGSIWIDKKRPPAIDLVEVSTISQSMOASSSHHR 670

```

RESULT 6  
T30989  
serine/threonine protein kinase NTK - mouse  
N:Alternate names: Nck interacting kinase  
C:Species: Mus musculus (house mouse)  
C:Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 22-Oct-1999  
C:Accession: T30989  
R:Su, Y.C.; Han, J.; Xu, S.; Cobb, M.; Skolnik, E.Y.  
E:Bio. J. 16, 1279-1290, 1997  
A:Title: NTK is a new Ste20-related kinase that binds NCK and MEK1 and activates the  
A:Reference number: Z20954; MUID:97280817; PMID:9135144  
A:Accession: T30989  
A:Status: preliminary: translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-1233 <SU>  
A:Cross-references: EMBL:U08984; NID:g1872545; PID:g1872546; PIDN:AAC53165.1  
A:Keywords: protein kinase

```

Query Match 12.7% Score 651.5; DB 2; Length 1233;
Best Local Similarity 24.3%; Pred. No. 8e-13;
Matches 251; Conservative 141; Mismatches 272; Indels 367; Gaps 39;

QY 7 AGSLKDPVAELFFKDDPEKLFSLDREIGHGSGFAGVVFARDVRNSEVAIAIKMSYSGKQS 66
Db 7 AKSLVDIDLSSL--RDPAGIFELVEVNGMGTGYGVKGRHVK--TVMAAIKVMV----T 58
QY 67 NEKKODIIKEVRFLOKL-RHNPITQVRCGYLR-----EHTAWLVMEYC-LGASLDLEY 118
Db 59 EDEEBEELTLENMLKKTSHHNRNIATYYGAFIKKSPRHNDQMLVMEFCAGSITTDLVKN 118
QY 119 HK-KPLOEVEIAAATVHGALOGLAYLHSHNMIRPVKAGNILLSEPGVLKIGDFG-SASI- 175
Db 119 TKGWTKMEDWIAVYSREILRGLAHLHIVHINRIKQONVLTPEMAEVKLVDFGVSQOLD 178
QY 176 --MAPANSFGCTPYWMAPEVYLADE--GOYDGKVDVWSIGTCTELAEKRRPLFMMNA 230
Db 179 RTVGRNRTFICTPYWMAPEVI-ACDENPDATYDYSRLMSGCIATAIMAGGRLCDMHP 237
QY 231 MSALYHIAONSPALOGSHMSEYFRNFVDSIOKIPQDRPTSEVLKRNHRYLRP---- 286
Db 238 MRALFLLPRNDPRPLKSKKSKKSFTEEGLVAKNYKORPSTDELLNRPY-KDQPERO 296
QY 287 -PIVIMDLIORTKDAVELDNLQYRKMKKILFQEPARNPGAEAPREEEERPMYHNRAGTL 345
Db 297 VRIQKOHIDRTKRKKRGEKDETEY----- 320
QY 346 TLESLSHSVFSMSISASSOSSVNSLADASDNEEEEEEEEEEEEEEEBESPERSEMANMO 405
Db 321 -----EYSGSEEEEEEEYDE-----Q 335
QY 406 EGEHTVTSHSIIHRLPGSDNLVDDPYQPEMTPEPLQPPAAPRTSTSSSARRAYCR-- 463
Db 336 EGE-----PSSIVN-VGESTL-----RRDPLRLQ 359
QY 464 --NRDHFATIRTSALVSROIOEHNEODSALREODLSGYKRMKROHOKOLLA-LESRLNGER 520
Db 360 QENKERSEALRPOOL-----QEOQLREQ-----EYKROLAERQKRIEQQKE 403
QY 521 EHSRLRLDLAORAGCTEAELKARRHQALIGEKEAAMAAEERKKTQOHLIGQOKKELAA 560
Db 404 Q-----RRRLRLEDO-----RRERARROQ-----BREQRRRQDEERK----- 435

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[illegible]

Db	304	IAEAAEVTVEEDQKEDEEEEAENLPIPIKRRASSDLSIASSEEDKLSONACILESV	1:::	363
QY	308	QYR-----KMKILFQEAR-NGP-----GAE-----		327
Db	364	SERTQOSTSEDKFSFKILNEKPTTGDPEKAVDEHADVDNLLETAAINDQTGVIHENGREK		423
QY	328	-----APEEE-----		332
Db	424	KRPKLLENLPDQDQTVDVNSVSEENNNVTLETNTDCLKPEEDKNKNEQETLESKLIQ		483
QY	333	-----EEAEPYMRAGT---LTSLESS		351
Db	484	SEEDINDHIQTMDLVSOETGEKEADFOAVDNEVGLTKEFTQEKLGDKGTAKQVITSDRSS		543
QY	352	HSVPMSISASSOSSSVNSLADASDNDEE-----DEEEEEEEEEE		392
Db	544	EYGTDEALDDTQAKAEISKAAQSGDEALVPTQLAEKPTGEPGAGAEPEPPGERVE		603
QY	393	EEGPEPSRMAMMOEGEHTVT-----SHSIIHRLP-----		422
Db	604	DKQEPQCPAVCEAGQSLTSETTRATLEQPEPDENVQVSENSIDELRLVTGAERA		663
QY	423	-GS-----DNLVDPEQPE-MTPGDLPPAAPTSTSSSSARRRAYCRNMD		466
Db	664	LGSEGEAATEVDLERKENMAKVFKAESQAPASQPEEPHPLIPISINSET--TENKE		722
QY	467	HEATIRTSILVSRQIOEHE-----QDSSA-----		489
Db	723	EMGALPKPETTLPEPEHEKNDTSGTSGTVENSSGDLNLSTSELSKAKQSGVSIQE		782
QY	490	IREQLSGYKR-----MRQHQKOLLALLESRLGE		518
Db	783	TRRQKKTLKTRKRFIVDSVEVSTTSKIYVDSQSKTEBELRFLRQRLRELRLLQKEBORA		842
QY	519	REESHSGLQRELEAORAGFGTEAEKLARRH--QAIGEKARAAQAEEKFOOH-----		569
Db	843	QOOLNGKLQOQREQIFRRF--EDEMLSKKRQYDQIEINLEKQKQOTIERLEQEHNRLLRD		900
QY	570	-----ILGQKKELALAEAKQKTKLKEBQLEKLEIDENSTPRKEAEMLLQKEQLOQC		625
Db	901	EAKRIRGEQEKELSKF-----QNLKLNKKKEVMNEVEKAPRELRELTK--RRKEBELAQ		953
QY	626	QAEFEAGLRKROROYFELQCRQ--YRKRMILARHSIDODLREDLNRKQOTQKQDLEQALL		683
Db	954	QHAQOEQEVQAOQDBQSLKTIQQAELA-----NRECKLNNKQ-----LM		999
QY	684	ROHEAT-RELELRQDAVQR-----TRAETLRLOHETELGNOLEYNNKREOEL		730
Db	1000	RAREAAIWELEERHLOEKNOLKQOLKDXQYFMQRHOLK-RHEKETQEQMQRNORLIEL		1058
QY	731	RQKHAQVQRQPK-----SLKYRAGQLPMGRPALGALGPLSTGLSEQPCSSGQERAILIQ		786
Db	1059	KNRQTOEARPKRQLORSEATGRAMFKRSRLINSTAP-----		1096
QY	787	RMLGEEEAVERMILKEGTTLEPEBORILOEEMQTFSSPOKHRSLNEEDWDISKEM		846
Db	1097	---DQDRKKIQ-----FAAQEKRRKKNERM--AQDNKHSQM--KDLQLOCEA		1133
QY	847	KESRVPSTIASQERNITGOEENAGANNIMEKEHG-NLYDMEFKLGWQGVPLTVPEEEBE		905
Db	1139	NVRELHONKCKHLVENHETQKLIKELDEHSEQLKEMWREKLR-----PKTKTLE		1188
QY	906	EE 907		
Db	1189	EE 1190		

C:Accession:U34021  
R:Fukami, Y.; Yamamoto, H.; Ichihara, T.; Mori, K.; Gomi, T.; Sato, K.  
Submitted to the EMBL Data Library: April 1997  
A:Description: SK1, a putative rat homologue of yeast protein kinase NRK1  
Reference number: 221463

Query Match	12.2%	Score 625.5	DB 2	Length 1206
Best Local Similarity	21.3%	Pred. No. 4.6e-12		
Matches 288	Conservative 162	Mismatches 326	Indels 465	Gaps 37

Qy	6	RAGSLKDDVDVALEFPKD--DPEKLSDLREIHSGSFGAVYFARDVYRNSVVAIKKMSISGK	64
Db	11	KLGSEKKKROYEHVKRDN--PPEEFWEIIGELDGFAGKYKKAQNNETVNLAAAKYD--T	67
Qy	65	QSNEMKODIIEKVEFRFLQKLRPNITQYGCYLREHTAVLVQCYLGASD--LLEVEHKP	122
Db	68	KSEELDEIYMEIDLACSDHPNIVYKLLDAFYENNMLILIEFCAGAVDAVMEL--ERP	122
Qy	123	LOEVEIAAVTHGALOGVALYHSHNMHRDVAKAGNILLSEPLVKGDFG---SASIMAP	178
Db	127	LTESOIQVVCQOTLEALNYLHDNKKIHHDLKAGNILLFTIDGDIKLADFGVSAKNTPTIQR	186
Qy	179	ANSFPGFYWMAPEYL--AMDEQGYCKVWVSLGITCIEJARCKPPLFMMNMSALYH	236
Db	187	RDSFGITTYWMAPEYVWKECTSKDRPYDKAIVWSLGLTLEMALIEPHEHLMRYVLLK	246
Qy	237	IAONESPAL--QSGHWSEYFRNFVDSCLQIKIPDRPTSEVLKXHFV---LREPRPT	288
Db	247	IAKSEPPTLAPSRMWSNFKDFLCKLEKNVDAKWTYSQLLQHPFYVYDSNKPVRELIAE	306
Qy	289	VIMDLQITKRAVRELD-----	305
Db	307	AKAEYTEVEEGKEDEDDDETESALPIPAKRASSDSLASSEBDKLSQNACLIESYER	366
Qy	306	---NLOYEKMKKILFQEPANPGAEAPE-----EEEAEPY---MHRAGFLTS	347
Db	367	TEHNTSGKFNKNYLISEKPRPEGEKTYVDVGRANDVLEVAAPNQAQVFNHNGEKK	426
Qy	348	LESSHVVSMSITSASSOSSVNSIADASN-----EEEEEEEE--	387
Db	427	RPOLESQD---TEDQOTVDVNLVGEGDSNIVILETNTDCLKPEEDRNEENOETIENKL	483
Qy	388	-----EEEE-----	393
Db	484	TQSEIKDIIHQMDLVSOETGEKEADFOAIDNEVGFTKEETQEKLGKDKTJKHVVISDI	543
Qy	394	-----EGPES-----	398
Db	544	TSEVGTDEPPDQKSAQSQDAGGAGEAPQAQTLTEKATGPRAHGAEEPRNGER	603
Qy	399	-----RMMAMOGCEHTVT-----SHSSTIHLR-----	422
Db	604	VEDKOLEQOASVCGEGQYVSTSESTRATTEEPETDEVDQSEBNSIELERLGVGAEE	663
Qy	423	---GS---DNLVDYPOPE--MTPEPLQPPAAP-----	448
Db	664	QALSGKGEAATELDEREENAOELPVKAEPOAPASQASEPPVLPISINHSENTENKG	723
Qy	449	-----TSTSSS-----	455
Db	724	EMGALPKRETIILPEPENGKNDPDSGFGVSEKSSDMLNISTISFLTKTKDGSVSLQE	783
Qy	456	-ARRARICRANRDNH-----ATITASLVSRQIOIEHEDSALREQ--LSGTYKMRROHQO	507
Db	784	TRRQKTLTKTRKIVDQEVSVTTSKIVDSQSKTELEFLFKROEJLRELRLQKEKROKA	843

Qy	508	LLALESLRGREHSHSRLORELEAQRAGSGTAEKILARRHQAIGEKARQAQAQAEKRFQ	567
Db	844	QOOLNGKLOQOREQIFRRFEQEMLSKROQDOETENL-----EKQOKOTTEREQ	893
Qy	568	QH-----LIGQOKKEALMALEAKRTYKILRKREOLKEELOENSPYPR-----EKAE	613
Db	894	EHTNRLRDEAKRIGEBQEKELSKFQNNLRKKKEBEPYQOKQOELGALKKIIQOQKAE	953
Qy	614	-----WLNRQK-----QLOQSOAEBAQILBRQ--ROYFELQSRQYKMYL	654
Db	954	LANIERECLNKKOQLLRABEAIMELEERHLEQKHOLLKQOLKDYF-----IQRHQLL	1007
Qy	655	ARHSIDDLR-----EDLNKKQYQKDYCEALMLRQENAR-----	690
Db	1008	KRHEKEETQMYRQYQNRLLIEELKRNQYQTERARLPKIQRSEAKRYMAFMKSLRINSTAPD	1067
Qy	691	-----ELEBROLQVORTAELRL-ONOT-----ELQNO-----LEY	722
Db	1068	ODREKIQFAAQEKKRQKNERNMAHQKNSQMDLQDQCEANVRELHOLQNEKCHLYEH	1127
Qy	723	NKRREOLROKHAQVQQRPSKVLVAGOLPMGLPATGALGRLSTGLSEBQPCSSGOEA	782
Db	1128	ETQKTELDEHSHQELKEMWEKILRPKRTL-----EEEFARKIQEQ	1168
Qy	783	ILGQRMIGEEF	793
Db	1169	EVFFRMGTGESE	1179

RESULT 9  
 S71886  
 Ste20-like protein kinase - human  
 C:Species: Homo sapiens (man)  
 C:Date: 29-Jan-1998 #sequence-revision 06-Feb-1998 #text-change 21-Jul-2000  
 C:Accession: S71886; G01022  
 R:Pombo, C.M.; Bonventre, J.V.; Molnar, A.; Kyriakis, J.; Force, T.  
 EMO J. 15, 4537-4546, 1996  
 A>Title: Activation of a human Ste20-like kinase by oxidant stress defines a novel st  
 A:Reference number: S71886; MUID:97042345; PMID:8887545  
 A:Accession: S71886  
 A:Molecule type: mRNA  
 A:Residues: 1-426 <POM>  
 A:Cross-references: EMBL:X99325; NID:g1430821; PID:CAA67700.1; PID:g1430822  
 A:Experimental source: cell type B cell  
 A:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom  
 C:Keywords: ATP; autophosphorylation; phosphotransferase; protein kinase; stress-indu  
 F:18-270/Domain: protein kinase homology <KIN>

Query Match	11.5%;	Score 592;	DB 2;	Length 426;
Best Local Similarity	36.4%;	Pred. No. 2e-11;		
Matches 154;	Conservative 69;	Mismatches 128;	Indels 72;	Gaps 16;

[illegible]

```

QY 317 FOAPNPGAEAPBEER---EAE-----PR---MIRACTLTSLESSHS 353
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 293 -----ESHGEESSESDSIDGEADGROGIMTFPTIRSPHSKILHKG---TALHSOK 344
QY 354 VPSMSIASOSSSVNSLADASDNEEEEEE-----EEEE-----EEBPEREM 401
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 345 -PDAYAKROFRSCLTLVPRVFGELKEKHKGSGSGVGALEBENAFSLAESCPGISDK 403
QY 402 AMM 404
      |||:
Db 404 LMV 406

RESULT 10
JC6316
Probable protein kinase (EC 2.7.1.-) - fruit fly (Drosophila melanogaster)
C:Species: Drosophila melanogaster
C:Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 21-May-1999
C:Accession: JC6316
R:Treisman, J.E.; Ito, N.; Rubin, G.M.
Gene 186, 119-125, 1997
A:Title: mishapen encodes a protein kinase involved in cell shape control in drosophila
A:Reference number: JC6316; MID:97199378; PMID:9047354
A:Accession: JC6316
A:Status: nucleic acid sequence not shown
A:Molecule type: DNA
A:Residues: 1-1102 <TR>
A:Experimental source: third instar eye-antennal disk cosmid library
A:Note: the cited accession number, 1076485, is not in Genbank release 111.0
C:Genetics:
A:gene: msn
C:Keywords: phosphotransferase

Query Match 11.5%; Score 591.5; DB 2; Length 1102;
Best Local Similarity 23.9%; Pred. No. 4.3e-11;
Matches 241; Conservative 124; Mismatches 293; Indels 351; Gaps 37;
QY 23 DPEKLSDLREIGHSGFAYFARADYNSSEVAIKKMSYSGKOSNEKMODIIKEVRELQK 82
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 27 DPAGIFELIEVNGVNGYGVYKGRHNTKGQLAIKVMYD---TEDEEEELKLEINVLK 82
QY 83 L-KHPNTIYRGCYL-----REHTAMLVMEYC-LGSASDLELVHK-KPIQVEITAAVTH 133
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 83 YSNHRNATATYGAFFIKKSPGKDQDLVMEYCGASGVTLVSTKQOSKEEVIATYCR 142
QY 134 GALOGLAYLHSHNMIRHDYKAGNILLSEPGVLKIDGFC-SASI---MAPNSFVGTYMM 189
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 143 EILRGSLYLSKNVYIHRDIGNVLLTDNAEVLKVDGVSNAQDRTIGRRNTFTGTYMM 202
QY 190 APEVILAMDE---GOYDGKVDVMSLGTICIELAEKRPPLFNMAMSALYHIAONESPALQ 246
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 203 APEVIL-ACDENPDATYDNRSDDLMSLIGITALEMAESQPLDLDHMRALFLIPRNSPRLK 261
QY 247 SGHMSEFRNFVDSCLQIKQDRTSEVLKHFVLEREPYVIMDLQRTKDAVRELDN 306
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 262 SKKMSKHFHFIDTVLVKDYHQRPTYENLLKHGI--KDDPTFRQVRIQ-LKD---HIDR 315
QY 307 LOYRKMKKILFOAPNPGAEAPBEERAPYMRAGTLNLSLESSHSVPSMSTIASOSS 366
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 316 CKRRK-----QEKEREDYK----- 330
QY 367 SVNSLADASDNEEEEEEDEEPESSREMAAMQGEHTVYSHSIIHRLPGSDN 426
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 331 -----SGSDNDDDEPLAGE-----HSSIV-QAPRGDT 357
QY 427 LYDDPTQPEMTFPGLPDPAAPPTSTSSSARRRAYCNRNDHPATITPASLVSRQIQHEQ 486
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 358 L-----RRNF----- 366
QY 487 DSALREQLSGYKRMKROHOKOLLALBSRLGEREHSGRLORELEAORAGFTAEKTLAR 546
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 367 -----EGRLAAEQOQOQHNLMAQOQAAAAAHHAAQAOQAOQ 401

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QY 547 RHQ-----AIGKEAPAAQAEERKFOQHILIGQCKEELALILEAKRTYKLRQOLKEEL 600
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 402 LQOQOQOQAAAAAHHAAQAOQAOQAOQAOQ-----QANROPKPPSRQVBE-- 452
QY 601 QENSTKREAEVLL-----RQKEQLQCCAEFEAGILRRQRYFELQCKQYRKRM 652
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 453 ---PGPARPPQRLIIVDPDPHANRPLPPPKC---GEPAGQTPQOQO----- 494
QY 653 LLARHSLDQDLREDLKKQTKQDLECALLRQEHATRELETRQLQVQRTARELTRLOH 712
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 495 -----RNSQNNFKPSLPPRRREDHLDVLAOLSELGVYFSQ--QPOP 534
QY 713 QTELGNQLEYKRRREQLRKHAAQVROPKSLKVARAGOLPMGLPATGALPSTGTLSLSE 772
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 535 QTAGGQ-----GSOQAQPEAPPPRNNQSSGLSSGGSASAGGG----- 573
QY 773 EQPCSSGQEFALIGRMIGEEBEAVPEKMLIGKETTLEPEEQRLQDEMT--PSSSPKH 831
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 574 ---SSKPAALPQOSNNHIGOPVNPPLDPLDSSDSEDEPDPNRRANNDGTLIASDPPK- 628
QY 832 RSLVNEEDWDISKRMKESRVPSLASOERNIIQGEAAGANNIMEKHGNIYDMERKLGWQ 891
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 629 -----PLPGL-----GPVSEDAANTTTPLSHG-----G 651
QY 892 GPVLTTPYEEEEEEBERG-----CAPITGPRDPGD 921
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 652 GPRNRPPLPPRPDDDDQAGDRTLMKRRNGGGGGGGGGSSGVADGTGLG---PGT 708
QY 922 GCPS--PDI-----PPEPPSHLRQYPASQLPGLSHGLTGLSFAVGSS 964
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 709 RTSSVLPLDLLSQASPAATPPRHDKSSSEKORSFYLTFG-----FGAGGS 751

RESULT 11
C96572
Protein F12M16.4 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: C96572
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon
Chen, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
ansen, N.F.; Hughes, B.; Hultzer, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marzia
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MID:21016719; PMID:11130712
A:Accession: C96572
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-690 <STO>
A:Cross-references: GB:AE005173; MID:g7769851; PIDN:AAF69529.1; GSPDB:GN00141
A:Genetics:
A:gene: F12M16.4
A:Map position: 1

Query Match 11.4%; Score 585; DB 2; Length 690;
Best Local Similarity 28.4%; Pred. No. 4.6e-11;
Matches 194; Conservative 110; Mismatches 243; Indels 135; Gaps 25;
QY 28 FSDLRIGHSGFAYFARADYNSSEVAIKKMSYSGKOSNEKMODIITK-----EV 77
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 15 FSGPELLGRSGFGVYKAFPTLKNKDAIVKIDL--EESDELEIDIKVSLLETLVLEI 72
QY 78 RFLQKLRHPTIYRGCYLREHTAMLVMEYCL-GSASDLEVHKKPIQVEITAAVTHGAL 136
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 73 SVLSQGCPTTTEYGSYLQTKMIITMETMAGSVADLLQ-PGNPLDEFSTIACITDDL 131
QY 137 QGLAYLHSHNMIRHDYKAGNILLSEPGVLKIDGFC-SASI---MAPNSFVGTYMMAPE 192
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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RESULT 14
A53714
protein kinase (EC 2.7.1.37) BL44 - human
N:Alternate names: GC kinase
C:Species: Homo sapiens (man)
C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 24-Sep-1999
C:Accession: A53714
R:Katz, P.; Whalen, G.; Kehrl, J.H.
J. Biol. Chem. 269, 16802-16809, 1994
A:Title: Differential expression of a novel protein kinase in human B lymphocytes. Prefe
A:Reference number: A53714, MIMD:94266900, PMID:7515885
A:Accession: A53714
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-819 <KAT>
A:Cross-references: GB:U07349; NID:9531819; PIDN:AAA20968.1; PID:9531820
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
C:Keywords: ATP; phosphotransferase
F:13-272/Domain: protein kinase homology <KIN>
F:21-29/Region: protein kinase ATP-binding motif

Query Match          10.9%; Score 561.5; DB 2; Length 819;
Best Local Similarity 31.7%; Pred. No. 2,6e-10;
Matches 147; Conservative 71; Mismatches 176; Indels 69; Gaps 13;

QY 23 DPEKLESDLEIGHSGFAGVYFARDVNSFVAIKKMSYSGKSNKMDIIEKVEFLQK 82
DB 10 DPREDELLQVAGAGTGYDYKARDVTSBLAVKTKVL---DPGDISLQOETITLRE 66
QY 83 LRHPNTIQYRGCVLRHNTAMLVMEYCLGSASDLLEVHK--PLQVEYIAVHTGALQGLA 140
DB 67 CRHPNVAVIGSYLRNDRLMICMEFCGGS--LQETIHATGPLEHQIAYVCERIKGLH 124
QY 141 YLHSHMHHRDVKAGNILLSEPLVKGDFG-----SASIMAPANSFVGTPYMAPEVIL 195
DB 125 HLHSQKRIHRDKIGANLLTLTGQEDVLADEGVSGELTASV-AKRRSFICGTPYMAPEVAA 183
QY 196 AMDEGOYDGKVDVWSLGTICIELAEKRPPLFNMMNSALYHIAON--ESPALQ-SGHWSF 252
DB 184 VERKSGYNELCQVWALGITAIEIGELQRPFLHPRKALMLSKSSFOPKLNDKTRWTO 243
QY 253 YRRNFVDSCLQKIPQDPTSEVLKHFVLRERPTVINDLTQRTD-----AVRELDN 306
DB 244 NHHNFKLALTKNPKKRPFAEKLLQHPFTTQQLPRALTLQILDKASDPHIGTSPEDCEL 303
QY 307 LQYRKAKTLLFQEARPGFAEAEF-----EEBAEPY---MHRAGTLLTLESS 351
DB 304 ETYDMFPDTHSRKQGHGPAERPTSETQFQVKGAPRRKRTDPLNPEWEETLLGKE-- 361
QY 352 HSNVSMSTASASSSVNSLADASONEEEEEEEEEEEEGSPSRKEMAMQEGHTY 411
DB 362 -----ELSGSLQSYQVQLLEERSLITRSASSEFQELDSDPDITWG----- 399
QY 412 TSHSSLIHRLPGSDNLYDDPYQPE--MTGPIQAPPAAPTST 451
DB 400 -----TIKRAPFLGPLPTDPPAEPLSPPGTLPPSPGPNSS 437

RESULT 15
T18897
hypothetical protein C04A11.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
C:Accession: T18897
R:McMurray, A.
submitted to the EMBL Data Library, November 1996
A:Reference number: 219041
A:Accession: T18897
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1228 <WIL>

```

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A:Cross-references: EMBL:281460; PIDN:CAB03829.1; GSPDB:GM00028; CESP:C04A11.3
A:Experimental source: clone C04A11
C:Genetics:
A:Gene: CESP:C04A11.3
A:Map position: X
A:Introns: 25/3; 107/3; 198/2; 409/3; 542/1; 624/1; 832/2; 1024/2; 1100/3; 1147/3; 11

Query Match          10.1%; Score 520.5; DB 2; Length 1228;
Best Local Similarity 21.1%; Pred. No. 5,7e-09;
Matches 261; Conservative 180; Mismatches 379; Indels 419; Gaps 47;

QY 23 DPEKLESDLEIGHSGFAGVYFARDVNSFVAIKKMSYSGKSNKMDIIEKVEFLQK 82
DB 29 NPREDHNNIIGELDGAFFGKKEKAVSRDPLFAASKSIEI--QEGELEDVLEIETLSE 86
QY 83 LR-HPTNIQYRGCVLRHNTAMLVMEYCLGSASDLLEVH-KKPLQVEYIAVHTGALQGLA 140
DB 87 CKGHPVWMLGLYSTYFPEENKLTLLLEFCGGGAVNNIIVELGHVLAKEQIRYIGYVCDALK 146
QY 141 YLHSHMHHRDVKAGNILLSEPLVKGDFG--SASIMA---PANSFVGPYMAPEVIL- 195
DB 147 WLHSQVNIHRDLKAGNILLTGQGVRLADPGVSAKLKSEKEDDTITGTPYMAPEVMAC 206
QY 196 -AMDEGOYDGKVDVWSLGTICIELAEKRPPLFNMMNSALYHIAONESPA-LQSGHWSF 253
DB 207 ETRKQDPYDCISDIWSFGLTILMAQGEPRHSDVSVWRIKQYKSEPTLLQPSHWTRS 266
QY 254 FRNFVDSCLQKIPQDPTSEVLKHFVLRERPT---YIMDL-----IORT 297
DB 267 FSDILTRCLVKKDRNRPFAEIRKQWF--QNAPSRKMTIMDLAMVADVQEEVYIDGD 324
QY 298 KDAVRELDNLYRKMK-----KILFQEAR--NGFAEPEEEEAEP- 337
DB 325 EESVAGSDELISQRRGDSWSASDPRATSDGFKVPLVSPITETPPDPIHKKRAAPP 364
QY 338 ---YMR-----AGT-----LTS 347
DB 385 PQEVNMRQGPVNVGKPAENSPAEFSFNSNTSSGTAFSTPTNKKSAQLSTPAVLS 444
QY 348 LEES----- 351
DB 445 LNTSGSPSSANEFVSPRRALSLDELITTLTLDDEQSTFENSPSSASPPROSPRSHES 504
QY 352 -----HSV-----PSMS-----TSASSQSS- 367
DB 505 PRHSPPNSPOKEOLFESHTDITMASRSRSLSPQLKQLSPSSASAFDESVLSHKLE 564
QY 368 -----VNSLADASNEEEEEEEEEEEEGSPSRKEMAMQEG 407
DB 565 PAEHAGYVMAHQOMEKTTAQLNRAVAVSNIRQOMEKTIADSSNSQRPISQITETIPEG 624
QY 408 -----EITVTHSSSIHRLPGSD-----NLDDPYQP-----EMTGPLOPPAP 447
DB 625 IYAQKVSREAEAVQVSNALFFKPKPSQDMSASLTVDMAQKTELRYSSASSTPTKTRAP 684
QY 448 P-----TSSSSARRRAYCNRDHEAF----- 470
DB 685 PKRAENOSYRTISGSSNVQVHSASSSTDVPTVSVAVPYFDGPRNGEQKVPPEPPV 744
QY 471 -----IRTSILVSRQIOEHEDQSALRQOLSGKRRMRQ--- 503
DB 745 DYEGNAKENAAPSVPVPKISQKVPPTPS--TSIDVQKTSNVNAPR-PLGKRKGNQOTIT 802
QY 504 -----HOKQLALESRLGGEREHSGLQRE---LE 531
DB 803 KKTRTYIMIDGVQVSTTVVHLGVKDKDVQKQDLHRLRLQREAROKOQLAQEGIKLVE 862
QY 532 AQRAFGTEAEKLAR-----RHQALGEKAAQAQAEF-RKQOQHTLQKQKKEILA 560
DB 863 EQARKTTSQTNLTTRTSELMDAMERRQREKIEDTGAQEHETRNQKRLTIEQEKDMA 922
QY 581 LLEAQRTYKLRKEQLK--EELQENSTPKRE--KAEWLLRQKQLOLOCOAEPEEGLLR 635

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Db 923 EKERLKQEKIKFQELTMSKVORCDALKQKKEQLEIEHQLEKEDFLMOLOQNAEA-MIQ 981
QY 636 RORQYFELQCRQYKRRMLARHSIDODLLREDLNK--KOTOKDLBCALLRQHEATRELE 693
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 982 RMAEKHEKEMASIEKQFLMOKH-----NLRAKENNIWELEDKQMRKEFVLHHRKLEFDEY 1037
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 694 LKQLOAVQRTAELTRLOHOTELEGNOLEYKRRBEQELROKHAQVROQPKSL---KVRA 749
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1038 LIRTOMLAR-----HOREMAQIEKIHQEEEDDLIRALTIDRKLIPKMLRSETKTRS 1088
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 750 GOLPMGLPATGALPLSTGTLSQPCSSGQEAIIIGORMLGEEEAVERMTLGKGTTL 809
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1089 VAFKESL-----RISAVNMSNAEM---QERT--RRF--DEQEXL--RMRALEDHDL 1131
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 810 EPEEO-RIQEEMGTFSSPQKHSIIVNEEDWDISKEMKESRVPISLASOERNIIGOEAG 868
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1132 KQOKKIQILKE-----RHQEAIIELD-----EMQNEKRKQLEKERNIMKEHEA- 1175
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 869 ANNLMEKEHGNLVDMFKLGWQGPVLPVPEPEEEEEEE 907
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1176 -----KYH-----EMRELMOENLIARKTVLEKEFEDE 1202
    | : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

Search completed: November 22, 2002, 12:27:14  
 Job time : 36.804 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 22, 2002, 12:18:20 ; Search time 15.3915 Seconds  
(without alignments)  
2675.892 Million cell updates/sec

Title: US-09-686-346A-4

Perfect score: 5140  
Sequence: 1 MPAGRAGSLNDPVALELF.....LLPLPLPRRWRLASTACP 993

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Prod. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1416.5	27.6	982	1	SUOL_CAEEL
2	695	13.5	968	1	ST10_HUMAN
3	692.5	13.5	966	1	ST10_MOUSE
4	619	12.0	487	1	STK4_HUMAN
5	598	11.6	491	1	STK3_HUMAN
6	597.5	11.6	426	1	STZ2_MOUSE
7	594	11.6	443	1	ST24_HUMAN
8	591	11.5	426	1	ST25_HUMAN
9	510	9.9	544	1	PAK1_RAT
10	508	9.9	545	1	PAK1_HUMAN
11	508	9.9	545	1	PAK1_MOUSE
12	505	9.8	544	1	PAK3_RAT
13	504	9.8	544	1	PAK3_HUMAN
14	500	9.7	544	1	PAK3_MOUSE
15	499	9.7	490	1	SPS1_YEAST
16	498.5	9.7	1080	1	ML15_CAEEL
17	497.5	9.7	1080	1	NRK1_YEAST
18	491	9.6	524	1	PAK2_HUMAN
19	491	9.6	524	1	PAK2_RABIT
20	489	9.5	524	1	PAK2_MOUSE
21	463	9.0	1062	1	CC7_SCHPO
22	450.5	8.8	553	1	SPAK_RAT
23	450.5	8.8	1230	1	ST20_CANAL
24	449	8.7	658	1	PAK1_SCHPO
25	447	8.7	939	1	ST20_YEAST
26	446	8.7	547	1	SPAK_HUMAN
27	444	8.6	556	1	SPAK_MOUSE
28	438.5	8.5	591	1	PAK4_HUMAN
29	438	8.5	589	1	SHK2_SCHPO
30	431	8.4	971	1	CLA4_CANAL
31	430	8.4	719	1	PAK7_HUMAN
32	421.5	8.2	1258	1	NEK1_HUMAN
33	418.5	8.1	974	1	CC15_YEAST

34	418	8.1	655	1	SKM1_YEAST	012469 saccharomyc
35	415	8.1	842	1	CLA4_YEAST	P48562 saccharomyc
36	407	7.9	1401	1	WISA_SCHPO	014299 schizosacch
37	399.5	7.8	1501	1	NINC_DROME	P10676 drosophila
38	399	7.8	774	1	NEK1_MOUSE	P51954 mus musculu
39	394.5	7.7	626	1	M3K3_HUMAN	Q99759 homo sapien
40	388.5	7.6	626	1	M3K3_MOUSE	061084 mus musculu
41	387	7.5	841	1	NEK4_HUMAN	P51957 homo sapien
42	382	7.4	1478	1	BCK1_YEAST	001389 saccharomyc
43	374	7.3	506	1	NEK3_HUMAN	P51956 homo sapien
44	373.5	7.3	618	1	M3K2_HUMAN	Q99745 homo sapien
45	372.5	7.2	619	1	M3K2_MOUSE	061083 mus musculu

## ALIGNMENTS

## RESULT 1

ID	SUOL_CAEEL	STANDARD:	PRT:	982 AA.
AC	P46549;			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Serine/threonine-protein kinase SUOL (EC 2.7.1.1.-).			
GN	KIN-18 OR SUOL OR T17E9.1.			
OS	Caenorhabditis elegans.			
OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;			
OC	Rhabditidae; Peloderae; Caenorhabditis.			
OX	NCBI_TaxID=6239;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Bristol N2.			
RA	Du Z.;			
RL	Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Bristol N2.			
RA	Cope W.J.T.V., Kendrick-Jones A.;			
RL	Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.			
CC	-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
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CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>			
CC	or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).			
CC	-----			
CC	EMBL: U11280; AAA19437.1; -			
DR	EMBL: U32275; AAA75370.1; -			
DR	WormPep: T17E9.1; CE01405.			
DR	InterPro: IPR000719; Euk.pkinase.			
DR	InterPro: IPR002290; Ser_thr.pkinase.			
DR	Pfam: PF00069; pkinase; 1.			
DR	ProDom: PD000001; Euk.pkinase; 1.			
DR	SMART: SM00220; S_TKc; 1.			
DR	PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.			
DR	PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.			
DR	PROSITE: PS00108; PROTEIN_KINASE_ST; FALSE_NEG.			
KW	Transferase; Serine/threonine-protein kinase; ATP-binding.			
FT	DOMAIN 30			
FT	NP_BIND 36			
FT	NP_BIND 44			
FT	ACT SITE 59			
FT	ACT SITE 153			
SO	SEQUENCE 982 AA; 112870 MW; 745CE1E2E690977D CRC64;			

Query Match 27.6%; Score 1416.5; DB 1; Length 982;

Best Local Similarity 34.8%; Pred. No. 1.7e-50;

Matches 333; Conservative 162; Mismatches 346; Indels 115; Gaps 17;

QY 6 RAGSLNDPVALELFKDDPEKLSDLREIGHGSGFAGVYFARDVNSEVAIKMSTSGKO 65

```

Db      8 KPEVINDPSITAALEFSKKNDPQRTQDIREIGHGSGFVAYRAYDKKNQOTYAIKKMNSGQ 67
Qy      66 SNEKMODIIKEVYFLOKLRHPNTIYRGCYLREHTAMLVEMCYLGSASDLLEVHKKPLQ 125
Db      68 AVEKMDILKEVSFLVTYVHPHYVDKACFLKQTCMLVMEYCISGAADIVLKRGMGE 127
Qy      126 VETAAVTHGALOGLAYLHSHNMHRDVKAGNILLSEPLVKLQDFGSGASIMAPANSFVGT 185
Db      128 VETAAICSOFLALRYLHSLKRIHRDKAGNILLSHAIVKTLADFGSASIVDPAQFFIGT 187
Qy      186 PYMAPEVILAMDEGOYDKVDWVSGITCIELAEKRPPLFNNMANSALYHTAQNPSPL 245
Db      188 PFMAPEVILAMDEGHYTDADWLSLITCIELAEKRPPLFNNMANSALYHTAQNNDPPL 247
Qy      246 -----QSGHWESEYFNPNVSCLOKIPDPRPTEVLKHFREYRERPPVIMDLIORTKD 299
Db      248 SPIDTSEGEOMSLSEYQVFLDKCRKPAERMSAESECFRHPFIORSRPSDTIQELLIORTN 307
Qy      300 AYRELDNLOIRKKKTLF-----QAPNGPGA-----EAPPEEBAEPYHRAGT 344
Db      308 MYLELDNFOYKKRKRLMYLDETEGEGSEGNASDLDLFGHNANSGRAGDSASRSAS 367
Qy      345 LVSLESHPVMSISASSOSSVNSLADSDNEEEEEEEEEEEEEEEEGPESRMAMM 404
Db      368 LVSFNSMSSGGAGLLVNTTIGAMDNHSGSGYSSSTSSARRPPISQMLSTVS 427
Qy      405 QGSEHTVTHSSIIHRLPGSDNLYDDPYQEMTPGLOP-PAAPRSTSSSA----- 456
Db      428 TSGVGTMPHSGV-----GASITATAVNP--TPSPSEPIPTISQPTSKSSSSILETAND 479
Qy      457 -----RRRAYCRRNDHATRTASLVSROIQEHQDSALREQLS 495
Db      480 DPLDTIRAPVYDLHMPHRAVERITLQNHKFAFLRSORIIHQEEYEYTKENMYEOMS 539
Qy      496 GYKRMROKOLLESRLRGREHSGRLQRELAQAGCTEKLARRHQAGEK 555
Db      540 KTKHLQAHKELQOFEERSCALDRELRVKMDELEQLTTTY--SKEKRVKCSQNNELD 597
Qy      556 ARAAQAE--ERKFOHILGOQKELALALAEOKRYTKLREKDELEQNPSTPKREKAE 613
Db      598 KKKKDIEDKKKKKKKNSQNOQOMKLYSAQOLKEKVKYKKEQKTKLR-SLMPKRYTYN 656
Qy      614 WLLRQKLOQCOAEBEAGLLRRQROYFELQCRQYKMKLARHSLDODLREDLNNKOT 673
Db      657 AKKEVYADINRYKDAENPFDEKLRLEDELYRYRQOLSMHLEQDLDEDVAVVGR 716
Qy      674 OKDLECALLRQHEATRELEQLQDAVQRTRAELTQLQHOTELGQNLBYNKRREQELRK 733
Db      717 QMDTRHGLLSKQHEMTRELEIQLHNLHMKKRHLETOHEAHSASQNEVYTORQODELARK 776
Qy      734 HAAQYRQPKSLKVRAGOL-----PGLRATGALGPLS-----TGLTSEE 773
Db      777 HAMQSQQRDLKIQEAQIRKQYRQVVKTORQFKLYLQWQVYKPKDQKELTSLAKD 836
Qy      774 Q-----PCSSGQBALIGQRLGEEEAVERPMILKEGT-- 807
Db      837 QOKQVALLASQYESQIKKMWQDKTYVLESWQED--EQVLSKLEKELELBELLAYQKTRA 894
Qy      808 TLEPE---EORTLOEMGFSSSPQKHSRLVNEEDMDISKEKESVPLAQOERN 860
Db      895 TLEBOIKERIALERIGT--RRAMLEQKILIEREQMGEMRRLKQDIRHRSQOERN 949

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## RESULT 2

```

ST10_HUMAN
ID ST10_HUMAN STANDARD; PRT; 968 AA.
AC 094804; G901W4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Serine/threonine-protein kinase 10 (BC 2.7.1.37) (Lymphocyte-oriented
kinase)..

```

```

GN STK10 OR LOK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99216434; PubMed=10199912;
RA Kuramochi S., Matsuda Y., Okamoto M., Kitamura F., Yonekawa H.,
RA Karsenty H.
RT "Molecular cloning of the human gene STK10 encoding lymphocyte-
RT oriented kinase, and comparative chromosomal mapping of the human,
RT mouse, and rat homologues."
RL Immunogenetics 49:369-375(1999).
RN [2]
RP SEQUENCE OF 814-968 FROM N.A.
RC TISSUE=Testis;
RA Blocker H., Boecher M., Brandt P., Mewes H.-W., Gassenhuber J.,
RA Wiemann S.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -! FUNCTION: CAN ACT ON SUBSTRATES SUCH AS MYELIN BASIC PROTEIN AND
CC HISTONE IIA ON SERINE AND THREONINE RESIDUES (BY SIMILARITY).
CC -! CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphorylated
CC -! TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN LYMPHOID ORGANS.
CC -! PTM: AUTOPHOSPHORYLATED (BY SIMILARITY).
CC -! SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC STE20 SUBFAMILY.
CC -----
CC This SWISS-Prot entry is copyright. It is produced through a collaboration
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CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; AB015718; BA35073.1; -
DR EMBL; AL133081; CAB61400.1; -
DR HSP; P24941; IHCL.
DR Genew; HGNC:11388; STK10.
DR MIM; 603919; -
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase.1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR Transferrase; Serine/threonine-protein kinase; ATP-binding;
KW phosphorylation; Coiled coil.
FT DOMAIN 36 294 PROTEIN KINASE.
FT DOMAIN 573 947 COILED COIL (POTENTIAL).
FT DOMAIN 750 884 GLN-RICH.
FT NP_BIND 42 50 ATP (BY SIMILARITY).
FT BINDING 65 65 ATP (BY SIMILARITY).
FT ACT_SITE 157 157 BY SIMILARITY.
SO SEQUENCE 968 AA; 112134 MW; 15E24513ECC553D CRC64;

```

Query Match 13.5%; Score 695; DB 1; Length 968;

Best Local Similarity 24.4%; Pred. No. 1.8e-21;

Matches 253; Conservative 174; Mismatches 366; Indels 244; Gaps 37;

```

Qy 23 DEKLFSDIREIGHGSGFVAYFARDVNSEVVAIKMSYSGKQSNKMODIIKEVRFLOK 82
Db 31 DPNEWEIVGELGDAFGAAYKYKA--KNKKGALAAAVIETKSPSEPLEDYIVETIELAT 87
Qy 83 LHRPNTIYRGCYLREHTAMLVEMCYLGSASD--LLEVHKKRPLQDVEVLAATYHGLQGLA 140
Db 88 CDHPYIVKLGAYYHDGKLMIMIEFCPGAVDAIMLEL--DRGLTEPQIYVVCROMLEALN 146

```



QY	141	YIHSNMHHRYKAGNLLISPGLYKIDGDC---	SASIMAPANSFVGTYMMAAPRYVL-	195
Db	147	FLHSRIIRHRLKGGNVLMTLEGIRLADGVS	AKNLTLOKDRSPGTYMMAPEVVMK	206
QY	196	-AMDEGOYDGVVDVWSLGTICIEIAEKRP	PLFENNANMASHYHIAONESPLAS-GHWSEY	253
Db	207	ETMDPTPYDADKADISLGTILTEMAQLE	RPHEHNLNPPRYLLTAKSPPLTLTPSKMSYE	266
QY	254	FRNFVDSLOKRIPODRPTSEVLKHFV----	IRE---RPPTYIMDLIO-----R	296
Db	267	FRDFLKIALDKNPETRPSAOLLBHPVYS	ITSKALRELVAEAKAVMEIEDGRDEGE	326
QY	297	TKDAYRELDNIQYKMKKILFQEPANPG	APAEPEEEEAAPYMHRACTLTSLESSHSY--	354
Db	327	EDADAASLTLENHTONS--SEVSPSL	INDKRPLEESPSTP-----LAP	377
QY	355	--PSWSISASSOSSVNSLADASN-----	DEEEEEEDEEEEEEDEEPEES	398
Db	378	PCSQPSGGRSLQTTSPRYVANGENGLAV	PRPLKSKPYSDMARIGVQAQKOVAEAGGL	437
QY	399	REMANMDEGEHTVTHSSIIHRLPGS	NDLYDDPYQPEMTGPLOP--AAPPT	456
Db	438	SPAAIRSQAKASPRNSSALETIGE-----	KLANGSLEPPAQAAPGSKRSDC	487
QY	457	RRRATCRNRDH-----	FATIRASL	476
Db	488	SLCTSEMDGTNLSTDLSLNKEMGSL	IKDPKLYKTLKRTKRFYVDGEVSEYITTSKI	547
QY	477	VSROLQHEODSALREO--LSGYKEM	ROHOKOLLATESRLRGEHEESGRLQELEORA	535
Db	548	ISEDKKKEEMKRFRLROGLRELRLQ	KEHNHOTQLSNKHELQLEQHNKKFED	607
QY	536	GTGTAEKLARRHQAIGEK-----	EARAAQAE--RKFOOHLGOOKKELAA	580
Db	608	FEDTLEMLERQOKQOYKEMQDHA	VRRBEARIRLEODRDYTRFQEQ--TKLMKKEVKN	666
QY	561	LLBAOKRTYKLKREQLKELOENST	PKREKAEMYLQKEOLOOQCAEEBA	640
Db	667	--EYAEKLPRQOKESMKQKMEHNQ	OKOLDRDVAKQEDLE-----	707
QY	641	FELQCRKRYKMLLARRHSLOD	LREDLNKQOTQKQDLECAL---LIRONEATR-ELCLR	695
Db	708	-----LAMKLTITDNKREICDKR---	ECLMKQOELLRDREALWMEEH	749
QY	696	QLOAVOR-----	TRAEITRLQHOTELGNOLEYNKRROEL	743
Db	750	QLOEHNQVLVQKQOLKQOYRLO	GHNELLR--KHKEEROMQRYNGRM	808
QY	744	----SLKYRAGOLPMGLRATGALCP	RLSTGLTSEBQPCSSGOEALILG	808
Db	809	IQRSEGRTRMAYKSKSLHING-----	GSAABQ-----REKI--KQFSQOEK	849
QY	800	MILGEGTTLPEBQRILQOEMGTF	SSPQKHSRLVNEEDMDISKEMKESRVS	859
Db	850	-----RQKSERLOOQ-----	QKHQOM--RDMLAQESNMSELQLOLEKC	888
QY	860	NIIGOEAGANMIMKEHG-NLVME	FKLGWQSPVLTPEVEEEEEE-----EEGAP	912
Db	889	HLIVHEHQXKLKADESINQMLKEM	ROKLRTKRAKALEBDLNQKRRBDM	945
QY	913	IGTPRDPGDCPSDIP	929	
Db	946	-----ECPPNPSTP	953	
RESULT 3				
ID	ST10_MOUSE	STANDARD;	PRT;	966 AA.
AC	055098;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Serine/threonine-protein kinase 10 (EC 2.7.1.37) (Lymphocyte-oriented			

```

DE      (kinase) OR LOK.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090.
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Thymus;
RX      MEDLINE=97426413; PubMed=9278426;
RA      Karasuyama H.;
RT      "LOK is a novel mouse STE20-like protein kinase that is expressed
RT      predominantly in lymphocytes."
RL      J. Biol. Chem. 272:22679-22684(1997).
CC      -I- FUNCTION: CAN ACT ON SUBSTRATES SUCH AS MYELIN BASIC PROTEIN AND
CC      HISTONE IIA ON SERINE AND THREONINE RESIDUES.
CC      -I- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC      -I- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN LYMPHOID ORGANS
CC      SUCH AS SPLEEN, THYMUS, AND BONE MARROW.
CC      -I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC      STE20 SUBFAMILY.
-----
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CC      or send an email to license@sdb-sdb.ch).
-----
DR      EMBL; D89728; BAA24073.1; -.
DR      HSSP; P24941; ICRP.
DR      MGD; MGI:1099439; SEK10.
DR      InterPro; IPR000719; Euk_pkinase.
DR      InterPro; IPR002290; Ser_thr_pkinase.
DR      Pfam; PF00069; pkinase; 1.
DR      ProDom; PD000001; Euk_pkinase; 1.
DR      SMART; SM00220; S_TKC; 1.
DR      PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR      PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR      PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW      Transferase; Serine/threonine-protein kinase; ATP-binding;
KW      Phosphorylation; Coiled coil.
FT      DOMAIN 36 294 PROTEIN KINASE.
FT      DOMAIN 588 936 COILED COIL (POTENTIAL).
FT      DOMAIN 749 883 GLN-RICH.
FT      NP_BIND 42 50 ATP (BY SIMILARITY).
FT      BINDING 65 65 ATP (BY SIMILARITY).
FT      ACT_SITE 157 157 BY SIMILARITY.
SQ      SEQUENCE 966 AA; 111992 MW; 7115EAC01032BP4 CRC64;

Query Match 13.5%; Score 692.5; DB 1; Length 966;
Best Local Similarity 24.3%; Pred. No. 2.3e-21;
Matches 245; Conservative 174; Mismatches 347; Indels 243; Gaps 34;

OY      23 DEEKLFSDRLREIGHGSEFGAVFYARADVNRSEVVAIKKMSYSGKSNKEMKODIIKEVFLQK 82
DB      31 DPDWWEIYGEJGDGDFGAVYKA--KNEETGALAARAKYIEFKSEEDDYIVELIILAT 87
OY      83 LRHPNTIQYRGCVLRHREHTMVLMEYCLGASD--LLEVHKRPLOJEVEIAAIVHGALOGIA 140
DB      88 CHPRYIVKLGAAYYDGKAMIMIEFGPGAVDAIMEL-DRLGLEPQIQVCRQMLEALN 146
OY      141 YLHSHNMIRHDYKAGNILLSEPGYLVKLGDFG---SASIMAPANSFVGTPTYMAPEVIL- 195
DB      147 FTLGKRIIHRDKAGNVLNLTLEGDIRLAFEGSAKRLKTLQRKDSFICGPIYMAAEVYVLC 206
OY      196 -AMDEQYQYGVKDVWSLGTCTEIAERKRPRLNNMNASLLYHIAONESALDS-GHWSEY 253
DB      207 ETMKADAPYDKADWSLGTITLEMAQIEPPHHELMNPRVLLKIAKSDPTJLLTPSKWSYE 266

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QY	254	FRNFVDSCLQIQIDRPPSYEVLLKHFRLVREPRPTVIMDLQIRK	-DAVEIDLQYRK	312		
Db	267	FRDLFKILADNPNPRTSRSAOLLDPHYVSKTYSKALRELVAAEKAAVMEETD	-----	320		
QY	313	KKILQEPANPGGAAREEEEA	--PYMHRA	-----TLTSLSSHVSYSMS--ISAS	362	
Db	321	-----	-----GREDDGEEDAVDAVPLVNHQDSDANVTQPSLDSKKLLQSDSTPLPS	368		
QY	363	SOSSSVN	-----SLADSDNEEE	-----EEEEEE	368	
Db	369	QPOEVPNPGCSGPGDGPLOTTSPADGSKNDNDLKVPLRKSRLPSMDARIOMEKO	-----	428		
QY	369	EEEEEEGESREMMQMOGEHTVSHSHIIRLGLSGNSLVDDPQRPMTBGPLOPAPR	448			
Db	429	IPDDENPS	--PAASKOKANQSPNSALETTLGE	-----ALTNGLE---	472	
QY	449	TSTSSSARRAYGRN	-----	RDHFATIR	472	
Db	473	SSVTPSHSKRASDGSNLTSTSEMSYGTSLADSLNKTETSLKSGSKLINTLTAKTRRF	532			
QY	473	-----	-----TASLVSRQIQEHEDDSALRED	-----LSGYRMRRQHKOLLALESRLGEREE	521	
Db	523	VVDGEVSYITTSKIISIEDEKDEEMRFLRQRELRLLQKEEHRNQTOLSSKHEILOEQ	592			
QY	522	HSGRLQRELEORAGFGFEAKTLAR	-----	HQAIGEEARAQAEE	---RKF	566
Db	593	MHKREQDITNAKKFPYDELENTLRQOKOQVEKEDHSVRRKEAKRIRLEDQRYAKF	652			
QY	567	QOHLIGQOKKSLAALLLEAKRTYRLRKLEQLKEIQENPSTPRKREKAWLLRQKEOLOQC	626			
Db	653	QEQ_LKQKKKTVKS	---EVEKTLPRQGRKESMKQKKEHSQKKRLDRQFAKQKDELEAM	709		
QY	627	AEEBAGLLRQRYFELQCYKRMMLARHSLDQDLREDLUNKQOTQKDECALLRQH	666			
Db	710	-----	-----KLTLENREICDEKREDSLSKOE	-----LLDR	738	
QY	667	EATR-ELETRQLOAVQR	-----	TRAELTRQHQTELGNQLEYKRRQDELRQK	733	
Db	739	EALAMEWEDLOERHOLVQOLKDOYFLQHNHLLR	---KHKEERQOMORYOMIMEQIKVR	797		
QY	734	HAQVROOPKSLK	-----VRAGQLPMGAPGALGPLSTGLTSEEPQSSQOEALIGRML	789		
Db	798	QOQEKARLPKIQRBDDGETRAMMYKKSLLHNGA	-----GSASE	-----QREKIKQFSQ	844	
QY	790	GEEDBAVERMIITKEGTLEPEBQRIQDEMGTFSSSPQKHS	-----	LVNEE	838	
Db	845	QOEKROKAEKL	-----	QOQKHEHQMRDMVACESNSSELOQLQNEKCYLLVEH	893	
QY	839	DMDLSKEKESRVPYSLASQENIITIGQEDAGAMNMEKHNLDVMEKL	887			
Db	894	ETQKIALDESHNOSLKEWRDKLPRKKALEEDLNQKREO	---EMFQKL	940		
RESULT 4						
STK4_HUMAN						
ID	STK4_HUMAN	STANDARD:	PRT:	487 AA.		
AC	Q13043; Q15802; Q9NTZ4;					
DT	16-OCT-2001 (Rel. 40, Created)					
DT	16-OCT-2001 (Rel. 40, Last sequence update)					
DT	16-OCT-2001 (Rel. 40, last annotation update)					
DE	Seiine/threonine protein kinase 4 (EC 2.7.1.37) (STE20-like kinase MS1) (MST-1) (Mammalian STE20-like protein kinase 1)					
DE	(Serine/threonine protein kinase Krs-2).					
OS	Homo sapiens (Human).					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.					
OX	NCBI_TaxID=9606;					
RN	[1]					
RA	SEQUENCE FROM N.A.					
RA	MEDLINE=95394929; PubMed=7665586;					
RT	Creasy C.L., Chernoff J.,					
	"Cloning and characterization of a human protein kinase with homology					

RT	J. Biol. Chem.	270:21695-21700(1995).
RN	SEQUENCE FROM N.A.	
RP	MEDLINE=96413604; PubMed=8816758;	
RA	Taylor L.K., Wang H.C., Erikson R.L.;	
RT	"Newly identified stress-responsive protein kinases, Krs-1 and Krs-	
RT	2."	
RL	Proc. Natl. Acad. Sci. U.S.A. 93:10099-10104(1996).	
RN	[3]	
RP	SEQUENCE OF I-435 FROM N.A.	
RA	Laird G.;	
RL	Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.	
CC	-I- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.	
CC	-I- ENZYME REGULATION: THE C-TERMINAL NON-CATALYTIC REGION INHIBITS	
CC	THE KINASE ACTIVITY.	
CC	-I- SUBCELLULAR LOCATION: Cytoplasmic (by similarity).	
CC	-I- TISSUE SPECIFICITY: UBICITOUSLY EXPRESSED.	
CC	-I- PM: AUTOPHOSPHORYLATED ON SERINE AND THREONINE RESIDUES.	
CC	-I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.	
CC	STE20 SUBFAMILY.	
CC	-----	
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CC	entities requires a license agreement (see <a href="http://www.isb-sib.ch/announce/or_send_an_email_to_license@isb-sib.ch">http://www.isb-sib.ch/announce/ or_send_an_email_to_license@isb-sib.ch</a> ).	
CC	-----	
DR	EMBL: U18297; AAA83254.1; -	
DR	EMBL: U60207; AAB17262.1; -	
DR	EMBL: AL109839; CAB89421.1; -	
DR	HSSB: P24941; IHCL.	
DR	GeneW: HGNC:11408; STK4.	
DR	MIM: 604965; -	
DR	InterPro: IPRO00719; Euk_pkinase.	
DR	InterPro: IPRO02290; Ser_thr_kinase.	
DR	InterPro: IPRO01245; Tyr_kinase.	
DR	pfam: PF00069; pkinase.1.	
DR	PRINTS: PR00109; TYRKINASE.	
DR	ProDom: PD000001; Euk_pkinase.1.	
DR	SMART: SM00220; S_TKC_1.	
DR	PROSITE: PS00107; PROTEIN_KINASE_ATP_1.	
DR	PROSITE: PS00108; PROTEIN_KINASE_ST; FALSE_NEG.	
DR	PROSITE: PS50011; PROTEIN_KINASE_DOM_1.	
KW	Transferase; Serine/threonine-protein kinase; ATP-binding.	
FT	DOMAIN 30 281	
FT	NP_BIND 36 44	
FT	BINDING 59 59	
FT	ACT_SITE 149 149	
FT	DOMAIN 373 378	
FT	CONFLICT 222 222	
FT	CONFLICT 312 312	
SQ	SEQUENCE 487 AA: 55630 MW: 150756BEC5F77D5C CXC64;	
Query Match	12.0%; Score 619; DB 1; Length 487;	
Best Local Similarity	29.5%; Pred. No. 1e-18;	
Matches 169; Conservative 88; Mismatches 191; Indels 124; Gaps 14;		
QY	10 LKDPPVAELFFDD-----PEKLFSDLREIGHGSGFGAYFRADRVNSEVNAIKMSTISG 63	
Db	1 LKNPRRLOKTLDESLTKQPEEVDVEKLEEGSYGYKAIHKEETOIVAIIKQVPV-- 63	
QY	64 KQSNKKMODIIEVFPLKLRHPNTIOYRGCLRHEHTAMLVWYC-LGSASDLLLVHKKP 122	
Db	64 ---ESDLOEIIEIKSIIMOCCDSFHVKTYGSTFKNTDLMIWEIVYGASVSIDIIRLNKT 120	
QY	123 LOEVELIAVTGAGLOGVLASHNNHIHDVYKAGNILLSEPGVLKDFGSA----SIMAP 178	
Db	121 LTDEELATILGSTLKGLDELHFMRKIHRDIKAGNILLMTBEGRAKLDAGVGAGQLDTDMAK 180	
QY	179 ANSFVGTPYMADEVILAMDGEQYDGKVDMVSLGITCIELAERRPKPLEFNMMNASLYHYIA 238	

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Db 181 RMTVIGTPWMAPEVI---OEIGYNCVADIMWSIGITAIEMAEKPPYADIHPRATFMIIP 237
OY 239 QNESPALQSGH-WSEYFRNPVDSCLQKIPQDRPTSEVLKLRHRYLREPRPTVIMDLQRT 297
Db 238 TNDPPFRFRPELMSDNFTPVKQCLVKSPEQRTATQLOHPVRSKAKVSIILDLINEA 297
OY 298 KPAVRELMDLQYRKMKKILFQEPANPGCAEAPPEEEAEPEYHRA-----342
Db 298 MDVKLKRQSSQQRVDQ-----DDEENSEDEMDSGTMRARAQDDEMGYTRVASTMT 348
OY 343 -GTUITSLESSHSVPSMSISASSOSSVNSLADASNEEEEEEEEEEEEEEGPESREM 401
Db 349 DGANTMIHDDTLP-----SOLGTMTVINADEDEEGTKMRDETQPAKPSFLEX 398
OY 402 AMMOEGEHVTVSHSSIIHRLPGSDNLYDPTQPEMTPPGLQPPAAPPTSISSASARRAY 461
Db 399 FEQKREKQINSFGKSV-----PGPLK-----NSSDMK-----426
OY 462 CRRMRHFAFTRFASLYSRQIOEHQDSALREOLSGYKRMK---ROHOKOLLLESRLRG 517
Db 427 -----IPQGDYEPFLKSWVEDLQKRLALDPMMEQ 457
OY 518 EREHSGRLQRELEAQRAGFGTEAKRLARRHQ 549
Db 458 EIEE---IROKYOSKRQPLTDAIEAKRRQ 485

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RESULT 5
STK3_HUMAN
ID STK3_HUMAN STANDARD; PRT; 491 AA.
AC Q13188; Q15801; Q15445;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Serine/threonine protein kinase 3 (EC 2.7.1.37) (STE20-like kinase
DE MST2) (MST-2) (Mammalian STE20-like protein kinase 2)
DE (Serine/threonine protein kinase Krs-1).
GN STK3 OR MST2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96144292; PubMed=8566796;
RA Creasy C.L., Chernoff J.;
RT "Cloning and characterization of a member of the MST subfamily of
RT Ste20-like kinases.";
RL Gene 167:303-306(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96413604; PubMed=8816758;
RA Taylor L.K., Wang H.C., Erikson R.L.;
RT "Newly identified stress-responsive protein kinases, Krs-1 and Krs-
RT 2.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:10099-10104(1996).
RN [3]
RP SEQUENCE OF 96-203 FROM N.A.
RX MEDLINE=94100173; PubMed=8274451;
RA Schultz S.J., Nigg E.A.;
RT "Identification of 21 novel human protein kinases, including 3 members
RT of a family related to the cell cycle regulator nimA of Aspergillus
RT nidulans.";
RL Cell Growth Differ. 4:821-830(1993).
CC -1- FUNCTION: OXIDANT STRESS-ACTIVATED SERINE/THREONINE KINASE THAT
CC MAY PLAY A ROLE IN THE RESPONSE TO ENVIRONMENTAL STRESS (BY
CC SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN ADULT KIDNEY,
CC SKELETAL AND PLACENTA TISSUES AND AT VERY LOW LEVELS IN ADULT
CC HEART, LUNG AND BRAIN TISSUES.

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CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC STE20 SUBFAMILY.
CC -----
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CC EMBL; 026424; AAC50386.1; -
CC EMBL; 060206; AAB17261.1; -
CC EMBL; 225422; CAA80909.1; -
CC HSSP; P24941; 1HCU.
CC Genew; HGNC:11406; STK3.
CC MIM; 605030; -
CC InterPro; IP000719; Euk_pkinase.
CC InterPro; IP002290; Ser_thr_pkinase.
CC Pfam; PF00069; pkinase; 1.
CC Prodom; PD000001; Euk_pkinase; 1.
CC SMART; SM00220; S_TKc; 1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; FALSE NEG.
CC PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
CC Transferase; Serine/threonine-protein kinase; ATP-binding.
CC DOMAIN 27 278
CC NP_BIND 33 41
CC BINDING 56 56
CC ACT_SITE 146 146
CC DOMAIN 308 314
CC DOMAIN 370 375
CC CONFLICT 96 98
CC CONFLICT 121 121
CC CONFLICT 203 203
CC CONFLICT 303 303
CC CONFLICT 332 334
CC SEQUENCE 491 AA; 56261 MW; 9CA3B0644F3C14A9 CRC64;

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Query Match 11.6%; Score 598; DB 1; Length 491;
Best Local Similarity 32.7%; Pred. No. 7.2e-18;
Matches 144; Conservative 76; Mismatches 157; Indels 64; Gaps 11;

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OY 24 PEKFLDRLREIGHSGFAYVEARDVNRSEVATKKMSYSGKQSNKMODIKREFLQKL 83
Db 23 PEEVFDYLEKLGEGSGYFKAHKSGQYVALTKQVPV-----ESDLQETIKETISMQOC 77
OY 84 RHPNTIQRCYLRHTAWLMEYC-LGSASDLEVHKRPLOVEIAAVTHGALQIAYL 142
Db 78 DSPYVVKYGYSPKNTDMLWMEYCCAGSYDIIRLRNTKLIEDETATIKSLKGLLEYL 137
OY 143 HSHNMTHRDYKAGNILLSEGLVKGDFGSA---SIMPANFVGTPYMAPEVIAMD 198
Db 138 HPMRKIHRIKAGNIILNTEGHAKLADFGVAGOLTPTMARNRNVIGTFPMMAPEVI---Q 194
OY 199 EGOYDGKVDVWSLGTICIELAEKRPPLFNMMNSALYHIAQNSPALQSGH-WSEYFRNF 257
Db 195 EIGYNCVADIMWSIGITSIEMAEKPPYADIHPRATFMIPTNPPFRKPELMSDPTDF 254
OY 258 VDSCLQIPQDRPTSEVLKLRHRYLREPRPTVIMDLQRTKDAVRELNDLQYRKMKILF 317
Db 255 VKKCIYKNNPQGRATATQLOHPRIKAKNPYSILRDLITEMELKARHDDQGELE---311
OY 318 QEPANPGCAEAPPEEEAEPEYHRACTLSLESSHSVPSMSISASSOSSVNSLADASDN 377
Db 312 -----DEENSEDEDEL-----DSHTWVKTSGVECGTMRATSTMSGAQT 349
OY 378 EEEEEEEEEE-----EEEEEEEGPESRE-----MAMQGEHVTVSHSS 416
Db 350 MIEHNSMTLESDLGTWVINSDEDEEDGTMKRNAATSPQVRPSFMDYFDKQDKRNSHEN 409
OY 417 I---IHR-LPGSDNLYDDPYQ 433

```



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 CC -----  
 DR EMBL: AF024636; AAB82560.1; -  
 DR EMBL: AF083420; AAD42039.1; -  
 DR HSSP: P24941; ICRP.  
 DR GeneW: HGNC:11403; STRK24.  
 DR MIM: 604984; -  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR002290; Ser\_thr\_pkinase.  
 DR InterPro: IPR001245; Tyr\_pkinase.  
 DR Pfam: PF00069; pkinase; 1.  
 DR PRINTS: PR00109; TYRKINASE.  
 DR ProDom: PD000001; Euk\_pkinase; 1.  
 DR SMART: SM00220; S\_TKc; 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; FALSE\_NEG.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR Transferrase: Serine/threonine-protein kinase; ATP-binding;  
 KW Phosphorylation; Alternative splicing.  
 FT DOMAIN 36 286 PROTEIN KINASE.  
 FT NP\_BIND 42 50 ATP (BY SIMILARITY).  
 FT BINDING 65 65 ATP (BY SIMILARITY).  
 FT ACT\_SITE 156 156 BY SIMILARITY.  
 FT MOD\_RES 18 18 PHOSPHORYLATION (BY PKA).  
 FT VARSPPLIC 1 26 MDSRAOLMGLALNKRATLPHPGSGT -> MAHSPVQSLGP  
 FT MUTAGEN 18 18 T->A: LOSS OF PHOSPHORYLATION BY PKA.  
 FT CONFLICT 414 414 A -> V (IN REF. 2).  
 FT SEQUENCE 443 AA; 49307 MW; 4A9F1F6B8A88A97 CRC64;  
 SQ  
 Query Match 11.6%; Score 594; DB 1; Length 443;  
 Best Local Similarity 45.8%; Pred. No. 9,4e-18;  
 Matches 130; Conservative 48; Mismatches 92; Indels 14; Gaps 7;

QY 21 KDDPEKLSDLREIGHSGFAYFARDVNSEVAIKKMSYSGKSNKMODIIKEVRF 80  
 | | | | | : : : | | | | | : : : | | | | : : : : : | | : |  
 DB 29 KADPEELFTLEKIGSGFGEVFGIDNRTQKVAIKITDL--EEADEDEDIQDEITVL 86  
 | | | | | : : : | | | | | : : : | | | | : : : : : | | : |  
 QY 81 QKLRHNTIOYRGCVLRHNTAMLVMEYC-LGSASDLEVKKRLQVEIAAATHGALQGL 139  
 | | | | | : : : | | | | | : : : | | | | : : : : : | | : |  
 DB 87 SQDCSPYVTKYISYKLDKRLMTIMEYLGGSALDLE--PGPLDETQIATILREILKGL 144  
 | | | | | : : : | | | | | : : : | | | | : : : : : | | : |  
 QY 140 AYLSHNMTHRDYKAGNIILSEPLVKGDFGSASIMAPA---NSFVGTPYMMAPVIL 195  
 | | | | | : : : | | | | | : : : | | | | : : : : : | | : |  
 DB 145 DYLSHSEKTHRODKANVILSEHGEVKLADFGVAGOLITQIKRNTVGGPPMMAPEVT- 203  
 | | | | | : : : | | | | | : : : | | | | : : : : : | | : |  
 QY 196 AMDEGQDGVNDVSLGITCIELAEKRPPLFNANMSALYHIAQNSPALQSGHMSFYR 255  
 | | | | | : : : | | | | | : : : | | | | : : : : : | | : |  
 DB 204 --QOSAYDSKADIMSLGITFIELARGPSEHLPKMKVLEFLPKNPPLE-GNYSKPLK 260  
 | | | | | : : : | | | | | : : : | | | | : : : : : | | : |  
 QY 256 NFDVSLQKIPQDRPTSEVILKHFVLERPPV-VIMDLIQRK 298  
 | | | | | : : : | | | | | : : : | | | | : : : : : | | : |  
 DB 261 EFVEACLNKEPSRPTAKELKFLIRNAKTSYTELIDRYK 304  
 | | | | | : : : | | | | | : : : | | | | : : : : : | | : |  
 RESULT 8  
 STR25\_HUMAN STANDARD; PRT; 426 AA.  
 ID STR25\_HUMAN Q15522;  
 AC 000506; Q15522;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Serine/threonine protein kinase 25 (EC 2.7.1.37) (Sterile 20/oxidant  
 stress-response kinase 1) (Ste20/oxidant stress response kinase-1)  
 DE (SOK-1) (Ste20-like kinase).  
 GN STR25 OR SOK1 OR YSK1.  
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97042345; PubMed=8887545;  
 RA Pomo C.M., Bonventure J.V., Molnar A., Kyriakis J., Force T.;  
 RT "Activation of a human Ste20-like kinase by oxidant stress defines a  
 RT novel stress response pathway.";  
 RL EMBO J. 15:4537-4546(1996).  
 RN (2)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97304522; PubMed=9160885;  
 RA Osada S.-I., Izawa M., Saito R., Mizuno K., Suzuki A., Hirai S.-I.,  
 RA Ohno S.;  
 RT "YSK1, a novel mammalian protein kinase structurally related to Ste20  
 RT and SPK1, but is not involved in the known MAPK pathways.";  
 RL Oncogene 14:2047-2057(1997).  
 CC -1- FUNCTION: OXIDANT STRESS-ACTIVATED SERINE/THREONINE KINASE THAT  
 CC MAY PLAY A ROLE IN THE RESPONSE TO ENVIRONMENTAL STRESS.  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein -> ADP + a phosphoprotein.  
 CC -1- ENZYME REGULATION: ACTIVATED BY PHOSPHORYLATION. PROBABLY  
 CC AUTOPHOSPHORYLATION. THE C-TERMINAL NON-CATALYTIC REGION INHIBITS  
 CC THE KINASE ACTIVITY.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- TISSUE SPECIFICITY: UBICUOUSLY EXPRESSED. HIGHEST LEVELS ARE  
 CC FOUND IN TESTIS, LARGE INTESTINE, BRAIN AND STOMACH FOLLOWED BY  
 CC HEART AND LUNG.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC STE20 SUBFAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: X99325; CA67700.1; -  
 DR EMBL: D63780; BAA20420.1; -  
 DR HSSP: P12931; IFMK.  
 DR GeneW: HGNC:11404; STRK25.  
 DR MIM: 602255; -  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR002290; Ser\_thr\_pkinase.  
 DR Pfam: PF00069; pkinase; 1.  
 DR ProDom: PD000001; Euk\_pkinase; 1.  
 DR SMART: SM00220; S\_TKc; 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; FALSE\_NEG.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR Transferrase: Serine/threonine-protein kinase; ATP-binding;  
 KW Phosphorylation.  
 FT DOMAIN 20 270 PROTEIN KINASE.  
 FT NP\_BIND 26 34 ATP (BY SIMILARITY).  
 FT BINDING 49 49 ATP (BY SIMILARITY).  
 FT ACT\_SITE 140 140 BY SIMILARITY.  
 FT CONFLICT 347 348 EP -> DA (IN REF. 1).  
 FT SEQUENCE 426 AA; 48111 MW; 183CE5700FCEAV16 CRC64;  
 SQ  
 Query Match 11.5%; Score 591; DB 1; Length 426;  
 Best Local Similarity 36.4%; Pred. No. 1,2e-17;  
 Matches 154; Conservative 68; Mismatches 129; Indels 72; Gaps 16;

QY 23 DPEKLSDLREIGHSGFAYFARDVNSEVAIKKMSYSGKSNKMODIIKEVRF 82  
 | | | | | : : : | | | | | : : : | | | | : : : : : | | : |  
 DB 15 DPEELFTKDRIGKSGFGEVFGIDNRTQKVAIKITDL--EEADEDEDIQDEITVLSQ 72  
 | | | | | : : : | | | | | : : : | | | | : : : : : | | : |  
 QY 83 LRHPNTIOYRGCVLRHNTAMLVMEYC-LGSASDLEVKKRLQVEIAAATHGALQGL 141  
 | | | | | : : : | | | | | : : : | | | | : : : : : | | : |  
 DB 73 CDSPPYITRRYGSYKSLKRLMTIMEYLGGSALDLK--PGPLETYIATILREILKGLDY 130  
 | | | | | : : : | | | | | : : : | | | | : : : : : | | : |



DE kinase 1) (PAK-1) (p65-PAK) (Alpha-PAK).  
 GN PAK1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RP [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97199447; PubMed=9395435;  
 RA Sells M.A., Knaus U.G., Bagrodia S., Ambrose D.M., Bokoch G.M.,  
 RA Chertoff J.;  
 RT "Human p21-activated kinase (PAK1) regulates actin organization in  
 RT mammalian cells.";  
 RL Curr. Biol. 7:202-210(1997).  
 RP [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=96398842; PubMed=8805275;  
 RA Brown J.L., Stowers L., Baer M., Trejo J., Coughlin S., Chant J.;  
 RT "Human Ste20 homologue hPAK1 links GTPases to the JNK MAP kinase  
 RT pathway.";  
 RL Curr. Biol. 6:598-605(1996).  
 CC -I- FUNCTION: THE ACTIVATED KINASE ACTS ON A VARIETY OF TARGETS.  
 CC LIKELY TO BE THE GTPASE EFFECTOR THAT LINKS THE RHO-RELATED  
 CC GTPASES TO THE JNK MAP KINASE PATHWAY.  
 CC -I- SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND  
 CC CDC42/P21 AND RAC1.  
 CC -I- PTM: AUTOPHOSPHORYLATED WHEN ACTIVATED BY CDC42/P21.  
 CC -I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC STE20 SUBFAMILY.  
 CC -I- SIMILARITY: CONTAINS 1 CRIB DOMAIN.  
 CC -----  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch))  
 CC -----  
 DR EMBL: U24152; AAA65441.1; -;  
 DR EMBL: U51120; AAC50590.1; -;  
 DR HSSP: P24941; 1CKP.  
 DR GeneW: HGNC:8590; PAK1.  
 DR MIM: 602590; -;  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR000095; Pakbox/Rhobndg.  
 DR InterPro: IPR002290; Ser\_thr\_pkinase.  
 DR Pfam: PF00069; pkinase; 1.  
 DR Pfam: PF00786; PBD; 1.  
 DR ProDom: PD000001; Euk\_pkinase; 1.  
 DR SMART: SM00285; PBD; 1.  
 DR SMART: SM00220; S\_TKc; 1.  
 DR PROSITE: P550108; CRIB; 1.  
 DR PROSITE: P500107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: P550011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE: P500108; PROTEIN\_KINASE\_ST; 1.  
 KM Transphosphatase; Serine/threonine-protein kinase; ATP-binding;  
 KM Phosphorylation.  
 KW DOMAIN  
 FT DOMAIN 134 269 CRIB.  
 FT DOMAIN 270 521 LINKER.  
 FT NP\_BIND 276 284 PROTEIN KINASE.  
 FT BINDING 299 299 ATP (BY SIMILARITY).  
 FT ACT\_SITE 389 389 ATP (BY SIMILARITY).  
 FT MUTAGEN 107 107 L->F: CONSTITUTIVELY ACTIVE.  
 FT CONFLICT 26 26 V -> A (IN REF. 2).  
 FT CONFLICT 237 237 R -> L (IN REF. 2).  
 FT CONFLICT 379 379 F -> S (IN REF. 2).  
 FT CONFLICT 503 503 D -> E (IN REF. 2).  
 SQ SEQUENCE 545 AA; 60661 MW; 14AE70E6480CD7E CRC64;  
 Query Match 9.9%; Score 508; DB 1; Length 545;

Best Local Similarity 40.9%; Pred. No. 3.3e-14;  
 Matches 117; Conservative 51; Mismatches 104; Indels 14; Gaps 6;  
 QY 23 DPEKLFSDIREIGHGSGFAGVYFARDVNSEVVAIKMSTSGSKOSNEKMODIIKEVFLQK 82  
 DB 265 DPKKKTYREKIGQSGVGYMTADVATGOEVAIKQMN1---QQQPKKELLINELLIMRE 321  
 QY 83 LRHPNTIOYRGCYLRHHTAMLVMEYCL-GSASDLLEVHKKPLEVEFLAIVTHGALGLAY 141  
 DB 322 NKNPNTIVTLDSTLVDELWVMEYLAGSLTDV--VTEFCMDGQIAVACRECLDALEF 379  
 QY 142 LHSNMIHRDVKAGNILLSEPLVKLGDFGSASIMAPANS---FPGTPYMAPEVITLAM 197  
 DB 380 LHSNQYIHRDIDKSNILLGMDSVKLTDFGFCQGITPEQSKRSTMTGTPYMAPEVY--- 436  
 QY 198 DEQGYDKVDVMSLGITCTELAEKRPPLFNMAASLYHIAQNEPALQSGH-WSEYFRN 256  
 DB 437 TRKAYGPKVDIWSLGIMAEIMEGEPYPYENPLRALYLAITNGTEPLQNPKEKLSAIFRD 496  
 QY 257 FVDSCLQKIPQDRPTSEVLKKHREVLREPPYIMLIQRTKQAVR 302  
 DB 497 FLNRCLDMQVYKRSKAKELLQHOFLKIAKPLSLPLIAAKKATK 542  
 RESULT 11  
 PAK1\_MOUSE  
 ID PAK1\_MOUSE STANDARD: PRT; 545 AA.  
 AC 088643;  
 DT 15-DEC-1998 (Rel. 37, created)  
 DT 15-DEC-1998 (Rel. 37, last sequence update)  
 DT 15-JUN-2002 (Rel. 41, last annotation update)  
 DE Serine/threonine-protein kinase PAK 1 (Ec 2.7.1.-) (p21-activated  
 DE kinase 1) (PAK-1) (p65-PAK) (Alpha-PAK) (CDC42/RAC effector kinase  
 DE PAK-A).  
 GN PAK1 OR PARA.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99282526; PubMed=10352232;  
 RA Burdelo P.D., Kozak C.A., Finegold A.A., Hall A., Piroe D.M.;  
 RT "Cloning, central nervous system expression and chromosomal mapping of  
 RT the mouse PAK-1 and PAK-3 genes.";  
 RL Gene 232:209-215(1999).  
 CC -I- FUNCTION: THE ACTIVATED KINASE ACTS ON A VARIETY OF TARGETS.  
 CC LIKELY TO BE THE GTPASE EFFECTOR THAT LINKS THE RHO-RELATED  
 CC GTPASES TO THE JNK MAP KINASE PATHWAY (BY SIMILARITY).  
 CC -I- SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND  
 CC CDC42/P21 AND RAC1 (BY SIMILARITY).  
 CC -I- PTM: AUTOPHOSPHORYLATED WHEN ACTIVATED BY CDC42/P21 (BY  
 CC SIMILARITY).  
 CC -I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC STE20 SUBFAMILY.  
 CC -I- SIMILARITY: CONTAINS 1 CRIB DOMAIN.  
 CC -----  
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 CC -----  
 DR EMBL: AF082077; AAC32375.1; -;  
 DR HSSP: P24941; 1CKP.  
 DR MGD: MGT:1339975; PAK1.  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR000095; Pakbox/Rhobndg.  
 DR InterPro: IPR002290; Ser\_thr\_pkinase.  
 DR Pfam: PF00069; pkinase; 1.  
 DR Pfam: PF00786; PBD; 1.







```

DR PROSITE: P550011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: P500108; PROTEIN_KINASE_SF; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW SH3-binding; Phosphorylation.
FT DOMAIN 70 83
FT DOMAIN 129 267
FT DOMAIN 268 519
FT NP_BIND 274 282
FT BINDING 297 297
FT ACT_SITE 387 387
FT CONFLICT 161 161
FT CONFLICT 361 361
FT CONFLICT 493 493
FT CONFLICT 525 525
SQ SEQUENCE 544 AA; 60683 MW; C4AEB71DD33EE6988 CRC64;

Query Match
Best Local Similarity 40.2%; Score 500; DB 1; Length 544;
Matches 115; Conservative 52; Mismatches 105; Indels 14; Gaps 6;

QY 23 DEPEKLSDLREIGHSGFAGVYFARDVNRSEVVAIKKMSYSGKSNKMODIIKEVFLQK 82
DB 263 DPKKKTRLEKIQGASGYTYTADATGQVAKOMNL---QOQPKKELITIELIVME 319
QY 83 LRHPNTIYRGCYLRHTAMLVMEYCLGSASDLEVKKPKLOEV-BIAAVTHGALQGLAY 141
DB 320 NKPKNIVNYLDSYVGLDELAVVMEYLAGS--LTDVYETECMDVGQIAVCRECLQALDF 377
QY 142 LHSNMHHRDVKAGNILLSEPGVYKIDGSGASIMAPANS---FVGTYYMAPEVITLAM 197
DB 378 LHSNOYIHRDINSDNILLGDSGVKLTDFGCAQITPEQSKRTWGTGYMAPEV--- 434
QY 198 DEQYDKYDWSLGTICIEIAERKPPLEFNMMASALYIAQNESPALOS-GHMSYEFN 256
DB 435 TRKAYGPXYDWSLGTICIEIAERKPPLEFNMMASALYIAQNESPALOS-GHMSYEFN 256
QY 257 FVDSCLQKIPQDRPTSEVLKHKRFVLRERPPVYIMDIQRTDAVR 302
DB 495 FLNRCLMDVDRGSAKELLQHPFLKLAFLPSLITPLITAAKRAIK 540

RESULT 15
SPSL_YEAST STANDARD; PRT; 490 AA.
AC P08458;
DT 01-AUG-1988 (rel. 08, Created)
DT 01-NOV-1995 (rel. 32, Last sequence update)
DT 30-MAY-2000 (rel. 39, Last annotation update)
DE Sporulation-specific protein 1 (Ec 2.7.1.-).
GN SPS1 OR YDR523C OR B9719.27.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;

[1]
RN RP SEQUENCE FROM N.A.
RA Friesen H., Lutz R., Doyle S., Segall J.;
RL Submitted (Aug-1994) to the EMBL/GenBank/DBJ databases.
[2]
RN RP SEQUENCE FROM N.A.
RA Dietrich F.S., Mulligan J., Allen E., Araujo R., Aviles E.,
RA Berron A., Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M.,
RA Hunnicke-Smith S., Hyman R., Komp C., Lashkari D., Lew H., Lin D.,
RA Mosedale D., Nakahara K., Namath A., Oefner P., Oh C., Petel F.X.,
RA Roberts D., Schramm S., Schroeder M., Shogren T., Shroff N.,
RA Winant A., Yelton M., Botstein D., Davis R.W.;
RL Submitted (Aug-1995) to the EMBL/GenBank/DBJ databases.
[3]
RN RP SEQUENCE OF 396-490 FROM N.A.
RX MEDLINE=87064542; PubMed=3023934;
RA Percival-Smith A., Segall J.;
RT "Characterization and mutational analysis of a cluster of three genes
expressed preferentially during sporulation of Saccharomyces

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RT cerevisiae."
RL Mol. Cell. Biol. 6:2443-2451(1986).
CC -!- FUNCTION: SERINE/THREONINE PROTEIN KINASE REQUIRED FOR SPORE WALL
CC DEVELOPMENT.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC STE20 SUBFAMILY.
CC -----
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CC -----
DR EMBL: U13018; AAA64833.1; -
DR EMBL: U13057; AAA64963.1; -
DR EMBL: M13629; AAA35079.1; -
DR PIR: B25376; B25376.
DR SGD: S0002931; SPS1.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase.1.
DR ProDom: PD000001; Euk_pkinase.1.
DR SMART: SM00220; S_TKc.1.
DR PROSITE: P500107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: P500108; PROTEIN_KINASE_SF; 1.
DR PROSITE: P550011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: P550011; PROTEIN_KINASE_DOM; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Sporulation; Meiosis.
FT DOMAIN 18 272
FT NP_BIND 24 32
FT BINDING 47 47
FT ACT_SITE 141 141
FT CONFLICT 454 454
FT CONFLICT 469 469
SQ SEQUENCE 490 AA; 55704 MW; 6143055E85BA4FF CRC64;

Query Match
Best Local Similarity 36.4%; Score 499; DB 1; Length 490;
Matches 135; Conservative 67; Mismatches 129; Indels 40; Gaps 14;

QY 24 PEKLFSDLEIGHSGFAGVYFARDVNRSEVVAIKKMSYSGKSNKMODIIKEVFLQK 83
DB 14 PSKLVSIQSCIGRGNFGDYKAVDRVQEIYAKVNL--EHSDDIELLAQEIFLAEI 71
QY 84 RHPNTIYRGCYLRHTAMLVMEYCLGSASDLE-VHKKPKLOEVIATVTHGALQGLAY 141
DB 72 KSLPTTNYIATMLDEVSMWIVMEYCGGSCDILKRSYVNGIPREKVSFIITHEVTGLKY 131
QY 142 LHSNMHHRDVKAGNILLSEPGVYKIDGSGASIMAPANS---PANSFVGTYYMAPEVITLAM 198
DB 132 LHEQKRIHRDIAANILLNEBSGVKLGDSVSGHIRSTLYLKRTPVGTYYMAPEVCCV 191
QY 199 EQQYDKYDWSLGTICIEIAERKPPLEFNMMASALYIAQNESPALOSGHMSYEFN 258
DB 192 DG-YNEKADWSLGTITTELLKGLPLSKYDPMKMTMLPRKRPKLO-GFESDAKAFV 249
QY 259 DSCLOKIPQDRPTSEVLKHKRFVLRERPPVYI---MDLIQRTDAVRDLNIOYRKM 313
DB 250 AGCLVKTPTADRPASVNLSPFEV--KNITITNLKSDVLDIKOK--VOE---RYTKVP 300
QY 314 KI-----FQEQAPNPGAE-----APEEEEAEPYIMHRAGLIT-SLESHSPS 356
DB 301 KYPLONRILYKNSNVYRGKFWNFESTRLSTQISKELSPTODSPSLNMESEPYLLHG 360
QY 357 MSISASQSSS 367
DB 361 QTVPTITPSS 371

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Search completed: November 22, 2002, 12:24:12  
Job time : 22.3915 secs



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OM protein - protein search, using sw model

Run on: November 22, 2002, 12:20:50 ; Search time 55.1115 Seconds  
(without alignments)  
3712.361 Million cell updates/sec

Title: US-09-686-346a-4

Perfect score: 5140  
Sequence: 1 MPAGRAGSLKDPDVALLFF.....LLPLPLLRWRWLAAGTAGP 993

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%  
Listing first 45 summaries

Database :

SPTREMBL\_21:\*

- 1: sp.archaea:\*
- 2: sp.bacteria:\*
- 3: sp.fungi:\*
- 4: sp.human:\*
- 5: sp.invertebrate:\*
- 6: sp.mammal:\*
- 7: sp.mhc:\*
- 8: sp.organelle:\*
- 9: sp.phage:\*
- 10: sp.plant:\*
- 11: sp rodent:\*
- 12: sp.virus:\*
- 13: sp.vertebrate:\*
- 14: sp.unclassified:\*
- 15: sp.virus:\*
- 16: sp.bacteriopl:\*
- 17: sp.archaeop:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5054	98.3	1235	11 Q9JLS3	Q9JLS3 rattus norv
2	4676	91.0	1235	4 Q9UL54	Q9UL54 homo sapien
3	3785.5	73.6	1049	4 Q94957	Q94957 homo sapien
4	3530	68.7	1062	4 Q9NSW2	Q9NSW2 homo sapien
5	2812.5	54.7	1005	4 Q9P216	Q9P216 homo sapien
6	2805.5	54.6	1001	11 Q88664	Q88664 rattus norv
7	2802.5	54.5	1001	4 Q9H2K7	Q9H2K7 homo sapien
8	2442.5	47.5	898	4 Q9H2K7	Q9H2K7 homo sapien
9	2442.5	47.5	898	4 Q9H2K7	Q9H2K7 homo sapien
10	2432.5	47.3	898	4 Q9H2K7	Q9H2K7 homo sapien
11	2427.5	47.2	898	13 Q919E0	Q919E0 gallus gall
12	2385.5	46.4	898	4 Q9UHG7	Q9UHG7 homo sapien
13	1841.5	35.8	1039	5 Q9VWG8	Q9VWG8 drosophila
14	1413	27.5	398	4 Q9H7S5	Q9H7S5 homo sapien
15	778	15.1	438	6 Q9BH01	Q9BH01 macaca fasc
16	735.5	14.3	1305	4 Q9UK63	Q9UK63 homo sapien

17	723	14.1	1276	4 Q9UK61	Q9UK61 homo sapien
18	722.5	14.1	1297	4 Q9UKD9	Q9UKD9 homo sapien
19	717	13.9	1360	4 Q9UK65	Q9UK65 homo sapien
20	715.5	13.9	473	11 Q91VG7	Q91VG7 mus musculus
21	709	13.8	1352	4 Q9UK62	Q9UK62 homo sapien
22	708.5	13.8	1331	4 Q9UK64	Q9UK64 homo sapien
23	701	13.6	1268	4 Q9UKD8	Q9UKD8 homo sapien
24	693.5	13.5	950	13 Q9YHC9	Q9YHC9 xenopus lae
25	692	13.5	1165	4 Q95819	Q95819 homo sapien
26	691.5	13.5	1323	4 Q9UK60	Q9UK60 homo sapien
27	681.5	13.3	842	10 Q9FNU3	Q9FNU3 oryza sativ
28	663	12.9	1231	11 Q95092	Q95092 cavia porce
29	662.5	12.9	836	10 Q24527	Q24527 arabidopsis
30	658	12.8	1120	10 Q910A1	Q910A1 arabidopsis
31	651.5	12.7	1233	11 P97820	P97820 mus musculu
32	649	12.6	1235	4 Q9H2G2	Q9H2G2 homo sapien
33	643	12.5	1233	11 Q54988	Q54988 mus musculu
34	642	12.5	809	10 Q8VYC1	Q8VYC1 arabidopsis
35	641.5	12.5	497	11 Q9J110	Q9J110 mus musculu
36	641	12.5	1300	11 Q9JMG2	Q9JMG2 mus musculu
37	640.5	12.5	669	5 Q8T0S6	Q8T0S6 drosophila
38	637	12.4	1308	11 Q9JMG2	Q9JMG2 mus musculu
39	635	12.4	1295	4 Q9P2R8	Q9P2R8 homo sapien
40	635	12.4	1303	4 Q9P1X1	Q9P1X1 homo sapien
41	634.5	12.3	445	11 Q60877	Q60877 mus musculu
42	632	12.3	1175	4 Q75172	Q75172 homo sapien
43	630.5	12.3	825	10 Q8SAE1	Q8SAE1 triticeum mo
44	629.5	12.2	825	10 Q9ARL7	Q9ARL7 hordeum vul
45	627.5	12.2	1202	11 Q9WU41	Q9WU41 mus musculu

## ALIGNMENTS

### RESULT 1

Q9JLS3 PRELIMINARY: PRT: 1235 AA.

Q9JLS3: 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)

DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)

DE Serine/threonine protein kinase TAO2.

GN TAO2.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-99428563; PubMed-10497253;

RA Chen Z., Hutchison M., Cobb M.H.;

RT "Isolation of the protein kinase TAO2 and identification of its

RT RT mitogen-activated protein kinase/extracellular signal-regulated kinase

RT kinase binding domain.";

RL J. Biol. Chem. 274:28803-28807(1999).

RN [2]

RP SEQUENCE FROM N.A.

RA Chen Z., Hutchison M., Cobb M.;

RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

DR EMBL: AF140556; AAD39480.2; -.

DR HSSP: P24941; 1B38.

DR InterPro: IPR000719; Euk\_pkinase.

DR InterPro: IPR001899; Gram\_pos\_anchor.

DR InterPro: IPR003006; Ig\_MHC.

DR InterPro: IPR002290; Ser\_thr\_pkinase.

DR InterPro: IPR001245; Tyr\_pkinase.

DR Pfam: PF00069; pkinase\_1.

DR PRINTS: PR00109; TYRKINASE.

DR ProDom: PD000001; Euk\_pkinase; 1.

DR SMART: SM00220; S\_TKc; 1.

DR PROSITE: PS00343; GRAM\_POS\_ANCHORING; UNKNOWN\_1.

DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_1.

DR PROSITE: P500107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE: P550011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: P500108; PROTEIN\_KINASE\_ST; 1.  
KW ATP-binding; Kinase: Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 1235 AA; 138750 MW; 426960D0812518MD CRC64;

Query Match 98.3%; Score 5054; DB 11; Length 1235;  
Best Local Similarity 99.9%; Pred. No. 6e-285;  
Matches 979; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPAGRAGSLKPDVAELFFKDDPEKLSDLREIGHSGFAYFARDVNSEVVAIKKMS 60  
DB 1 MPAGRAGSLKPDVAELFFKDDPEKLSDLREIGHSGFAYFARDVNSEVVAIKKMS 60  
QY 61 YSGKSNEMKMODIIKEVRFLQKLRHNTIYRGCTLRHTAMLWMEYCGASDLEVHK 120  
DB 61 YSGKSNEMKMODIIKEVRFLQKLRHNTIYRGCTLRHTAMLWMEYCGASDLEVHK 120  
QY 121 KPLQVEIAAVTHGALQGLAYLHSHNMIRDVAKGNILLSEPGVLKDFGASASIMAPAN 180  
DB 121 KPLQVEIAAVTHGALQGLAYLHSHNMIRDVAKGNILLSEPGVLKDFGASASIMAPAN 180  
QY 181 SFVGPYMAPEVILLAMDGOYDKVDVWSLGITCTIELAEKRPPLFNMMASALYHIAON 240  
DB 181 SFVGPYMAPEVILLAMDGOYDKVDVWSLGITCTIELAEKRPPLFNMMASALYHIAON 240  
QY 241 ESPALQSGHMSYFRNFVDSCLQKIPQDRPTSEVLKHFVLRERPPYIMDLQRTKDA 300  
DB 241 ESPALQSGHMSYFRNFVDSCLQKIPQDRPTSEVLKHFVLRERPPYIMDLQRTKDA 300  
QY 301 VRELNLQYRKKKKILFQEPAPNGCAEAPDEEAPYMHKAGTILTSLSHSVPMSTIS 360  
DB 301 VRELNLQYRKKKKILFQEPAPNGCAEAPDEEAPYMHKAGTILTSLSHSVPMSTIS 360  
QY 361 ASSQSSVNSLADASNEEEEEEEEEEEEGPESREMAAMOGERTVSHSIIHR 420  
DB 361 ASSQSSVNSLADASNEEEEEEEEEEEEGPESREMAAMOGERTVSHSIIHR 420  
QY 421 LFGSDNLXDDPYQPEMTGSLPPAPPTSTSSSARRAYCRNRDHFATITASLVSRQ 480  
DB 421 LFGSDNLXDDPYQPEMTGSLPPAPPTSTSSSARRAYCRNRDHFATITASLVSRQ 480  
QY 481 IOEHEDDSLRQSLGSKYKMRROHOKOLLALSRLGEEHSGRLQRELEQRAQFGTE 540  
DB 481 IOEHEDDSLRQSLGSKYKMRROHOKOLLALSRLGEEHSGRLQRELEQRAQFGTE 540  
QY 541 AKKLARRHQAIEKEKRAQAQAEERKFOQHILGQKKELAALEAQKRTYKLRQEKEL 600  
DB 541 AKKLARRHQAIEKEKRAQAQAEERKFOQHILGQKKELAALEAQKRTYKLRQEKEL 600  
QY 601 QENPSTPKREKAEMILLRQEQLOQCOAEDEAGLLRRQRYFELQCRQYRKMLARHSID 660  
DB 601 QENPSTPKREKAEMILLRQEQLOQCOAEDEAGLLRRQRYFELQCRQYRKMLARHSID 660  
QY 661 QDLLEPDLKKKTQDLECALLRQHEATRELELROLQAVQTRAEVTLQDQTELGNDL 720  
DB 661 QDLLEPDLKKKTQDLECALLRQHEATRELELROLQAVQTRAEVTLQDQTELGNDL 720  
QY 721 EYNNKREDELROKHAQVQOPKSLKVRAGOLPMGLPAGALGPSTGTSLSEOPCSSGO 780  
DB 721 EYNNKREDELROKHAQVQOPKSLKVRAGOLPMGLPAGALGPSTGTSLSEOPCSSGO 780  
QY 781 EAILQGRMLGEEBEAVPERMILGKEGTTLPEBORILQEMCTFSSSPQKHSLSVNEEDW 840  
DB 781 EAILQGRMLGEEBEAVPERMILGKEGTTLPEBORILQEMCTFSSSPQKHSLSVNEEDW 840  
QY 841 DLSKEKESRVSLSAQENIIGQEBAGAMNMEKEHGNLVMEFKLGAVQGPVLTYPVE 900  
DB 841 DLSKEKESRVSLSAQENIIGQEBAGAMNMEKEHGNLVMEFKLGAVQGPVLTYPVE 900  
QY 901 EEEEEEEGAGITGTPRDGDCSPDIPREPPSHLRQYPAQSOLPGFLSHGLTGLSFA 960  
DB 901 EEEEEEEGAGITGTPRDGDCSPDIPREPPSHLRQYPAQSOLPGFLSHGLTGLSFA 960

QY 961 VSSSGLLPLLLLLPLLLPLLA 980  
DB 961 VSSSGLLPLLLLLPLLLPLLA 980

## RESULT 2

Q9UL54  
ID Q9UL54 PRELIMINARY; PRT; 1235 AA.  
AC Q9UL54;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
DE Prostate derived STE20-like kinase PSK.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-BREAST CARCINOMA;  
RX MEDLINE=20127920; PubMed=10660600;  
RA Moore T.M., Garg R., Johnson C., Coppecoat M.J., Ridley A.J.,  
RA Morris J.D.H.;  
RT "PSK, a novel STE20-like kinase derived from prostatic carcinoma that  
RT activates the JNK MAPK pathway and regulates actin cytoskeletal  
RT organisation.";  
RL J. Biol. Chem. 275:4311-4322(2000).  
CC -1 - SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

DR EMBL: AF061943; AADA5616.1; -.  
DR HSSP: P24941; 1B38.  
DR InterPro: IPR000719; Euk\_pkinase.  
DR InterPro: IPR002290; Ser\_thr\_pkinase.  
DR InterPro: IPR001245; Tyr\_pkinase.  
DR Pfam: PF00069; pkinase.1  
DR PRINTS: PR00109; TYRKINASE.  
DR ProDom: PD000001; Euk\_pkinase; 1.  
DR SMART: SM00220; S-Trk; 1.  
DR PROSITE: P500107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE: P550011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: P500108; PROTEIN\_KINASE\_ST; 1.  
KW ATP-binding; Kinase: Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 1235 AA; 138232 MW; 3AB9E8690934307 CRC64;

Query Match 91.0%; Score 4676; DB 4; Length 1235;  
Best Local Similarity 93.0%; Pred. No. 5.1e-263;  
Matches 913; Conservative 23; Mismatches 40; Indels 6; Gaps 3;

QY 1 MPAGRAGSLKPDVAELFFKDDPEKLSDLREIGHSGFAYFARDVNSEVVAIKKMS 60  
DB 1 MPAGRAGSLKPDVAELFFKDDPEKLSDLREIGHSGFAYFARDVNSEVVAIKKMS 60  
QY 61 YSGKSNEMKMODIIKEVRFLQKLRHNTIYRGCTLRHTAMLWMEYCGASDLEVHK 120  
DB 61 YSGKSNEMKMODIIKEVRFLQKLRHNTIYRGCTLRHTAMLWMEYCGASDLEVHK 120  
QY 121 KPLQVEIAAVTHGALQGLAYLHSHNMIRDVAKGNILLSEPGVLKDFGASASIMAPAN 180  
DB 121 KPLQVEIAAVTHGALQGLAYLHSHNMIRDVAKGNILLSEPGVLKDFGASASIMAPAN 180  
QY 181 SFVGPYMAPEVILLAMDGOYDKVDVWSLGITCTIELAEKRPPLFNMMASALYHIAON 240  
DB 181 SFVGPYMAPEVILLAMDGOYDKVDVWSLGITCTIELAEKRPPLFNMMASALYHIAON 240  
QY 241 ESPALQSGHMSYFRNFVDSCLQKIPQDRPTSEVLKHFVLRERPPYIMDLQRTKDA 300  
DB 241 ESPALQSGHMSYFRNFVDSCLQKIPQDRPTSEVLKHFVLRERPPYIMDLQRTKDA 300  
QY 301 VRELNLQYRKKKKILFQEPAPNGCAEAPDEEAPYMHKAGTILTSLSHSVPMSTIS 360  
DB 301 VRELNLQYRKKKKILFQEPAPNGCAEAPDEEAPYMHKAGTILTSLSHSVPMSTIS 360  
QY 361 ASSQSSVNSLADASNEEEEEEEEEEEEGPESREMAAMOGERTVSHSIIHR 420

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|||||
Db 361 ASSOSSSVNSLADASDN--EEEEEEEEEEEGEPAREMAMOGEGHTVTSHSIIHR 418
421 LPSGSDMLYDDPYPEMTPGLOPPAPRPSTSSSSARRAYCNRNHFATIRTSLSVSRQ 480
419 LPSGSDMLYDDPYPEMTPGLOPPAPRPSTSSARRAYCNRNHFATIRTSLSVSRQ 478
481 IOEHEDSALREDSGKRRRROHOKOLLAESRLGGEREHSGRLORELEAORAGFGTE 540
479 IOEHEDSALREDSGKRRRROHOKOLLAESRLGGEREHSARLORELEAORAGFGAE 538
541 AEKLARRHOAIGEKARAAQAEEERKFOQHILGQKKELALALEAOKRTYKLRKEQKEEL 600
539 AEKLARRHOAIGEKARAAQAEEERKFOQHILGQKKELALALEAOKRTYKLRKEQKEEL 598
601 QENPSTPKREKAEWLLROKQEQLOOCCAEERAGLLRROROYFELQOCROYKKMLLARHSLD 660
599 QENPSTPKREKAEWLLROKQEQLOOCCAEERAGLLRROROYFELQOCROYKKMLLARHSLD 658
661 QDLREDLNKKOTQKDECALLRQHEATRELELROLOAVORTRAELTRLOHOTELGNOL 720
659 QDLREDLNKKOTQKDECALLRQHEATRELELROLOAVORTRAELTRLOHOTELGNOL 718
721 EYKKRREOELROKHAQVROQPSKLVKRAQOLPMG--LPATGALGPLSTGTLSEEQPCSS 778
719 EYKKRREOELROKHAQVROQPSKLVKRAQORPGLPLPIPALGPENGTPIEQDPCSP 778
779 GQAAIIGORMLGEEEAENPFRMLGKGTLLPEEQRILLOEMGTSSSSQOKRSLVNEE 838
779 GQAAVLDORMLGEEEAENPFRMLGKGTLLPEEQRILLOEMGTSSSSQOKRSLVNEE 838
839 DMDISKEMKESRVPSLASOERNITIGOEAGAWLMEKEHGNLVMDMEKLGWOGPVLTPTV 898
839 VMLPEIEELRPLPSLPQDRSIVGOEERAGTSLWGKEDSLDEEELGAWOGPALTPV 898
899 PEEEEEEREGAPIGTRPDGDCSPDIPRPPPSHLRQVAPASOLPGSLSHGLTGLS 958
899 PEEEEEEREGAPIGTRPDGDCSPDIPRPPPSHLRQVAPASOLPGSLSHGLTGLS 956
959 FAVGSSGGLPLLLLLPLLA 980
957 FAVGSSGGLPLLLLLPLLA 978

RESULT 3
094957 PRELIMINARY: PRT: 1049 AA.
AC 094957;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE KIA0881 protein (STE20-like kinase).
GN KIA0881.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE=9156230; PubMed=10048485;
RA Nagase T., Ishikawa K., Suyama M., Kikuno R., Hiroseawa M.,
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.,
RT "Prediction of the coding sequences of unidentified human genes. XII.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 5:355-364 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Yustein J.T., Robinson D., Templeton D.J., Kung H.-J.;
RT Characterization of a Subfamily of Human STE20-like kinases that
RT Selectively Activate p38 Through MKK3 and are Regulated via a PP2A-
RT dependent Mechanism.";

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RL Submitted (MAY-2000) to the EMBL/Genbank/DDBJ databases.
CC -1 SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AB020686; BA47904.1; -.
DR EMBL: AF263313; AAG38503.1; -.
DR HSSP: P24941; 1B38.
DR InterPro: IPR000719; Euk-kinase.
DR InterPro: IPR002290; Ser_thr_kinase.
DR InterPro: IPR001245; Tyr_kinase.
DR Pfam: PF00069; pkinase.1.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD000001; Euk-kinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE: PS50011; PROTEIN KINASE DOM; 1.
DR PROSITE: PS00108; PROTEIN KINASE-ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ
SEQUENCE 1049 AA: 119280 MW: D6C5062P47794030 CRC64;

Query Match 73.6%; Score 3785.5; DB 4; Length 1049;
Best local similarity 79.2%; Pred. No. 1.9e-211;
Matches 781; Conservative 35; Mismatches 110; Indels 60; Gaps 14;

QY 1 MPAGRAGSLKDPVALEFFKDDPEKLFSDREIGHSGFAYVFARDVNRSEVVAIKMS 60
Db 1 MPAGRAGSLKDPVALEFFKDDPEKLFSDREIGHSGFAYVFARDVNRSEVVAIKMS 60
QY 61 YSGKSNKQKODILKEVRLQKLRHNTIOYRCCTYREHTAWLMEXCJGASDILLEVHK 120
Db 61 YSGKSNKQKODILKEVRLQKLRHNTIOYRCCTYREHTAWLMEXCJGASDILLEVHK 120
QY 121 KPLQVEIAVTHGALQGLAYLHSHMIRHDVAKGNILSEPLVTLGDFGASIVAPAN 180
Db 121 KPLQVEIAVTHGALQGLAYLHSHMIRHDVAKGNILSEPLVTLGDFGASIVAPAN 180
QY 181 SFVGTPEYMAPEVILAMDEGOYDKVYVSLGTCIELERKPEPLFNMAASALYHIAQV 240
Db 181 SFVGTPEYMAPEVILAMDEGOYDKVYVSLGTCIELERKPEPLFNMAASALYHIAQV 240
QY 241 ESPALDSGHHSSEFRNFVDSCLQKITQDPRTSVLLKHRVLEBRPTVIMDIQRTKDA 300
Db 241 ESPALDSGHHSSEFRNFVDSCLQKITQDPRTSVLLKHRVLEBRPTVIMDIQRTKDA 300
QY 301 VRELDMILQYRKMKKILFOEAPNGPAGAEPEEEAEAPYMHRACTILTSLSHSPMSIS 360
Db 301 VRELDMILQYRKMKKILFOEAPNGPAGAEPEEEAEAPYMHRACTILTSLSHSPMSIS 360
QY 361 ASSOSSSVNSLADASDN--EEEEEEEEEEEGEPAREMAMOGEGHTVTSHSIIHR 420
Db 361 ASSOSSSVNSLADASDN--EEEEEEEEEEEGEPAREMAMOGEGHTVTSHSIIHR 418
QY 421 LPSGSDMLYDDPYPEMTPGLOPPAPRPSTSSSSARRAYCNRNHFATIRTSLSVSRQ 480
Db 421 LPSGSDMLYDDPYPEMTPGLOPPAPRPSTSSSSARRAYCNRNHFATIRTSLSVSRQ 478
419 LPSGSDMLYDDPYPEMTPGLOPPAPRPSTSSARRAYCNRNHFATIRTSLSVSRQ 478
481 IOEHEDSALREDSGKRRRROHOKOLLAESRLGGEREHSGRLORELEAORAGFGTE 540
479 IOEHEDSALREDSGKRRRROHOKOLLAESRLGGEREHSARLORELEAORAGFGAE 538
541 AEKLARRHOAIGEKARAAQAEEERKFOQHILGQKKELALALEAOKRTYKLRKEQKEEL 600
539 AEKLARRHOAIGEKARAAQAEEERKFOQHILGQKKELALALEAOKRTYKLRKEQKEEL 598
601 QENPSTPKREKAEWLLROKQEQLOOCCAEERAGLLRROROYFELQOCROYKKMLLARHSLD 660
599 QENPSTPKREKAEWLLROKQEQLOOCCAEERAGLLRROROYFELQOCROYKKMLLARHSLD 658
661 QDLREDLNKKOTQKDECALLRQHEATRELELROLOAVORTRAELTRLOHOTELGNOL 720
659 QDLREDLNKKOTQKDECALLRQHEATRELELROLOAVORTRAELTRLOHOTELGNOL 718
721 EYKKRREOELROKHAQVROQPSKLVKRAQOLPMG--LPATGALGPLSTGTLSEEQPCSS 778
719 EYKKRREOELROKHAQVROQPSKLVKRAQORPGLPLPIPALGPENGTPIEQDPCSP 778

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QY	540	EAERKLARHOAIGGEARAAQAEERKKPOONHLSGOKKELALLAEQAKRTYKIRKEOLKEE	599
Db	510	EMEKIKTKHQSMKEKAEKAVYMAEERKKPOONHQAQOKKELNSFESQAKREYKRLKEOLKEE	569
QY	600	LOENSTPRKKAEMVLLKOKBOLQOCQAEAEAGLLRRQORQYFELQCHQYKRMKLARHSL	659
Db	570	LNENQSTPKKEQEWLSKQKENGNIHQAEEDANILRRQORYLELECHRFKRMILGHNH	629
QY	660	DODLLREDLNKKQYQKQKDECLALLRQHEATRELEBOLQAVQRTAELTYLQHOTELGNQ	719
Db	630	BODLREELNKKQYQKQKDECLALLRQHEATRELEBOLQAVQRTAELTYLQHOTELGNQ	689
QY	720	LEYNKRROELROKHAQVROOPKSLVRAQOLPMGLPATGALGP-----LSTGT	769
Db	690	LEYNKRRELELRKHHVMEVROOPKSLVRAQOLPMGLPATGALGP-----LSTGT	749
QY	770	LSE-----EOPCSSGOEALIGARM-LGEEEAQVPE--RMILGKEG	806
Db	750	KSEHVAVLRLKEQOTRKLATILAQYDHSINEMLSQTQALRLDEQAQEAQVLMQLOQEL	809
QY	807	TLTEBEDRIQD-----EMGTFSSPOKRRVLEEDMDISKEM-----KESVPS	853
Db	810	ELLVAYQSKIKQAEQADHRELEBOLQAVQRTAELTYLQHOTELGNQ	866
QY	854	LASQERNITGOEEAGAMVMEKEH--GNLVDMERK-----LGWVGQPV-----L	895
Db	867	LLERQARIEAFDESMRLGPSNMVLSLSEAFSSHSPGASMSHNPPTGSGPRHGMHPM	926
QY	896	TPVPEEEEEEEGAGPIGTFRDQDCGP--SPDIPRPPSHLYQRYASQALPGLSHGL	954
Db	927	GGTPOAMGHPMQGGQRPQGHGSPGMOGVPRGSSIGVKNRSPQALRRTAGS---GTEGQMS	983
QY	955	TGLSFAVGSSSG	966
Db	984	RSTSVTSQISNG	995

RESULT 7

Q9H2K7 PRELIMINARY; PRT; 1001 AA.

AC Q9H2K7; 01-MAR-2001 (TREMblrel, 16, Created)

DT 01-MAR-2001 (TREMblrel, 16, Last sequence update)

DT 01-JUN-2002 (TREMblrel, 21, Last annotation update)

DE STE20-like kinase (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

OC NCBI\_TaxID:9606; [1]

RP SEQUENCE FROM N.A.

RA Yustein J.T., Rodinson D., Kung H.-J.;

RT "Characterization of a Subfamily of Human STE20-like Kinases that Selectively Activate p38 Through MKK3 and are Regulated via a PP2A-dependent Mechanism.";

RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.

DR EMBL: AF263312; AAC38502.1; -.

DR HSSP; P24941; 1B38.

DR InterPro; IPR000719; Euk\_pkinase.

DR InterPro; IPR002290; Ser\_thr\_kinase.

DR InterPro; IPR001245; Tyr\_pkinase.

DR Pfam; PF00069; pkinase; 1.

DR ProDom; PD000001; Euk\_pkinase; 1.

DR SMART; SM00220; S\_TKc; 1.

DR SMART; SM00219; TYKc; 1.

DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.

DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.

DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.

QY Kinase.

QY NON\_TER 1001 1001

QY SEQUENCE 1001 AA: 115957 MW: 7E0E534D3E7E159E CRC64:

Query Match	54.5%;	Score 2802.5;	DB 4;	Length 1001;
Best Local Similarity	59.68;	Pred. No. 2e-154;		
Matches 590;	Conservative 101;	Mismatches 202;	Indels 97;	Gaps 15

QY	1	MA6GASGLKOPDAVEALFFKDDPEKLESDLAELIGHGSGAVYFARDVANSFVNAIKKMS	60
Db	1	MBSTNAGSLKOPBEALFEKDEPEKLEFPLDLREIGHGSGAVYFARDVNTNVAIKKMS	60
QY	61	YSGKQNEKMODIKREVFRLKLRHNTLOYRGCYREHTAUMVEYCSGASDLELVK	12
Db	61	YSGKQTEKMODIKREVKLQRIKHNLSLEYGCYAREHTAUMVEYCSGASDLELVK	12
QY	121	KPLQVEIAAVTHGALQSLAYLHSHNMHRDYKAGNILLSEGLVKLGDGSGASIMAPAN	18
Db	121	KPLQVEIAAITHGALQSLAYLHSHMTMRDKAGNILLTEEGQVKLDFGSGASMAPAN	18
QY	181	SFPGPYMAAPVILLAMDGOYDKVDVSLSTICTELAEKRPPLFNNMAMALYHIAON	24
Db	181	SFPGPYMAAPEVILLAMDGOYDKVDVSLSTICTELAEKRPPLFNNMAMALYHIAON	24
QY	241	ESPALQGHMSEYFRNFVSCLOKIPVDPRTEVLKHFVLRERPPYIMDLQRTKDA	30
Db	241	ESPLOQSNEMSDYFRNVSVDCLQIPQDRPTEBELKHFVLRERETVLDLQRTKDA	30
QY	301	VRELNDLOYRKAKKILFQAPRPGABAREEBEABPYHNRAGTILTSLESSHVSQMSIS	36
Db	301	VRELNDLOYRKAKKILFQAHNHPRAVEAOEBEEDODHGFRGTGVNSVSGNOSIPMSIS	36
QY	361	ASSQSSSVSLDASANEEDSEEBEEDBEDEBQESREXMMOGEHTVYSHSHIHR	42
Db	361	ASSQSSSVSLDVSDDKELD-----MAGDHTVMSNSSVYHL	39
QY	421	LFGSDNLVDYPOREMPGP-LQPPAPPTSSSSARRAYCRRNDRPATIRTASLYSR	47
Db	400	KPEEEN-----YREEDGPRTASRDPSP-----QVSRKSHYRRNREHPATIRTSLYVR	44
QY	480	QIOEHNDQALREOLSGYRRMRQNDKOLLAEBSRLGRREHSGRLQRELAQAGST	53
Db	450	QIOEHNDQELREOBSGYRRMRQNDKOLMTLENKIKAMDENRRLQKDLDETQNRNPA	50
QY	540	EAEKILARRQAIGCEKARAQAQAEERFOOHLIGOOKETLAEALAEAKRTYKLRKEOLKEE	59
Db	510	EMBKILKRIQAAMEKAKYKMSNEKKFQOHLQAQOKKELNLSFESQKREYKIKRKEOLKEE	56
QY	600	LOENBPTKREKAEWLLROKEDLOOQOAEERAGLLRRQORYELOCCROYKRRMLARHSL	65
Db	570	LNEBOSTPKREKQEWLMSKQENIQHFOAEENLRLRRQORYLELBCRRKRYRMLLGRHNL	62
QY	660	DODDLREDLNKQOTKDLFCALLNQHNTRELEJROJAOVORTAEYLTRLOHONELGNO	71
Db	630	EODLVAREELNKQOTQDLNAMLKRNHESMOELERFHNLTQKMCCELTRLOHONELTNO	68
QY	720	LEYNKRREOELROKNAAYOORPKSLYVAGOLPMGLPATGALGP-----LSTGT	76
Db	690	LEYNKRREBELRKHNVEYRQRPKSLYSKELQIKKQOFOTCKIQTRYKALNHLLETPR	74
QY	770	LSE-----EORCSSGQALILGQRA-LGEEBEAVPE-RMLTSGEG	80
Db	750	KSEHKAUVRLEKEBQRTKLALIBAYDHSINMLSTOALRLDEAOEAOVUKMOLOEL	80
QY	807	TLLEPEBQRILOE-----EMGTSSSPQKARSL-----VNEEDMDISKEMESVPSLA	85
Db	810	ELLNAYQSKIKQAQAEONDRERLELDYRSLRALLBOKITEEMALONECTE-RIRSL	86
QY	856	SOERNILQEGANWLMKEKH--GNLVDMERK-----LGVQGPVLTLPVREEEBEEE	90
Db	869	EQQAETIEAFDESNRKLGSNNVNLSPKASHSYRPAASGSHNRPOTGPGP-----	92
QY	908	EGGAPITGRPD-----PGDSCSPDIPREPR	933
Db	921	HWGNHPRMGGRPAWGNHPRMOGGRPQWCHNSPGR	950

ID	Q9HC79	PRELIMINARY;	PRT;	898 AA.
AC	Q9HC79;			
DT	01-MAR-2001 (TREMBLrel. 16, Created)			
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)			
DE	01-JUN-2002 (TREMBLrel. 21, Last annotation update)			
OS	Serine kinase (STE20-like kinase).			
OC	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20384190; PubMed=10924369;			
RT	Zhang W., Chen T., Wan T., He L., Li N., Yuan Z., Cao X.;			
RT	"Cloning of DPK, a novel dendritic cell-derived protein kinase			
RT	activating the ERK1/ERK2 and JNK/SAPK pathways.";			
RT	Biochem. Biophys. Res. Commun. 274:872-879(2000).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=PLACENTA;			
RL	Submitted (Feb-2001) to the EMBL/GenBank/DBDJ databases.			
DR	EMBL; AF135158; AACG9131.1; -			
DR	EMBL; BC002756; AAH02756.1; -			
DR	HSSP; P24941; 1b38.			
DR	InterPro: IPR000719; Euk_pkinase.			
DR	InterPro: IPR002290; Ser_thr_pkinase.			
DR	InterPro: IPR00130; Tyr_pkinase.			
DR	InterPro: IPR000130; Zn_MtPdcase.			
DR	Pfam; PF00069; Pkinase; 1.			
DR	ProDom; PD000001; TYRKINASE.			
DR	PRINTS; PR00109; TYRKINASE.			
DR	SMART; SM00229; S_TKc; 1.			
DR	SMART; SM00219; TyrKc; 1.			
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.			
DR	PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.			
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.			
DR	PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.			
KW	ATP-binding; Kinase; Transferase.			
SEQ	SEQUENCE 898 AA; 105405 MW; AE7E30745B09763C CRC64;			
QY	Query Match	47.6%;	Score 2445.5;	DB 4; Length 898;
	Best local similarity	54.5%;	Pred. No. 9e-134;	
	Matches 505; Conservative 129; Mismatches 210; Indels 83; Gaps 10;			
QY	6 RAGSLKDPVALLEFRKDPEKFLFSDLRELGHSGFGAYFARPYRNRSEVVAIKKMSYSGKQ 65			
DB	2 RRGVGLKDEPIALDFLRKDPEELFLGILHGHGSGFAYVFATTAHNTSEVVAIKKMSYSGKQ 61			
QY	66 SNEKKODILKEVRFLOKILHPNTIOYRGCYLREHNTAMLVMEYCLCSASDLLEFVHKKPLQE 125			
DB	62 THEKKODILKEVRFLOKILHPNTIEKGCYCLEHNTAMLVMEYCLCSASDLLEFVHKKPLQE 121			
QY	126 VEIAAFTGALOGLAYLHSHNMIRHDYKAGNITLSEPLGLKIGDEGSGASIMAPANSFYGT 185			
DB	122 VEIAAITGHALGLAYLHSHALIRHDYKAGNITLLEPGVGLKADGSGASMAPANSFYGT 181			
QY	186 PTWMAPEVTLAMDEGOYDGKVDVYWSLGTCTELAERKPPLEFMMNAMSALYHTAONEPAL 245			
DB	182 PTWMAPEVTLAMDEGOYDGKVDIWSLGTCTELAERKPPLEFMMNAMSALYHTAONDSPTL 241			
QY	246 OGGHSEYFRNFTVDSCLQIKIPQDRPTSEVLLKHFVFLRPRPTVIMDLIQRTKDAVRELD 305			
DB	242 OSNEWTDFRRRVYDCLQIKIPQERTPSAELLKHDVRRRPRPLVILDLIQRTKDAVRELD 301			
QY	306 NLQYRKMKILFQEPANPGGAPAEPEEAEPEYMRAGTILTSLESHSVPSMSIASGQS 365			
DB	302 NLQYRKMKILFQETRNQPLNSQDEDEDSHGTSILNRMDSLGSNHSIPMSVSTGQS 361			
QY	366 SSVNSLADASDNEEEEEEEEEEEEEEEEPSSREKAMMOGEHNTVTSHGSLIHRKPGSD 425			

Db	362	SSVNSMGEVME-----SSSELVMMHDDDESTINSSSVYHK---KD	399
QY	426	NLYDDPYQPEMTPEGLPPAPAPTSTSSSSARRRAYCRNBDHPATITRTASVRSQIOENE	485
Db	400	HVF---IRDEAGHGDPREPPEPSTQVQSA---LHYRNEREFATIKSALFVROLIHEHE	452
QY	486	QDSALRELSGCKMKRRRQHOQOLLALSRLGEEENSGRLQRLFLQNRAGFTEAKLA	545
Db	453	QENELREMSQYKRRRRROHOKQLALENKKLAEMDEHRLKLOKEVTHANSSIELEKLA	512
QY	546	RROHAGKEKRAAOAEERKFOQIILQOKKELALALEAOKRTYKLRKEOLKELOENPS	605
Db	513	KQOAVITKEKAVAAADKKFOQOILQOQKOLLTFTELESQKQYKICKEXIKKEEMDHS	572
QY	606	TPRKREKAWLROKREOLQOCQAEAEAGILRRORQYFELQSGROYRKMLARHSLDQDLR	665
Db	573	TPRKQKQRIKSKHNENLOHTQAEDEAHLLTQQRILYUDKNCRFPRKIKIRHVEEQNIR	632
QY	666	EDLNKKQTCQKLECALLRQNEATRELELRLOAVQRTRAELRTFLQHOTELGNOLENKR	735
Db	633	BELNKKRKQKEMEMAMLRHDESTRLELEYROLHTLOKLRMDLRLOHOTELENOLEYNKR	692
QY	726	REOELRQKHAANOVRQORPSLVVRGAQYPMGLPATGALGPLS-----	766
Db	693	RERELHRRHNMELROQRPKNLAMEQIKQFORPCYKQVOTQOYKALKHNOLEVPKPKENKT	752
QY	767	-TGLTSEKQPPSCSGQEQALIGQRMIGEEEAVERPMIIGKEGTTLEPEEQRIT-LOEEMGT	824
Db	753	ILKTLTKDQD---TKRLALAQYQDOSTINEMASQALYLDEQAEHFCALMLQOQEMELL	809
QY	825	S-----SSPQKHSL-----VNEEDWDISKEMKESRVPASLQSE	858
Db	810	NAVQSKIMQTEAOEHERELQKLEQVRSLLRRALHLOKITEELIALQKESRIRIKMLERQE	869
QY	859	RNIQGEFAGAMNLMKEHGNLYVMEF	885
Db	870	REI---ETFMESILRMGFGMLVTLDF	892
RESULT 9			
Q9NZM9			
ID	Q9NZM9	PRELIMINARY;	PRT; 898 AA.
AC	Q9NZM9;		
DT	01-OCT-2000	(TREMBLrel, 15, Created)	
DI	01-OCT-2000	(TREMBLrel, 15, Last sequence update)	
DT	01-MAR-2002	(TREMBLrel, 20, Last annotation update)	
DE	Serine/threonine kinase.		
GN	KDS.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Carter T.G., Benton B., Fuhling D., Monks C.R.F., Windmiller D.,		
RA	Kupfer A., Manfredi J., Johnson G.L., Pleiman C.M.,		
RT	"KDS and TAO1, two related proteins with kinase domain homology to		
RT	STK20, differentially relocate in mitogen stimulated T lymphocytes.",		
RL	Submitted (Aug-1999) to the EMBL/GenBank/DBJ databases.		
CC	-1- SIMILARITY: ALPONGS to the SER/THR FAMILY OF PROTEIN KINASES.		
DR	EMBL; AF181985; BAF25817.1; -		
DR	HSSP; P24941; 1838.		
DR	InterPro: IPR000719; Euk.pkinase.		
DR	InterPro: IPR002290; Ser_thr.pkinase.		
DR	InterPro: IPR001245; Tyr_pkinase.		
DR	InterPro: IPR000130; Zn_MTPetdisc.		
DR	Pfam; PF00069; pkinase.1.		
DR	PRINTS; PR00109; TYRKINASE.		
DR	Prodom; PD000001; Euk.pkinase.1.		
DR	SMART; SM00220; S_TKC.1.		
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP_1.		
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM_1.		
DR	PROSITE; PS00108; PROTEIN_KINASE_ST_1.		



```
QY 486 QDSALREOLSGYKRMROHOKOLLATESRLGEREESHGRLQRELEAORAGFTGEAKLA 545
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 453 QENELREOMSGYKRMROHOKOLLATESRLGEREESHGRLQRELEAORAGFTGEAKLA 512
QY 546 RRHOAIGEKAPARAQAEEERKFOOHILGQOKKEALAEALAEAKRYKLRKEOLKEELOENPS 605
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 513 KQOVALTEBAKVAADEKFFQOOLLAQOKKDLTFPLESQKQYKICKKEKKEEMNEDHS 572
QY 606 TPKREKEMILROKEOLOQCOAEERAGILRRORQYFELQCRQYRKMLLAHSLDQDLR 665
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 573 TPKREKERSKHENLOHQAEEREAHLTQORLYYDKNCRFFKRTKIMIKHNEEQONIR 632
QY 666 EDLNKQKODLECALLRQHEATRELELRQAVORTRAELTLOHOTELQENLEYNKR 725
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 633 EELNKKTKQKEMEHAMLRHDESTRELETRYOLHTLRKLRMDLRLQHOTELENOLEYNKR 692
QY 726 REDELROKHAQVROQPSLKVRAQOLPMGLPATGALGPLS----- 766
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 693 RERELHRKHVMEILROQPKNLKAMEMQIKQOFODTCKVOTQOKYALKNHOLEVTPKNEHT 752
QY 767 -TGTLSEQSCSGQELILQORMLGEEEAVERPMILGEGTTLPEPEORI-LOEENGT 824
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 753 ILATLQDEQ---TRKLAILEQYEQSINEMMASQALRLDEQAEQECALRLQLOQEMELL 809
QY 825 S-----SSPQKHRSI-----VNEEDWDISKMKSRVPSLASOE 858
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 810 NAOQSKKMQTEAQHEHELOKLEORVSLBRAHLEQKIEELALQKRESEKIKLLEROE 869
QY 859 RNIIQGEAGAMNLMKEHGNLYDMER 885
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 870 REI----ETFDMESLRMGFGNLYTIDF 892
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RESULT 11
QY19E0 PRELIMINARY; PRT; 898 AA.
AC Q919E0;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE KFC (Fragment).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20162342; PubMed=10698516;
RA Yustein J.T., Li D., Robinson D., Kung H.J.;
RT "KFC, a Ste20-like kinase with mitogenic potential and capability to
activate the SAPK/JNK pathway."
RL Oncogene 19:710-718(2000).
DR EMBL; AF263314; AAF73045.1; -.
DR HSSP; P24941; 1B38.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR000130; Zn_MTpeptidase.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Euk_pkinase; 1.
DR SMART; SMO0220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.
FT NON_TER 898
SQ SEQUENCE 898 AA; 105289 MW; 46E265937F218A8 CRC64;
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Query Match 47.2%; Score 2427.5; DB 13; Length 898;
Best Local Similarity 54.5%; Pred. No. 1e-132;
Matches 504; Conservative 127; Mismatches 216; Indels 77; Gaps 10;
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QY 6 RAGSLKDPDVAELFFKDDPEKLSFDLREIGHGSGFVAYFARDVNSBVVAIKKMSYSGKQ 65

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Db 2 RKGVKDPDELADLFYKDDPEELFVGLHEIGHGSGFVAYFPATNSHTNENVAIVKMSYSGKQ 61
QY 66 SNEKWQDIIIEVRLQKLRHNTIYQNGCYREHTANLVMEYCSGASDLEVHKRPLQE 125
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 TNEKWQDIIIEVRLQKLRHNTIYQNGCYREHTANLVMEYCSGASDLEVHKRPLQE 121
QY 126 VEIATVHGALQGLAYLHSHNMIRHDKAGNILLSEGIYKLGFGSASITAPANSVGT 185
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 122 VEIATVHGALQGLAYLHSHNMIRHDKAGNILLSEGIYKLGFGSASITAPANSVGT 181
QY 186 PYMAPREVILLAMDEGOYDKGVDSLTGTCETLAERKPPFNMMAMALVHIAONESPAL 245
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 182 PYMAPREVILLAMDEGOYDKGVDSLTGTCETLAERKPPFNMMAMALVHIAONESPAL 241
QY 246 QSGHWSEYFRNFVDSCLQIPDRPTSEVLKHFVLRERPPVIMDLORTKDAVELD 305
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 242 QSNEMSDSFRGFVDYCLQIPDRPTSEVLKHFVLRERPPVIMDLORTKDAVELD 301
QY 306 NLOYRKMKKTLFOBARPGCAEAREEEREAERYNHKAGTILSLESSHSVPMSISASQS 365
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 302 NLOYRKMKKTLFOETRNGRPLTESQEEEDSEHGSNLSRKMDISGNSHSPMSVTSQS 361
QY 366 SSVASLADASDNEEEEEEEEEEEEEEGPESREMMAMOGCEHTYSHSIIHRLPGSD 425
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 362 SSVASMQEVLDE-----SPELVAMHSDSAVNSTSSVYVK---KD 399
QY 426 NLVDDPYOPEKTPGLPPAPAPTSTSSSARRARYARNRDFHTIRTASVRSQIOEHE 485
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 400 HVF---IRDEVGHDRRPREVPPTQSVONQ---LHYRNRERFATIKASIVTRQIHNE 452
QY 486 QDSALREOLSGYKRMROHOKOLLATESRLGEREESHGRLQRELEAORAGFTGEAKLA 545
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 453 QENELREOMSGYKRMROHOKOLLATESRLGEREESHGRLQRELEAORAGFTGEAKLA 512
QY 546 RRHOAIGEKAPARAQAEEERKFOOHILGQOKKEALAEALAEAKRYKLRKEOLKEELOENPS 605
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 513 KQOVALTEBAKVAADEKFFQOOLLAQOKKDLTFPLESQKQYKICKKEKKEEMNEDHS 572
QY 606 TPKREKEMILROKEOLOQCOAEERAGILRRORQYFELQCRQYRKMLLAHSLDQDLR 665
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 573 TPKREKERSKHENLOHQAEEREAHLTQORLYYDKNCRFFKRTKIMIKHNEEQONIR 632
QY 666 EDLNKQKODLECALLRQHEATRELELRQAVORTRAELTLOHOTELQENLEYNKR 725
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 633 EELNKKTKQKEMEHAMLRHDESTRELETRYOLHTLRKLRMDLRLQHOTELENOLEYNKR 692
QY 726 REDELROKHAQVROQPSLKVRAQOLPMGLPATGALGPLSTGTLSEQ---PCSSGOE 781
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 693 RERELHRKHVMEILROQPKNLKAMEMQIKQOFODTCKVOTQOKYALKNHOLEVTPKNEHT 752
QY 782 -----ALIGQRMIGEEEAVERPMILGEGTTLPEPEORI-LOEENGTFS-- 825
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 753 ILKSLKDEQTRKLAILEQYEQSINEMMASQALRLDEQAEQECALRLQLOQEMELLNGY 812
QY 826 -----SSPQKHRSI-----VNEEDWDISKMKSRVPSLASOERNI 861
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 813 QSKIKMQTEAQHEHELOKLEORVSLBRAHLEQKIEELALQKRESEKIKFLTEROEREI 872
QY 862 IGOEEAGAMNLMKEHGNLYDMER 885
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 873 ----ETFDMESLRMGFGNLYTIDF 892
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RESULT 12
QYUNG7
AC Q9UNG7;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE STE20-like kinase.
GN JIK.
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OS Homo sapiens (Human)  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20026851; PubMed=10559204;  
 RA Tassi E., Blesova Z., Di Fiore P.P., Gutkind J.S., Wong W.T.;  
 RT "Human JNK, a novel member of the STE20 kinase family that inhibits  
 RT JNK and is negatively regulated by epidermal growth factor."; J.  
 RL J. Biol. Chem. 274:33287-33295(1999)  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 DR EMBL; AF179867; AF174559.1; -;  
 DR HSSP; P24941; 1B38.  
 DR InterPro: IPR000719; Euk.pkinase.  
 DR InterPro: IPR002290; Ser\_thr.pkinase.  
 DR InterPro: IPR001245; Tyr.pkinase.  
 DR InterPro: IPR000130; Zn\_MTptplase.  
 DR Pfam; PF00069; pkinase; 1.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD000001; Euk.pkinase; 1.  
 DR SMART; SM00220; S\_TKc1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PSS0011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_SF; 1.  
 DR PROSITE; PS00142; ZINC\_PROTEASE; UNKNOWN.1.  
 KW ATP-binding; kinase; Serine/threonine-protein kinase; Transferase.  
 SO SEQUENCE 898 AA; 105657 MW; 61P0462871356025 CRC64;

Query Match	46.4%	Score 2385.5	DB: 4	Length 898
Best Local Similarity	53.3%	Pred. No. 2.7e-130		
Matches 494	Conservative 133	Mismatches 217	Indels 83	Gaps 10

QY	6	RAGSLKDPDAVELEFKDPDELTFSDLRIGGSGGAYFADVANSSEVALTKKXSYGKO	65
Dd	2	RKVGLKDPDLDTFYKDPDELLFTGLHEHIGSGGAYFATNATSEVALTKKXSYGKO	61
QY	66	SNEKWOIIEKVEPRLQKLRHNTIQRGCVLREHTAMLVMEYCGSASDLELVHKKPLOE	125
Dd	62	THEKMODILKEVEKLEROLKHPNTEIEYKGCVLKEHTAMLVMEYCGSASDLELVHKKPLOE	121
QY	126	VEIAVYHGALOGIAGLYHSHNMHIDVYKAGNIIILSEGLVKLSDFGSASIMAPRANSVGT	185
Dd	122	VEIAITHGALHAGLYHSHALHIDRIKAGNIIILTEGQVKLAFGASAMSPANSVGT	181
QY	186	PYMAPEVILIADGQYDGVKDVWSLGTCTIETAEKRPPELFENMAASALYHIAONESPAL	245
Dd	182	PYMAPEVILIADGQYDGVKDVIMSLGTCTELAEKRPPELFENMAASALYHIAONDSPTL	241
QY	246	QSGHMSYEFNRFVDSCLKIPQDRPTSEVLLKRRFVLRERPVIMDLIORTKDAVRELD	305
Dd	242	QSNMTDTSFRFRFVDSCLKIPQESRPTSELLRHDFVRDRPLVLDLIORTKDAVRELD	301
QY	306	NLOYRKMKKILIFQAPNPGGAEAREEELAEAPYHNRAGTILTSLESSHVSYSMSISASSQS	365
Dd	302	NLOYRKMKKILIFQETRNGPLNSEDDEBESHGTSILNRENDLSGNSHPSMSYTNV---	358
QY	366	SSVNSLADASNEEEEEEEEEEDEEGESESAMMOEGEHTVYSHSIIHRLPGSD	425
Dd	359	-----OPGONGOPGGOFRSHKIVRYVMHDEESTINSSSVYHK---KD	399
QY	426	NLYDDPYQPEKTPGRLPPAPRPTSGSSASRRAYCRNHDPEATRTIASLVSKOIDEHE	485
Dd	400	HVF---IRDEAGHGDPRPREPRPTSGVQSQA---LHNRNERPATITSASLVTRQIIEHE	432
QY	486	QDSALREOLSGYKMRROHOKOLIALESRLGEREHSGRLORELEAORAGFGEAEKLA	545
Dd	453	QENELREOMSGYKMRROHOKOLIALENKILKAEMDEHRLKLOKEVETHANNSSTIEKLA	512
QY	546	RRHRAIIEKERRAQAABERKFOQHIIIGQOKKELALALLAEAKRTYKLLKEDLKELEBNS	605
Dd	513	KQOYAILIEKEKKAQAABERKFOQIIIAQOKKDLTTFLESOKYOKYLOKEKIEKEMDHS	572

QY	ТРКРКАШМЛРКОЕОЛООСОЕБЕАГЛРНОЮУРЕЛОЮУРКАШМЛРНШДОДЛР	665
Db	573 ТРКЕКОЕРИШЕНЮОНОДБЕАНЛТООУРЛУУКНОСФЕРКАШМРННЕЮОНИР	6322
QY	ЕДЛНКЮОКОДЛЕАЛЛРНОЕАТРЕЛЕЛРОЛОАУОРТАЛРЕЛТРОТЕЛНОЛЕУНР	7255
Db	633 ЕЛНКРКЮОКМЕИМЛРНДНЕСТРЕЛЕУРОЛНТЛОКЛРМДЛРЛОНОТЕЛНОЛЕУНР	6922
QY	726 РЕОЕЛРКНААУВНОРПСЛКВРАГОДРМГПРАТАЛСРЛС	7666
Db	693 РЕРЕЛРКНУМЕЛНОРПНЛКАМЕНОЛКОРОДСКУЮУКАЛКННОЛЕУВРКНЕНКТ	7522
QY	767 -ТГЛСЕОРОССОЕОАЛГОРМЛГЕЕБЕАВРЕМЛЛГКСТЛРЕВРОГ-ЛОЕМКТР	8244
Db	753 ИЛТЛКЛЕО---ТКЛЛЛЛЕОУЕОСИНЕММАСОАЛРЛДЕАОЕАЕСОАЛРЛОДОЕМЛ	8099
QY	825 S-----SSPQKHSL-----VNEEDWDSKMKRSRVPJSLASOE	8588
Db	810 NAYOSKIMQTEAOHEHRLQLEORVSLRRAHLEOKITEELALOKERSERIRNLLROE	8699
QY	859 RNIIGOEAGAMLNLEKEHGLVMEF	885
Db	870 REI---ETPDMESLRMGFGVNLVTDL	892

### RESULT 13

ID	Q9VWG8	PRELIMINARY;	PRT;	1039	AA.
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DT	01-MAY-2000 (TREMblurel. 13, Created)
DT	01-MAY-2000 (TREMblurel. 13, last sequence update)
DT	01-MAR-2002 (TREMblurel. 20, last annotation update)

DE CG14217 protein.

05 *Drosophila melanogaster* (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Epnydroidea; Drosophilidae; Drosophila.

NCBI\_TaxID=7227;

RP SEQUENCE FROM N.A.

RX MEDLINE=20196006; Pubmed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.  
 April 1987  
 Abstracts of the 1987 Annual Meeting of the American Society of Tropical Medicine and Hygiene, San Francisco, California, December 1-5, 1987.

RA April J.F., Agdayani A., An H.-J., Andrews-Piannkoch C., Baldwin D.  
RA Ballaw P.M., Bason A., Bayondujo T., Baurath+awcoju T., Bessler E.V.

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.V., Borman P.D., Bhargava P., Bhatnagar S., Bhatnagar S.,  
RA Beeson K.V., Borman P.D., Bhargava P., Bhatnagar S., Bhatnagar S.,

KA Beeson K.I., Benos P.V., Berman B.P., Bhandardi D., Bolshakov S.,  
RA Borkova D., Botchan M.P., Bouck J., Brokstein P., Brottier P.

KA Borkova D., Bolchah M.R., Bouck J., Broksstein P.,  
RA Burtis K C, Busam D A, Butler H, Cadion F, Center A, Chandra T

Cherry J.M., Cawley S., Dahlke C., Davenport I. B., Davies P.  
Bulcic N.C., Busdini D.A., Butler H., Calieu E., Center A., Chandra I.

KA CHERLY J. M., CRAWLEY S., DANILKE C., DAVENPORT L. B., DAVIES P.,  
BA DE PABLOS B., DELICHER A., DENG Z., MAYES A. D., DEW I., NIETZ S. M.

RA  
na  
ue  
Dodson  
Downes  
Dugan-Bocha  
Dunkov  
Dunn

RA  
the  
beason  
Durbin  
K.J.,  
Evangelista  
C.C.,  
Ferraz  
C.,  
Fleischmann  
D.,  
Dobson  
D.E.,  
Downes  
M.,  
Dugan-Rochin  
S.,  
Dunkov  
B.C.,  
Dunn

Fosler C., Gabriellian A.E., Gard N.S., Gelbart W.M., Glasser K., RA

RA Glodex A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
Kocher C., Kudachellam A.B., Saig N.S., Seidatc W.M., Glassel R.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeqwan C., RA

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacleb J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.C.

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*.";  
 Science 287:2185-2195 (2000).  
 DR EMBL: AE003512; AAF48973.1; .  
 DR HSSP: p24941; 1B38.  
 DR Flybase: Fggn0031030; CG14217.  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR002290; Ser\_thr\_pkinase.  
 DR Pfam: PF00069; pkinase; 1.  
 DR ProDom: PD000001; Euk\_pkinase; 1.  
 DR SMART: SM00220; S\_TKc; 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR ATP-binding; Transferase.  
 KW SEQUENCE 1039 AA; 118298 MW; 391D15216D295F3A CRC64;

Query Match 35.8%; Score 1841.5; DB 5; Length 1039;  
 Best Local Similarity 46.5%; Pred. No. 1,2e-98;  
 Matches 391; Conservative 126; Mismatches 228; Indels 95; Gaps 12;

QY 1 MPAGRAGSLKDPVALEFEKDDPEKLFSDLRIGSGFGAVYFARDVRNSEVAIAKKMS 60  
 1 MS-ARPGSLKDEIDALDNKHPKIFEDLRIGSGFGAVYFARDVRNSEVAIAKKMS 59  
 QY 61 YSGKSNKEMKQDITKEVRLQKLRHNTQYRGYLRHTAWLMVMEYSGASDLLEVRK 120  
 60 YTGKQSGEMKQDITKEVRLQKLRHNTQYRGYLRHTAWLMVMEYSGASDLLEVRK 119  
 QY 121 KPLQGEVIAVNTGALQALYLSHNMIRHDVYAGNITLSEPLVYLGDPGSAIMAPAN 180  
 120 KPLHEDEIAICGLVSLGSLYSLHSIRHIDKAGNITLTDNGVVKIADPGSAIKCPAN 179  
 QY 181 SEFGYPMAPVEYILAMDEGQYDGKDVMSLGTICTEIAERKRPPLFNNMAMSLYHIAON 240  
 180 SEFGYPMAPVEYILAMDEGQYDGKDVMSLGTICTEIAERKRPPLFNNMAMSLYHIAON 239  
 QY 241 ESPALOSGMWSEYFRNFVDSCLQKIPQDRPTSEVLKHFVLRERPTVIMDLQRTKDA 300  
 240 ESPTLPKRNPMDSAFCSFVELCTKMPAERPSAKLLTHAVVTRPSDVTLLLEIARTKSA 299  
 QY 301 VRELDMVLRKMKKILFQEARNGPAGAEAREEAEAPYMRAGTLT---SLESHSVPSM 357  
 300 VRELDMVLRKMKKILFQEARNGPAGAEAREEAEAPYMRAGTLT---SLESHSVPSM 356  
 QY 358 SIS-ASSOSSSVSLADASDNEEEEEE-----EEDDEEESREMMAM 403  
 357 GYSAASSOSSSVSLADASDNEEEEEE-----EEDDEEESREMMAM 415  
 QY 404 MOGEHT---VTSHSITIR---LPGSDNLYDPPYQ---EMTGPRLPPRAPPT--- 449  
 416 -QOGQVPVPGAVSRNSRHRNRPPLPNIMHSMNNVTPTNSASVYAPAPAPVLPPISY 474  
 QY 450 -----STSSSA 456  
 DB 475 LPHLSAMGHVGGGTGTGSGGGSPASGGLADRIQVOPRYLTTPAAQAAYVAASASS 534  
 QY 457 RRAAYCRNRD-----PATRTASVROIOEHODSALRLOLSGYRMRORHOKOLLATE 512  
 513 QQAISNAVNDHGNPNATITTSIVTKQKEHQEE- MBDMSGYRMRREHDAHLKLE 593  
 QY 513 SRLGEREHSGLRQLELEAORAGFTEAKLARHQATIGEKARAAQAQAEERFQOHLIG 572  
 594 EKCVYMEAHKPTALDKREYDPLLNFTRDLRLFTKHQOVERAKQTSAAEKKILHETIL 653  
 QY 573 QCKKELALLAOKRTYLLKKEQLKELOENPSTPKREKAEWLLRQEKLOQCOAEBEAG 632  
 654 KOENDRKVVYDNLNKKKPKKREKRELSDMESTPKRQDLTLQOSKDNKLOHEAQEOR 713

QY 633 LRRRQYVELQCRQYRKMLARHSLDODLAREDLNKKOTOKOLECALLRQHEATREL 692  
 DB 714 MDAQOYVELEKRRKRMIMQNHEDQQLDELCKKEQOQOAHMILKHNKHTQEL 773  
 QY 693 ELRQLOAVORTAELRLQHQHLEGMOLEYKRRDELRKNAQVROOKSLKPAQOL 752  
 DB 774 EYKROKSVHOLREQINKQHDLEHNMOKYMDRIKKELVAKHVAELRPOPSIKQKLEOI 833

## RESULT 14

Q9H7S5 PRELIMINARY; PRI; 398 AA.

AC Q9H7S5;  
 DT 01-MAR-2001 (Tremblrel, 16, Created)  
 DT 01-MAR-2001 (Tremblrel, 16, Last sequence update)  
 DT 01-MAR-2002 (Tremblrel, 20, Last annotation update)  
 DE CDNA FL14314 f1s, clone PLACE3500350, weakly similar to  
 DE serine/threonine-protein kinase 50DU (EC 2.7.1.1).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=PLACENTA;  
 RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,  
 RA Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,  
 RA Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,  
 RA Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,  
 RA Wakamatsu A., Nakamura Y., Nagahara K., Masuno Y., Oshima A.;  
 RT "NEO human cDNA sequencing project.";  
 RL Submitted (Aug-2000) to the EMBL/GenBank/DDa databases.  
 DR EMBL: AK024376; BAB14901.1; .  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR002290; Ser\_thr\_pkinase.  
 DR Pfam: PF00069; pkinase; 1.  
 DR ProDom: PD000001; Euk\_pkinase; 1.  
 DR SMART: SM00220; S\_TKc; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 KW ATP-binding; Transferase.  
 KW SEQUENCE 398 AA; 46177 MW; BLADDIDA45D46FA4 CRC64;

Query Match 27.5%; Score 1413; DB 4; Length 398;  
 Best Local Similarity 66.8%; Pred. No. 2,6e-74;  
 Matches 284; Conservative 42; Mismatches 67; Indels 32; Gaps 4;

QY 177 APANSEVGTPIYMAPEVILAMDEGQYDGKDVMSLGTICTEIAERKRPPLFNNMAMSLYH 236  
 3 SPANSEVGTPIYMAPEVILAMDEGQYDGKDVMSLGTICTEIAERKRPPLFNNMAMSLYH 62  
 QY 237 IANESPALOSGMWSEYFRNFVDSCLQKIPQDRPTSEVLKHFVLRERPTVIMDLQRTKDA 296  
 63 IANESPTLOSNMTYDFRNFVDSCLQKIPQDRPTSEVLKHFVLRERPTVIMDLQRTKDA 122  
 QY 297 TKDAVEELDLQYRKMKKILFQEARNGPAGAEAREEAEAPYMRAGTLTSSSVPS 356  
 123 TKDAVEELDLQYRKMKKILFQEARNGPAGAEAREEAEAPYMRAGTLTSSSVPS 182  
 QY 357 MSISASSOSSSVSLADASDNEEEEEE-----EEDDEEESREMMAMQGEHTVTSHS 416  
 183 MSISASSOSSSVSLADASDNEEEEEE-----EEDDEEESREMMAMQGEHTVTSHS 221  
 QY 417 IIRRLGSDNLYDPPYQEPKTPGP-LQPPAAPRTSSSSARRRAYCRANDHATRTAS 475  
 222 VHLKPEEN-----YREEDPRTASDPQSP-----QVSRKSHYRNHEHATRTAS 271  
 QY 476 IYSROIOEHODSALRLOLSGYRMRORHOKOLLALERSLGRGEREHSGLRQLELEAORA 535  
 272 LVTRQMEHODSALRLOLSGYRMRORHOKOLLALERSLGRGEREHSGLRQLELEAORA 331  
 QY 536 GFGTEAKLARHQATIGEKARAAQAQAEERFQOHLIGQCKELALLAOKRTYLLKKEQ 595  
 332 NFAAEWKEKLKKNQAAWKEKAKYVNSDEKKFQOHIAQOKKELNSFLSGKRRYKLRKEQ 391





GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: November 22, 2002, 12:21:31 ; Search time 21.846 Seconds  
(without alignments)  
1337.406 Million cell updates/sec

Title: US-09-686-346a-4

Perfect score: 5140  
Sequence: 1 MPAGGRAGSLKDPVAVLELF.....LLPLAPRWRLAGTAGCP 993

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database :

1: Issued\_Patents\_AA:\*  
2: /cgn2\_6/ptodata/1/1aa/3A\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/3B\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5133	99.9	993	4	US-09-060-410-4
2	2805.5	54.6	1001	4	US-09-060-410-2
3	873.5	17.0	278	4	US-09-060-410-17
4	717	13.9	1360	4	US-09-393-569-2
5	614	11.9	487	2	US-08-712-709-8
6	614	11.9	487	3	US-09-111-444-8
7	614	11.9	487	4	US-09-411-228-8
8	594	11.6	431	4	US-09-211-930-5
9	594	11.6	431	3	US-09-340-993-5
10	594	11.6	431	4	US-09-152-406-3
11	594	11.6	431	4	US-09-468-442-5
12	592	11.5	426	2	US-08-852-743-2
13	592	11.5	426	2	US-09-211-930-4
14	592	11.5	426	3	US-09-340-993-4
15	592	11.5	426	3	US-09-185-370-2
16	592	11.5	426	4	US-09-152-406-4
17	592	11.5	426	4	US-09-468-442-4
18	576.5	11.2	416	2	US-09-211-930-11
19	576.5	11.2	416	3	US-09-340-993-11
20	576.5	11.2	416	4	US-09-468-442-11
21	571	11.1	416	2	US-09-211-930-3
22	571	11.1	416	3	US-09-340-993-3
23	571	11.1	416	4	US-09-468-442-3
24	560	10.9	403	2	US-08-712-709-3
25	560	10.9	403	3	US-09-111-444-3
26	560	10.9	403	4	US-09-411-228-3
27	555	10.8	270	2	US-08-852-743-5

28	555	10.8	270	3	US-09-185-370-5	Sequence 5, App11
29	516	10.0	276	2	US-08-852-743-7	Sequence 7, App11
30	516	10.0	276	3	US-09-185-370-7	Sequence 7, App11
31	505	9.8	545	2	US-08-935-760-4	Sequence 4, App11
32	503	9.8	545	2	US-08-114-555a-2	Sequence 2, App11
33	503	9.8	545	2	US-08-935-760-2	Sequence 2, App11
34	499	9.7	465	3	US-08-559-397a-2	Sequence 2, App11
35	497	9.7	544	3	US-08-559-397a-19	Sequence 19, App1
36	491	9.6	506	1	US-08-369-780-2	Sequence 2, App11
37	491	9.6	506	1	US-08-475-682-2	Sequence 2, App11
38	491	9.6	506	1	US-08-780-833-2	Sequence 2, App11
39	491	9.6	506	1	US-08-636-036-2	Sequence 2, App11
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41	491	9.6	506	3	US-09-108-262-2	Sequence 2, App11
42	491	9.6	524	2	US-08-615-942a-2	Sequence 2, App11
43	489	9.5	268	2	US-08-852-743-3	Sequence 3, App11
44	489	9.5	268	3	US-09-185-370-3	Sequence 3, App11
45	487.5	9.5	272	2	US-08-852-743-6	Sequence 6, App11

#### ALIGNMENTS

```
RESULT 1
US-09-060-410-4
; Sequence 4, Application US/09060410
; Patent No. 6165461
; GENERAL INFORMATION:
; APPLICANT: Cobb, Melanie
; APPLICANT: Hutchinson, Michele
; APPLICANT: Chen, Zhu
; APPLICANT: Berman, Kevin
; TITLE OF INVENTION: TAO PROTEIN KINASERS AND METHODS OF USE
; NUMBER OF INVENTIONS: THEREFOR
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/060,410
; FILING DATE: 14-Apr-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Makl, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 860098.421
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEO ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 993 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-060-410-4

Query Match 99.9%; Score 5133; DB 4; Length 993;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 99%; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPAGGRAGSLKDPVAVLELFSDLRREIGHSGFAGVYFARDVRNSEVAIKKMS 60
Db 1 MPAGGRAGSLKDPVAVLELFSDLRREIGHSGFAGVYFARDVRNSEVAIKKMS 60
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QY      61 YSGKSNKMODIIKEVRFLOKL RHPNTIOYRGCIYLRHNTAMLVMEYCLGSADLLEVHK 120
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QY      121 KPIQVEIYAIVTHGALQGLAYLHSHNMHHDVAKAGNILLSEPGVLKGDGSGASINAPAN 180
      |||
      121 KPIQVEIYAIVTHGALQGLAYLHSHNMHHDVAKAGNILLSEPGVLKGDGSGASINAPAN 180
QY      121 KPIQVEIYAIVTHGALQGLAYLHSHNMHHDVAKAGNILLSEPGVLKGDGSGASINAPAN 180
      |||
      121 KPIQVEIYAIVTHGALQGLAYLHSHNMHHDVAKAGNILLSEPGVLKGDGSGASINAPAN 180
QY      181 SPFGTPYMAPEVILAMDEGOYDGKDVMSLGTICIELAEKRPPLFNMMAMSLYHIAON 240
      |||
      181 SPFGTPYMAPEVILAMDEGOYDGKDVMSLGTICIELAEKRPPLFNMMAMSLYHIAON 240
QY      181 SPFGTPYMAPEVILAMDEGOYDGKDVMSLGTICIELAEKRPPLFNMMAMSLYHIAON 240
      |||
      181 SPFGTPYMAPEVILAMDEGOYDGKDVMSLGTICIELAEKRPPLFNMMAMSLYHIAON 240
QY      241 ESPALOSGHWSEYFRNFVDSCLQKIPDRPTSEVLLKHFVLEBRPPVIMDLIORTKA 300
      |||
      241 ESPALOSGHWSEYFRNFVDSCLQKIPDRPTSEVLLKHFVLEBRPPVIMDLIORTKA 300
QY      241 ESPALOSGHWSEYFRNFVDSCLQKIPDRPTSEVLLKHFVLEBRPPVIMDLIORTKA 300
      |||
      241 ESPALOSGHWSEYFRNFVDSCLQKIPDRPTSEVLLKHFVLEBRPPVIMDLIORTKA 300
QY      301 VRELDMIOYRKMKKILFOEAPNGGAEAPPEEAEAPYHRACTLTLSLSSHVSPTSIS 360
      |||
      301 VRELDMIOYRKMKKILFOEAPNGGAEAPPEEAEAPYHRACTLTLSLSSHVSPTSIS 360
QY      301 VRELDMIOYRKMKKILFOEAPNGGAEAPPEEAEAPYHRACTLTLSLSSHVSPTSIS 360
      |||
      301 VRELDMIOYRKMKKILFOEAPNGGAEAPPEEAEAPYHRACTLTLSLSSHVSPTSIS 360
QY      361 ASSOSSSVNSLADASDNEEEEEEDEEGEPESREMMAMOGERTVTSHTSIHR 420
      |||
      361 ASSOSSSVNSLADASDNEEEEEEDEEGEPESREMMAMOGERTVTSHTSIHR 420
QY      361 ASSOSSSVNSLADASDNEEEEEEDEEGEPESREMMAMOGERTVTSHTSIHR 420
      |||
      361 ASSOSSSVNSLADASDNEEEEEEDEEGEPESREMMAMOGERTVTSHTSIHR 420
QY      421 LPGSDMLYDDPYOPEMTPGPLQPPAPPTSTSSSARRRAYCNRDHPATIRTAASLVSRQ 480
      |||
      421 LPGSDMLYDDPYOPEMTPGPLQPPAPPTSTSSSARRRAYCNRDHPATIRTAASLVSRQ 480
QY      421 LPGSDMLYDDPYOPEMTPGPLQPPAPPTSTSSSARRRAYCNRDHPATIRTAASLVSRQ 480
      |||
      421 LPGSDMLYDDPYOPEMTPGPLQPPAPPTSTSSSARRRAYCNRDHPATIRTAASLVSRQ 480
QY      481 IOEHEDSALRELOSGYKRMROHOKOLLALESRLGEEHSGRLQRELEAORAGGTE 540
      |||
      481 IOEHEDSALRELOSGYKRMROHOKOLLALESRLGEEHSGRLQRELEAORAGGTE 540
QY      481 IOEHEDSALRELOSGYKRMROHOKOLLALESRLGEEHSGRLQRELEAORAGGTE 540
      |||
      481 IOEHEDSALRELOSGYKRMROHOKOLLALESRLGEEHSGRLQRELEAORAGGTE 540
QY      541 AEKLARRHQAIGKEKRAAQAEEERKFOQHILGOOKELALLAEOKRTYKLRKEQLKEEL 600
      |||
      541 AEKLARRHQAIGKEKRAAQAEEERKFOQHILGOOKELALLAEOKRTYKLRKEQLKEEL 600
QY      541 AEKLARRHQAIGKEKRAAQAEEERKFOQHILGOOKELALLAEOKRTYKLRKEQLKEEL 600
      |||
      541 AEKLARRHQAIGKEKRAAQAEEERKFOQHILGOOKELALLAEOKRTYKLRKEQLKEEL 600
QY      601 QENPSTPKRKAEWMLRQKQOLOOQAEERAGLLRRQRYFELQCRQYKRMKLARHSLD 660
      |||
      601 QENPSTPKRKAEWMLRQKQOLOOQAEERAGLLRRQRYFELQCRQYKRMKLARHSLD 660
QY      601 QENPSTPKRKAEWMLRQKQOLOOQAEERAGLLRRQRYFELQCRQYKRMKLARHSLD 660
      |||
      601 QENPSTPKRKAEWMLRQKQOLOOQAEERAGLLRRQRYFELQCRQYKRMKLARHSLD 660
QY      661 QDLRLDLNKKOKQKDEKCLLLRQEHATRELELROLOAORTRAELTRLOHOTEGLNOL 720
      |||
      661 QDLRLDLNKKOKQKDEKCLLLRQEHATRELELROLOAORTRAELTRLOHOTEGLNOL 720
QY      661 QDLRLDLNKKOKQKDEKCLLLRQEHATRELELROLOAORTRAELTRLOHOTEGLNOL 720
      |||
      661 QDLRLDLNKKOKQKDEKCLLLRQEHATRELELROLOAORTRAELTRLOHOTEGLNOL 720
QY      721 EYNNRREBELRQKHAQVROQPKSLYKVRAGOLPMGLPATGALGPLSTGLTSEQPCSSGQ 780
      |||
      721 EYNNRREBELRQKHAQVROQPKSLYKVRAGOLPMGLPATGALGPLSTGLTSEQPCSSGQ 780
QY      721 EYNNRREBELRQKHAQVROQPKSLYKVRAGOLPMGLPATGALGPLSTGLTSEQPCSSGQ 780
      |||
      721 EYNNRREBELRQKHAQVROQPKSLYKVRAGOLPMGLPATGALGPLSTGLTSEQPCSSGQ 780
QY      781 EAILGOMLGEEREAVERMILKEGTTLPEBORILQEEBMTFFSSPOKHRSLVNEEDW 840
      |||
      781 EAILGOMLGEEREAVERMILKEGTTLPEBORILQEEBMTFFSSPOKHRSLVNEEDW 840
QY      781 EAILGOMLGEEREAVERMILKEGTTLPEBORILQEEBMTFFSSPOKHRSLVNEEDW 840
      |||
      781 EAILGOMLGEEREAVERMILKEGTTLPEBORILQEEBMTFFSSPOKHRSLVNEEDW 840
QY      841 DISKEMKESVPSLAOERNITIGOEAGANLMEKEHGNLYDMEFKLGWQGVLPVPE 900
      |||
      841 DISKEMKESVPSLAOERNITIGOEAGANLMEKEHGNLYDMEFKLGWQGVLPVPE 900
QY      841 DISKEMKESVPSLAOERNITIGOEAGANLMEKEHGNLYDMEFKLGWQGVLPVPE 900
      |||
      841 DISKEMKESVPSLAOERNITIGOEAGANLMEKEHGNLYDMEFKLGWQGVLPVPE 900
QY      901 EEEEEEDEGAPIGTRPDGDCPPDIPEPPPSHLROYPAQOLGPGTSLHGLTGLSFA 960
      |||
      901 EEEEEEDEGAPIGTRPDGDCPPDIPEPPPSHLROYPAQOLGPGTSLHGLTGLSFA 960
QY      901 EEEEEEDEGAPIGTRPDGDCPPDIPEPPPSHLROYPAQOLGPGTSLHGLTGLSFA 960
      |||
      901 EEEEEEDEGAPIGTRPDGDCPPDIPEPPPSHLROYPAQOLGPGTSLHGLTGLSFA 960
QY      961 VGSSGILLPLLLPLPLAPRWRMLAGSTAP 993
      |||
      961 VGSSGILLPLLLPLPLAPRWRMLAGSTAP 993
QY      961 VGSSGILLPLLLPLPLAPRWRMLAGSTAP 993
      |||
      961 VGSSGILLPLLLPLPLAPRWRMLAGSTAP 993

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RESULT 2
US-09-060-410-2
: Sequence 2, Application us/09060410
: Patent No. 6165461
: GENERAL INFORMATION:
: APPLICANT: Cobb, Melanie
: APPLICANT: Hutchinson, Michele

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: APPLICANT: Chen, Zhu
: APPLICANT: Berman, Kevin
: TITLE OF INVENTION: TAO PROTEIN KINASES AND METHODS OF USE
: TITLE OF INVENTION: THEREFOR
: NUMBER OF SEQUENCES: 26
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: SEED AND BERRY LLP
: STREET: 6300 Columbia Center, 701 Fifth Avenue
: CITY: Seattle
: STATE: Washington
: COUNTRY: USA
: ZIP: 98104
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/060,410
: FILING DATE: 14-APR-1998
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Maki, David J.
: REGISTRATION NUMBER: 31,392
: REFERENCE/DOCKET NUMBER: 860098.421
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (206) 622-4900
: TELEFAX: (206) 682-6031
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1001 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-09-060-410-2

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Query Match      54.6%; Score 2805.5; DB 4; Length 1001;
Best Local Similarity 57.8%; Pred. No. 1.1e-177;
Matches 596; Conservative 108; Mismatches 225; Indels 103; Gaps 16;

QY      1 MPAGAGSLKOPDVALEPFKDDPEKLFSDREIGHSGFCAVYFARDVNRSEVATKKMS 60
      |||
      1 MPSTNRAGSLKDPKLELFFKDEPEKLFDTLREIGHSGFCAVYFARDVNRSEVATKKMS 60
QY      61 YSGKSNKMODIIKEVRFLOKL RHPNTIOYRGCIYLRHNTAMLVMEYCLGSADLLEVHK 120
      |||
      61 YSGKSNKMODIIKEVRFLOKL RHPNTIOYRGCIYLRHNTAMLVMEYCLGSADLLEVHK 120
QY      61 YSGKSNKMODIIKEVRFLOKL RHPNTIOYRGCIYLRHNTAMLVMEYCLGSADLLEVHK 120
      |||
      61 YSGKSNKMODIIKEVRFLOKL RHPNTIOYRGCIYLRHNTAMLVMEYCLGSADLLEVHK 120
QY      121 KPIQVEIYAIVTHGALQGLAYLHSHNMHHDVAKAGNILLSEPGVLKGDGSGASINAPAN 180
      |||
      121 KPIQVEIYAIVTHGALQGLAYLHSHNMHHDVAKAGNILLSEPGVLKGDGSGASINAPAN 180
QY      121 KPIQVEIYAIVTHGALQGLAYLHSHNMHHDVAKAGNILLSEPGVLKGDGSGASINAPAN 180
      |||
      121 KPIQVEIYAIVTHGALQGLAYLHSHNMHHDVAKAGNILLSEPGVLKGDGSGASINAPAN 180
QY      181 SPFGTPYMAPEVILAMDEGOYDGKDVMSLGTICIELAEKRPPLFNMMAMSLYHIAON 240
      |||
      181 SPFGTPYMAPEVILAMDEGOYDGKDVMSLGTICIELAEKRPPLFNMMAMSLYHIAON 240
QY      181 SPFGTPYMAPEVILAMDEGOYDGKDVMSLGTICIELAEKRPPLFNMMAMSLYHIAON 240
      |||
      181 SPFGTPYMAPEVILAMDEGOYDGKDVMSLGTICIELAEKRPPLFNMMAMSLYHIAON 240
QY      241 ESPALOSGHWSEYFRNFVDSCLQKIPDRPTSEVLLKHFVLEBRPPVIMDLIORTKA 300
      |||
      241 ESPALOSGHWSEYFRNFVDSCLQKIPDRPTSEVLLKHFVLEBRPPVIMDLIORTKA 300
QY      241 ESPALOSGHWSEYFRNFVDSCLQKIPDRPTSEVLLKHFVLEBRPPVIMDLIORTKA 300
      |||
      241 ESPALOSGHWSEYFRNFVDSCLQKIPDRPTSEVLLKHFVLEBRPPVIMDLIORTKA 300
QY      301 VRELDMIOYRKMKKILFOEAPNGGAEAPPEEAEAPYHRACTLTLSLSSHVSPTSIS 360
      |||
      301 VRELDMIOYRKMKKILFOEAPNGGAEAPPEEAEAPYHRACTLTLSLSSHVSPTSIS 360
QY      301 VRELDMIOYRKMKKILFOEAPNGGAEAPPEEAEAPYHRACTLTLSLSSHVSPTSIS 360
      |||
      301 VRELDMIOYRKMKKILFOEAPNGGAEAPPEEAEAPYHRACTLTLSLSSHVSPTSIS 360
QY      361 ASSOSSSVNSLADASDNEEEEEEDEEGEPESREMMAMOGERTVTSHTSIHR 420
      |||
      361 ASSOSSSVNSLADASDNEEEEEEDEEGEPESREMMAMOGERTVTSHTSIHR 420
QY      361 ASSOSSSVNSLADASDNEEEEEEDEEGEPESREMMAMOGERTVTSHTSIHR 420
      |||
      361 ASSOSSSVNSLADASDNEEEEEEDEEGEPESREMMAMOGERTVTSHTSIHR 420
QY      421 LPGSDMLYDDPYOPEMTPGPLQPPAPPTSTSSSARRRAYCNRDHPATIRTAASLVSRQ 480
      |||
      421 LPGSDMLYDDPYOPEMTPGPLQPPAPPTSTSSSARRRAYCNRDHPATIRTAASLVSRQ 480
QY      421 LPGSDMLYDDPYOPEMTPGPLQPPAPPTSTSSSARRRAYCNRDHPATIRTAASLVSRQ 480
      |||
      421 LPGSDMLYDDPYOPEMTPGPLQPPAPPTSTSSSARRRAYCNRDHPATIRTAASLVSRQ 480
QY      480 QIOEHEDSALRELOSGYKRMROHOKOLLALESRLGEEHSGRLQRELEAORAGGTE 539
      |||
      480 QIOEHEDSALRELOSGYKRMROHOKOLLALESRLGEEHSGRLQRELEAORAGGTE 539

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Db 450 OMOEHODSELRLBOMSGYKMRROHOKOLMTLLENKLAEMDEHRLDLKDFOTNNFAA 509
QY 540 EAEKLARHQAIGEKERRAQAQAEERKFOOHIIIOOKKELALLAEAKRYKLKEQLKEE 599
Db 510 EMEKLAKKHOASNEKAKVANEKFKFOOHIOQOKKELNSFLESREKREKLKEELKEE 569
QY 600 LOENPSTPKREKAEMLLRQEKLOQCAEBEAGLLRROROFYELQCRROYKRLARHSL 659
Db 570 LNNOSTPKREKQENLSKQENIQHQAEEANLLKROQYELLECRRFRRLGRHNL 629
QY 660 DODLREDLNKQOTOKDLBECALLRQHEATRELELRQLOAVOPTRAELRLQHOTELGNO 719
Db 630 EOLVREEELNKROTOKDLBHAMLLRQHESMQELFPRHLNTIQMRCELRLQHOTELTNQ 689
QY 720 LEVNRREQLRQKHAQVQOQPSKLVRAGOLPMGLPATGALGP-----ISTGT 769
Db 690 LEVNRREQLRQKHAQVQOQPSKLVRAGOLPMGLPATGALGP-----ISTGT 749
QY 770 LSE-----EOPCSSQGEALILGORM-LGEEEAAPVE--RMILGKEG 806
Db 750 KSKHAKVLRKKEQTRKALILAEQYDHSINEMISTOALDLBAQEBECOVLLKMOQL 809
QY 807 TLEPEEORILQD-----EMGTFSPPQKHSRLVNEEDMDISKEX-----KESKVP 853
Db 810 ELINAVQSKIKMOQAQHDRELRELEQVSLRALLQOK--LEEMLALQNRTERIRS 866
QY 854 LASQERNITGOEAGANLMEKEH--GNLYDMFK-----LWVOGPV-----L 895
Db 867 LLRQKRELLEAFSESRLGFSNMVLNLSPEAFSHSPGASMSHNPITGSGSPHMGHP 926
QY 896 TPVPEEEEEEGBGAPICPRDGDGCP--SPDIPEPPPSHLROYPASOLPGLSHGL 954
Db 927 GGPQAMGHMGGPQPGWHPGPGMGPVPRGSGIYVNSFOALRQASG---GRTEQMS 983
QY 955 TGLSFAVGSSSG 966
Db 984 RSTSVTSQISNG 995

RESULT 3
US-09-060-410-17
; Sequence 17, Application US/09060410
; Patent No. 6165461
; GENERAL INFORMATION:
; APPLICANT: Cobb, Melanie
; APPLICANT: Hutchinson, Michele
; APPLICANT: Chen, Zhu
; APPLICANT: Berman, Kevin
; TITLE OF INVENTION: TAO PROTEIN KINASES AND METHODS OF USE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/060,410
; FILING DATE: 14-APR-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 860098.421
; TELECOMMUNICATION INFORMATION:

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; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 278 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-09-060-410-17

Query Match 17.0%; Score 873.5; DB 4; Length 278;
Best Local Similarity 59.1%; Pred. No. 1.6e-50;
Matches 162; Conservative 47; Mismatches 56; Indels 9; Gaps 2;

QY 6 RAGSLNDPVVAELFFKDDPEKLFSDLRREIGHGSGFAGVYFARDVNRNSVVAIKKMSISGKO 65
Db 8 KPGVINDPSTIALFLSKNDPEQ---DLREIGHGSGFAGVYFARDVNRNSVVAIKKMSISGKO 64
QY 66 SNEKMODIIEKVEFLQKLRHPTIYRGYLRHTAMLVMEYCLGSASDLVEYHKRPLOE 125
Db 65 AVEKMDILKEVFLNTVYVPHIVDYKACFLKDTTCMLVMEYCLGSASDLVEYHKRPLOE 124
QY 126 VEIAAYTHGALQGLAYLHSHNMIRDVKAGNILLSEGLKLDGFSASIMAPANSFVGT 185
Db 125 VEIAAYTHGALQGLAYLHSHNMIRDVKAGNILLSEGLKLDGFSASIMAPANSFVGT 184
QY 186 PYMAPEVILLAMDEGQYDGVVSGITCIELAEKRPLENNAMSAHYHIAQNESPAL 245
Db 185 PFMMAPEVILLAMDEGQYDGVVSGITCIELAEKRPLENNAMSAHYHIAQNESPAL 244
QY 246 -----QSGHSEYFRNFVDSCLKIPDRPTSE 273
Db 245 SPIDTSEQPEWSLEFVQFLDKLRPAERMSAE 278

RESULT 4
US-09-393-569-2
; Sequence 2, Application US/09393569
; Patent No. 6277979
; GENERAL INFORMATION:
; APPLICANT: BINGHAM, SHARON
; APPLICANT: CASE, PATRICK
; APPLICANT: LAWSON, SALLY NEALE
; APPLICANT: NEWTON, RICHARD ANTHONY
; APPLICANT: PIERCE, VALERIE
; APPLICANT: RAUSCH, OLIVER LARS
; APPLICANT: RAYAL, PRAVIN
; APPLICANT: REITH, ALASTAIR DAVID
; APPLICANT: SANGER, GARETH JOHN
; TITLE OF INVENTION: NEW USE
; FILE REFERENCE: P32261
; CURRENT APPLICATION NUMBER: US/09/393,569
; CURRENT FILING DATE: 1999-09-10
; EARLIER APPLICATION NUMBER: GB 9907261.3
; EARLIER FILING DATE: 1999-03-29
; EARLIER APPLICATION NUMBER: GB 9819779.1
; EARLIER FILING DATE: 1998-09-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1360
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-393-569-2

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Query Match 13.9%; Score 717; DB 4; Length 1360;
Best Local Similarity 26.2%; Pred. No. 2.6e-39;
Matches 272; Conservative 158; Mismatches 372; Indels 238; Gaps 45;

QY 1 MPAGRAGSLKDDVAELFFKDDPEKLFSDLRREIGHGSGFAGVYFARDVNRNSVVAIKKMS 60
Db 1 MADSPARSDELDELDSLAL--RDPAGIFELVELVNGCTGYQVYKGRHVYKGLAIKIVMD 57

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[illegible]

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1 GENERAL INFORMATION:
2 APPLICANT: Au-Young, Janice
3 APPLICANT: Guegler, Karl J.
4 APPLICANT: Hawkins, Phillip R.
5 TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
6 NUMBER OF SEQUENCES: 9
7 CORRESPONDENCE ADDRESS:
8 ADDRESSEE: Incyte Pharmaceuticals, Inc.
9 STREET: 3174 Porter Drive
10 CITY: Palo Alto
11 STATE: CA
12 COUNTRY: U.S.
13 ZIP: 94304
14
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: Diskette
17 COMPUTER: IBM Compatible
18 OPERATING SYSTEM: DOS
19 SOFTWARE: FASTSEQ Version 1.5
20
21 CURRENT APPLICATION DATA:
22 APPLICATION NUMBER: US/08/712,709
23
24 FILING DATE: Filed Herewith
25 ATTORNEY/AGENT INFORMATION:
26 NAME: Billings, Lucy J
27 REGISTRATION NUMBER: 36,749
28 REFERENCE/DOCKET NUMBER: PF-0118 US
29 TELECOMMUNICATION INFORMATION:
30 TELEPHONE: 415-855-0555
31 TELEFAX: 415-845-4166
32 INFORMATION FOR SEQ ID NO: 8:
33 SEQUENCE CHARACTERISTICS:
34 LENGTH: 487 amino acids
35 TYPE: amino acid
36 STRANDEDNESS: single
37 TOPOLOGY: linear
38 MOLECULE TYPE: peptide
39 IMMEDIATE SOURCE:
40 LIBRARY: GenBank
41 CLONE: 1117791
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43 US-08-712-709-8
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Db 399 FEQKEKENQJNSFGKSV-----PGPLK-----NSSDWK----- 426  
QY 462 CRRNDHPTATIRTSLSVSRQIOEHEDSALREOLSGYKRM-----ROKOKOLLAESRLRG 517  
Db 427 -----IPQGDYEFELKSWTVEDLQKRLALDPAMEQ 457  
QY 518 EREHSGRLQRELEAORAGFGTEAEKRLARRHQ 549  
Db 458 EIEE-----IRQKYOSKROPILDAIEAKRRQO 485

RESULT 6  
US-09-111-444-8  
Sequence 8, Application US/09111444  
Patent No. 6045792  
GENERAL INFORMATION:  
APPLICANT: Au-Young, Janice  
APPLICANT: Guegler, Karl J.  
APPLICANT: Hawkins, Phillip R.  
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/111,444  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/712,709  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0118 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 487 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY: Genbank  
CLONE: 1117791  
US-09-111-444-8

Query Match 11.9%; Score 614; DB 3; Length 487;  
Best Local Similarity 29.5%; Pred. No. 4.8e-33;  
Matches 169; Conservative 87; Mismatches 192; Indels 124; Gaps 14;

QY 10 LKDDPALEFFKDD-----PEKLSFLREIGHSGFGAVYFARDVNSEVAIKRMSYSG 63  
Db 6 LRNDPRROLKLKEDSLTKQPEEFVLEKLGESYSYVKAHKETGQIVAIKQVPPV-- 63  
QY 64 KQSEKMODIKKEVRELOKLRHPTIOYRGCYLREHTAMLVMEYC-LGASADLLEVHKRP 122  
Db 64 ---ESDLQETIKETSTWQCDSPHVAVYGSYFKNLDMVMEYCGAGSVSDIIRLNKT 120  
QY 123 LOEVEIAAVHTGALOGIAYLHSHNMIRDVKAGNIILSEGLVTLGDFGSA----SIMAP 178

Db 121 LTEDETATILQSTLKGLELHYFMKRIHRDIKAGNILLNTEGHAKLADFGVAGOLDTPTMAK 180  
QY 179 ANSVGCTPYMAPEVILLAMEGOTDGKVDVWSIGITCIELAEKKRPPLFNNMANSALYHA 238  
Db 181 RNTVIGTFPMWAVEVI---OEIGNCVADIWISLGTIAIEMAEKRRPADIHPRALFMP 237  
QY 239 QNESPALOSGH-WSEYFRNRVDSLOKIPDRPTSEVLLNHRFLRREPTVIMDLQRT 297  
Db 238 TNPPTTRKRELMSDNTDTPVKQCLVSPQOKATATOLLHPYRSKAGVSIIRDLINEA 297  
QY 298 KDAVRELDNLQYRKMKILFOEAPNGPAGAEPEEEBAEPYMHRA----- 342  
Db 298 MDVKLRQESQOREMDQ-----DDEENSEDEMDSGTWAVRVDGEMGTAVASTMT 348  
QY 343 -GILTLESLSHVSPTSMSISASSQSSVNSLADSDNEEEDEEEDEEEDEECPESREM 401  
Db 349 DGANTMLEHDDTLR-----SOLGTWVINAEDDEEGTKMRREDTQPAKPSLEY 398  
QY 402 AMQGEHTVTSHSIIHRLPGSDNLVDPPYQPEMPGPIOPAPAPTSTSSSARRRAY 461  
Db 399 FEQKEKENQJNSFGKSV-----PGPLK-----NSSDWK----- 426  
QY 462 CRRNDHPTATIRTSLSVSRQIOEHEDSALREOLSGYKRM-----ROKOKOLLAESRLRG 517  
Db 427 -----IPQGDYEFELKSWTVEDLQKRLALDPAMEQ 457  
QY 518 EREHSGRLQRELEAORAGFGTEAEKRLARRHQ 549  
Db 458 EIEE-----IRQKYOSKROPILDAIEAKRRQO 485

RESULT 7  
US-09-541-228-8  
Sequence 8, Application US/09541228  
Patent No. 6232077  
GENERAL INFORMATION:  
APPLICANT: Au-Young, Janice  
APPLICANT: Guegler, Karl J.  
APPLICANT: Hawkins, Phillip R.  
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/541,228  
FILING DATE:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/712,709  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0118 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 487 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide

IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 1117791  
US-09-541-228-8

Query Match 11.9%; Score 614; DB 4; Length 487;  
Best Local Similarity 29.5%; Pred. No. 4.8e-33;  
Matches 169; Conservative 87; Mismatches 192; Indels 124; Gaps 14;

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10 LKPDVALEFFKDD-----PEKLFSDLRIGHSGGAYVFARDVNSEVVAIKKMSYSYG 63
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
   6 LKPPKRLKLDLDESLTKOPPEEVDLEKLGSGSYKAIHKETGQVATKQV-- 63
QY 64 KQSNKMODIKREVLQKLRHNTQYRCGYLREHTAMLVMEYC-LGSASDLELVHKRP 122
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
   64 ---ESDLOEIKRISIMQCDSPHVKKYGSYFKNTDLMVMEYCGASVSDIIRLNK 120
QY 123 LOEVEIAAYTHGLOGIATYHSHNMTHRDYKANNILSEFGLVKLDFGSA----S 178
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
   121 LTEDETATITQSTLKGLEYLHFRKRIHDKIKAGNILLNTEGHAKLADFGVAG 180
QY 179 ANSFVGTPTWMADEVILLAMDEGQYDGKVDVWSLGTICIELAEKRPPLFN 238
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
   181 RNTVIGTFPMMAPEVI---QELGYNCAVDIWSIGITAIEMAEKRRYADIHPR 237
QY 239 QNESPALQSGH-WSEYFRNFVDSCLKIPQDRPTSEVLKHFVLRPRPTVIM 297
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
   238 TNPPPTFRKPELMSDNFTDFVKQCLVSPQORATATQQLQHPREBSAKGV 297
QY 298 KDAVRELDNIQYKMKKILFQEARPNFGAARPEEEEAERYMRA----- 342
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
   298 MDVKLRQESQOQEMDQ-----DDEENSEDEMDSGTAVRAVDEMGTV 348
QY 343 -GTLTLESLSHVSYSMSISASSSVNSIADASDNEEEEEEEEEEEEEEP 401
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
   349 DGNMTIAEHDDITP-----SOLGTVITAEDEBEEGTKKRDETMQPKP 398
QY 402 AMMOGEHVTSHSSIIHRLPGSDNLYDPQPEMTPGLPPADPTSSSSARR 461
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
   399 FEQEKENQINSRGSV-----PGLK-----NSSDMK----- 426
QY 462 CRRRDFATIRTSLSVSRQIHEHDSALREQLSGYKRM-----RQ 517
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
   427 -----IPQGDYEFLLKSWTEVDLQKRLALLADPM 457
QY 518 EREHSGRLQRELEAORAGFGTEAKLARRHQ 549
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
   458 EIEE-----IRQYQSKRPILDAIEAKKRQ 485
Db
```

RESULT 8  
US-09-211-930-5  
Sequence 5, Application us/09211930  
Patent No. 5962265  
GENERAL INFORMATION:  
APPLICANT: Tyrell E. No. 5962265tis  
APPLICANT: William Craig Moore  
APPLICANT: David Shay Silberstein  
TITLE OF INVENTION: HUMAN SIGNAL TRANSDUCTION  
FILE REFERENCE: PHM 70296  
CURRENT APPLICATION NUMBER: US/09/211,930  
EARLIER FILING DATE: 1998-12-15  
EARLIER APPLICATION NUMBER: GB 9726851.0  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 5  
LENGTH: 431  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-211-930-5

Query Match 11.6%; Score 594; DB 2; Length 431;  
Best Local Similarity 45.8%; Pred. No. 8.6e-32;  
Matches 130; Conservative 48; Mismatches 92; Indels 14; Gaps 7;

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21 KDDPEKLFSDLRIGHSGGAYVFARDVNSEVVAIKKMSYSYGKQSNKMODIK 80
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
   17 KADPEELFTKLEIKGSGEYFKGIDNRTQKVAAIKITDL--EEADEIEDIQ 74
QY 81 OKLRHNTQYRCGYLREHTAMLVMEYC-LGSASDLELVHKRPLOEVEIAAY 139
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
   75 SQCDSPYVTKYKGYSLKDTKMLIMEYLGGSALDLE--PGLDETQATITRE 132
QY 140 AYLSHNMTHRDYKANNILSEFGLVKLDFGSAIIMADA---NSFVGTPT 195
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
   133 DYLSSEKTIHRDIKANVILSEHGEVKLADFGVAGQLTDTQIKRNTFVGT 191
QY 196 AMDEGQYDGKVDVWSLGTICIELAEKRPPLFNMMASALYHIAQNSP 255
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
   192 --KQSAVDSKADIWSLGTITAIELARGEPPHSELHPKVLFLLPKNPP 248
QY 256 NFVDSCLKIPQDRPTSEVLKHFVLRPRPT-VIMDLIQRK 298
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
   249 EFVEACLNKPEPSRPTAKELKKHFIIRNAKKTSTYLETIDRYK 292
Db
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RESULT 9  
US-09-340-993-5  
Sequence 5, Application us/09340993  
Patent No. 6034228  
GENERAL INFORMATION:  
APPLICANT: Tyrell E. No. 6034228tis  
APPLICANT: William Craig Moore  
APPLICANT: David Shay Silberstein  
TITLE OF INVENTION: HUMAN SIGNAL TRANSDUCTION SERINE/THREONINE KINASE  
FILE REFERENCE: PHM 70296.N1  
CURRENT APPLICATION NUMBER: US/09/340,993  
CURRENT FILING DATE: 1999-06-25  
EARLIER APPLICATION NUMBER: GB 9726851.0 & US 09/211,930  
EARLIER FILING DATE: 1997-12-19 & 1998-12-15  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 5  
LENGTH: 431  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-340-993-5

Query Match 11.6%; Score 594; DB 3; Length 431;  
Best Local Similarity 45.8%; Pred. No. 8.6e-32;  
Matches 130; Conservative 48; Mismatches 92; Indels 14; Gaps 7;

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21 KDDPEKLFSDLRIGHSGGAYVFARDVNSEVVAIKKMSYSYGKQSNKMODIK 80
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
   17 KADPEELFTKLEIKGSGEYFKGIDNRTQKVAAIKITDL--EEADEIEDIQ 74
QY 81 OKLRHNTQYRCGYLREHTAMLVMEYC-LGSASDLELVHKRPLOEVEIAAY 139
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
   75 SQCDSPYVTKYKGYSLKDTKMLIMEYLGGSALDLE--PGLDETQATITRE 132
QY 140 AYLSHNMTHRDYKANNILSEFGLVKLDFGSAIIMADA---NSFVGTPT 195
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
   133 DYLSSEKTIHRDIKANVILSEHGEVKLADFGVAGQLTDTQIKRNTFVGT 191
QY 196 AMDEGQYDGKVDVWSLGTICIELAEKRPPLFNMMASALYHIAQNSP 255
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
   192 --KQSAVDSKADIWSLGTITAIELARGEPPHSELHPKVLFLLPKNPP 248
QY 256 NFVDSCLKIPQDRPTSEVLKHFVLRPRPT-VIMDLIQRK 298
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
   249 EFVEACLNKPEPSRPTAKELKKHFIIRNAKKTSTYLETIDRYK 292
Db
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RESULT 10

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US-09-152-406-3
: Sequence 3, Application US/09152406
: Patent No. 6265560
: GENERAL INFORMATION:
: APPLICANT: William Craig Moore
: APPLICANT: Tyrell E. No. 6265560r1s
: APPLICANT: David Shay Silberstein
: TITLE OF INVENTION: HUMAN STRE20-LIKE STRESS ACTIVATED
: TITLE OF INVENTION: SERINE/THREONINE KINASE
: FILE REFERENCE: PHM 70272
: CURRENT APPLICATION NUMBER: US/09/152.406
: CURRENT FILING DATE: 1998-09-14
: EARLIER APPLICATION NUMBER: 9719920.2
: EARLIER FILING DATE: 1997-09-19
: NUMBER OF SEQ ID NOS: 9
: SOFTWARE: FASTSEQ for Windows Version 3.0
: SEQ ID NO 3
: LENGTH: 431
: TYPE: PR1
: ORGANISM: Homo Sapiens
US-09-152-406-3

```

Query Match 11.6%; Score 594; DB 4; Length 431;  
Best Local Similarity 45.8%; Pred. No. 8.6e-32;  
Matches 130; Conservative 48; Mismatches 92; Indels 14; Gaps 7;

Qy	21	KDDEKLESDLEIREIGHGSEGVAVYFARVARNSEVAIAIKMSYSGSGSEKKODIKEYRFL	80
Db	17	KADPELEFLTKLEIKGSGSEGVFKGIDNRQKVAIKITDL--EADAEDEHDIQOETTVL	74
Qy	81	QKLRHPNTIQYRGCLREHTAMLYMEYC-IGSASDILLEHKKPLQVEIAVAYTHGALQGL	139
Db	75	SQCSPPVTKYKYGSLKDTKMTIMELYGGGSADLLE--PGPLDFQATILNELIKGL	132
Qy	140	AYLSHNMTIHRDVAAGNLTLEPGLVKIGDGSASIMAPA---NSFVGPAPYMAPEVIL	135
Db	133	DYLHSEKTIHMDIKAAVNLSEHEEYVLADPGVAGQLTDPOIKNTYTVGPIEFMAAPYIT-	120
Qy	196	AMDEQYDGVKDVVMSLGITICIELAEKRPPLFNMMAMGALYHIAONESPALQSGHSEYFR	255
Db	192	--KQASYSKADIWSLGTITAEIELARGEPPHSELHPMKVFLIPKNNPPTLE-GNYSPLK	248
Qy	256	NFVDSCLQIKPDQRPSTSVLLKHFVLEREPPY-VIMDLIQRTK	258
Db	249	EEVEACLNKKESEPPYAKELLKHFILIRNAKTSYUVELLIDRYK	292

```

RESULT 11
US-09-468-442-5
? Sequence 5, Application US/09468442
? Patent No. 6300098
? GENERAL INFORMATION:
? APPLICANT: Tyrell E. No. 6300098-ris
? APPLICANT: William Craig Moore
? APPLICANT: David Shay Silberstein
? TITLE OF INVENTION: HUMAN SIGNAL TRANSDUCTION SERINE/THREONINE KINASE
? FILE REFERENCE: PHM. 70296. N1
? CURRENT APPLICATION NUMBER: US/09/468,442
? CURRENT FILING DATE: 1999-12-21
? EARLIER APPLICATION NUMBER: US 09/340,993
? EARLIER FILING DATE: 1999-06-25
? EARLIER APPLICATION NUMBER: GB 9726851.0
? EARLIER FILING DATE: 1997-12-19
? EARLIER APPLICATION NUMBER: US 09/211,930
? EARLIER FILING DATE: 1998-12-15
? NUMBER OF SEQ ID NOS: 14
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 5
? LENGTH: 431
? TYPE: PR1
? ORGANISM: Homo sapiens
US-09-468-442-5

```

Query Match	11.6%	Score 594;	DB 4;	Length 431;
Best Local Similarity	45.8%;	Pred. No. 8.6e-32;		
Matches 130;	Conservative 48;	Mismatches 92;	Indels 14;	Gaps 7;

0y	21	KDDEKFEESDLREIGHGSGFGVAVYARVURNSEVAIIKMSYSGOSNEKKODIIKEYRFL	80
	17	KADPEELFTKLEIKGSGFGEVFKGIDNRQKVAIKIIDL--BEADELEJEDIQOETTVL	74
0y	81	OKLRHPNTIQYRGCLREHTAMLYMEYC-LGSASDLEHVRKPLQVEVIAAVTHGALQGL	139
Dd	75	SQCSPPYTKYGGSLKDPKTLMIIMEYLGSGSADLDE--PGPLDEFQATILREILKGL	132
0y	140	AYLHSHNMHHVDKAGNLTLESPGVKRGDGSGASIMAPA----NSPVGAPYMAPEVIL	135
Dd	133	DYLSEKKIHHDIRANVYLSHEHEVKLADFGVAGQLTDPQIKRNTYVGVIPFWMAPEVY-	191
0y	196	AMDEGQYDGKVDVMSLTGTCIELAEKRPPLFNMMAMSLYHIAONESPALOSGHMSEYFR	255
Dd	192	--KQASVDSKADIMSLGTATLELRGEPHSELHPMKVLFILPKRNPDLTE-GWYSKPLK	248
0y	256	NFYVSCLOKIQODRPTSEVLLKHFVLEREPPY-VINDLIQRTK	298
Dd	249	EVEVACLNNKESPEFRTAKELLKHFILIRNAKRTYVLELLEIDRYK	292

RESULT 12  
US-08-852-743-2

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QY 354 VPSMSISASSQSSSVNSLADASDNEEEEEEE-----EEEE-----EEGPPSREM 401  
 Db 345 -PADAVKRPQRSQCLSTLVRPVPGELKEKHKGSGSVGALFELENNFSLAEESCPIGSDX 403  
 QY 402 AMM 404  
 Db 404 LMV 406

RESULT 15  
 US-09-185-370-2  
 ; Sequence 2, Application US/09185370  
 ; Patent No. 6093560  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Force, Thomas  
 ; APPLICANT: Kyriakis, John M.  
 ; APPLICANT: Pombo, Celia M.  
 ; APPLICANT: Bonventure, Joseph  
 ; TITLE OF INVENTION: SOK-1 AND METHODS OF USE  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Fish & Richardson, P.C.  
 ; STREET: 225 Franklin Street  
 ; CITY: Boston  
 ; STATE: MA  
 ; COUNTRY: US  
 ; ZIP: 02110-2804  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: Windows95  
 ; SOFTWARE: FASTSEQ for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/185,370  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/852,743  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Fraser, Janis K.  
 ; REGISTRATION NUMBER: 34,819  
 ; REFERENCE/DOCKET NUMBER: 00786/327001  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 617/542-5070  
 ; TELEFAX: 617/542-8906  
 ; TELEX: 200154  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 426 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; FRAGMENT TYPE: internal  
 ; US-09-185-370-2

Query Match 11.5%; Score 592; DB 3; Length 426;

Best Local Similarity 36.4%; Pred. No. 1.2e-31;  
 Matches 154; Conservative 69; Mismatches 128; Indels 72; Gaps 16;

QY 23 DPELFSDLRIGHSFGAYFYFADVNSSEVVAIKKMSYSGKOSNEKMODIKKEVRFLOK 82  
 Db 15 DPELFKLRIGKSGEYKGDNHTKEVVAIKIIDL--EEADEIEDIOCEITVLSQ 72  
 QY 83 LRHPTIQYRGCYLREHTAWLVMEYC-LGSASDLLEVHKKPLQEVETAAVTHGALQGLAY 141  
 Db 73 CDSPIYTRFYGSYLKSKLWIMEYLGGSALDLK--PGPLEETVYATILREIKGLDY 130  
 QY 142 LHSNMTHRDYKACNILLSEPGVLYKLGDFGSASIMAPA---NSFVGTPTWMAPEVILAM 197  
 Db 131 LHSRKRTHRIDKANVILLSQGVKPLADFGVAGQLTDTQIKRNTFVGTPTWMAPEVI--- 187  
 QY 198 DEGOYDKVWVSLGICIELAEKRPPLFMNMAVSALYHTAQNPSPALQSGHWSEYFRNF 257

Db 188 KOSAYDFKADIVSLGITAIELAKGEPNSDLHPMRVFLIPKNSPPTLEGQH-SKPFKEF 246  
 QY 258 VDSCLQKIPQDREPTSVLLKHKREVLK-ERPPYIMDLIORTKQAVELNLOYRKMKKTL 316  
 Db 247 VEACLNKDDPFRPTAKELIKHKFTTYTKTSFTLELDR-----YKRWKS-- 292  
 QY 317 FORAPNGPAAEAPEEEE--EAE-----PY--MHRAGTLTSLSSHS 353  
 Db 293 -----EGHGEESSESDSDIDGEADGEGPIMTFPTTIRSPHSKLHG--TALHSQK 344  
 QY 354 VPSMSISASSQSSSVNSLADASDNEEEEEEE-----EEEE-----EEGPPSREM 401  
 Db 345 -PADAVKRPQRSQCLSTLVRPVPGELKEKHKGSGSVGALFELENNFSLAEESCPIGSDX 403  
 QY 402 AMM 404  
 Db 404 LMV 406

Search completed: November 22, 2002, 12:28:02  
 Job time : 28.096 secs

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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 22, 2002, 12:18:00 : Search time 60.573 Seconds  
(without alignments)  
2164.436 Million cell updates/sec

Title: US-09-686-346A-4

Perfect score: 5140

Sequence: 1 MPAGGRAGSLMDPDVALLEFF.....LLPLPLRWRWLAGSTAGP 993

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

A\_Geneseq\_101002:\*

- 1: /SID2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:\*
- 2: /SID2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*
- 3: /SID2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*
- 4: /SID2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:\*
- 5: /SID2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:\*
- 6: /SID2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:\*
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- 22: /SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*
- 23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	5133	99.9	993	20	AAV49897
2	4676	91.0	1235	21	AAAB41663
3	3769.5	73.3	1049	22	AAE04366
4	3728	72.5	758	20	AAW97677
5	3530	68.7	1062	21	AAAB40294
6	2812.5	54.7	1001	20	AA155942
7	2812.5	54.7	1001	23	AAAB97326
8	2805.5	54.6	1001	20	AAV49896
9	2743	53.4	748	20	AAV55938
10	2440.5	47.5	898	20	AAW97676

11	2437.5	47.4	898	21	AAV44244
12	2432.5	47.3	898	20	AAV55936
13	2408	46.8	899	21	AAAB4191
14	1841.5	35.8	1039	22	ABE69116
15	1778.5	34.6	786	20	AAV55937
16	1416.5	27.6	982	20	AAV55955
17	1413	27.5	398	22	AAV55955
18	1337.5	26.0	323	22	AAAB87114
19	1119	21.8	265	22	AAU87435
20	1119	21.8	265	22	AAU17256
21	816.5	15.9	363	22	AAW90795
22	777	15.1	438	22	AAV78656
23	765.5	14.9	453	22	AAW25915
24	740	14.4	256	21	AAAB4388
25	735.5	14.3	1306	22	AAAB68218
26	723	14.1	1277	22	AAAB68220
27	722.5	14.1	1298	22	AAAB68222
28	721	14.0	1385	22	AAW79405
29	717	13.9	1360	21	AAV85263
30	717	13.9	1360	22	AAV50059
31	709	13.8	1353	22	AAAB68219
32	708.5	13.8	1332	22	AAAB68217
33	701	13.6	1269	22	AAAB68223
34	698.5	13.6	1339	22	AAW78421
35	696	13.5	1239	20	AAV55931
36	695	13.5	968	20	AAV55966
37	692.5	13.5	911	20	AAV55957
38	692.5	13.5	1135	21	AAV68784
39	692	13.5	1165	22	ABG17470
40	691.5	13.5	1324	22	AAAB68221
41	682	13.3	912	22	AAV55939
42	679.5	13.2	1212	20	AAE04368
43	676	13.2	1297	20	AAE55932
44	673.5	13.1	824	23	AAE20277
45	672	13.1	1165	21	AAAB43016

#### ALIGNMENTS

RESULT 1  
ID AAV49897 standard: Protein: 993 AA.  
AAV49897;  
AC AAV49897;  
XX  
DT 27-JAN-2000 (first entry)  
XX  
XX  
DE Rat TAO2 kinase.  
XX  
XX  
KW TAO1; TAO2; MEK3; mitogen activated protein kinase; phosphorylation;  
KW p38; protein kinase; cancer; inflammation; autoimmune disease;  
KW neurodegeneration; insulin-resistant diabetes; metabolic disorder;  
KW neurodegeneration; MAP kinase; MAP/ERK kinase.  
XX  
OS Rattus sp.  
XX  
XX WO953076-A1.  
XX  
XX PD 21-OCT-1999.  
XX  
XX PF 14-APR-1999; 99WO-US08165.  
XX  
XX PR 14-APR-1998; 98US-0060410.  
XX  
XX PA (TEXA ) UNIV TEXAS SYSTEM.  
XX  
XX PI Cobb M, Hutchinson M, Chen Z, Berman K;  
XX  
XX WPI; 1999-633831/54.  
XX  
XX DR N-PDB; AA232436.  
XX  
XX PT New polypeptides that phosphorylate kinase, used to screen for

PT modulators for treating e.g. cancer or inflammation -  
 XX Claim 7: Page 84-87; 95pp; English.  
 XX  
 CC The present sequence represents rat TAO2 protein kinase, which is capable  
 CC of phosphorylating MEK3 (a MAP/ERK kinase). TAO kinases, and related  
 CC polypeptides, are used to screen for modulators of stress-responsive  
 CC mitogen activated protein (MAP) kinase pathways. These modulators are  
 CC potentially useful for treating or preventing: (1) inflammation,  
 CC autoimmune disease, cancer and degeneration (inhibitors of  
 CC phosphorylation); or (2) insulin-resistant diabetes, metabolic disorders  
 CC and neurodegeneration (enhancers of phosphorylation). TAO kinases are  
 CC also used to raise specific antibodies, useful therapeutically as  
 CC modulators and as immunosassay reagents for detecting TAO kinases.  
 CC TAO kinase polynucleotides can be used: (a) for recombinant expression  
 CC of TAO kinases; and (b) in the form of fragments, for detecting TAO  
 CC kinase polynucleotides in standard hybridisation and amplification  
 CC tests. TAO kinases are highly specific for MEK3.  
 XX  
 XX Sequence 993 AA:

Query Match 99.9%; Score 5133; DB 20; Length 993;  
 Best Local Similarity 99.9%; Pred. No. 3.8e-318;  
 Matches 992: Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPAGGAGSLKDPVAELFFKDDPEKLFSDLRIGHSGFAYFARDVARNSEVAIKKMS 60  
 DB 1 MPAGGAGSLKDPVAELFFKDDPEKLFSDLRIGHSGFAYFARDVARNSEVAIKKMS 60  
 QY 61 YGKOSNEKMOIIEKVRLOKLRHNTQYRGCYLREHTAMLYMEYCGSASDLEVRK 120  
 DB 61 YGKOSNEKMOIIEKVRLOKLRHNTQYRGCYLREHTAMLYMEYCGSASDLEVRK 120  
 QY 121 KPLQVEIAVTHGALOGALAYLHSHNMIRDVACNIISEPGLYLVGFGSASIMAPAN 180  
 DB 121 KPLQVEIAVTHGALOGALAYLHSHNMIRDVACNIISEPGLYLVGFGSASIMAPAN 180  
 QY 181 SFVGTPIYMAPEVILAMDEGYDGVVSLGTCIELAEKRRPPLFNMAAMSAHYHIAON 240  
 DB 181 SFVGTPIYMAPEVILAMDEGYDGVVSLGTCIELAEKRRPPLFNMAAMSAHYHIAON 240  
 QY 241 ESPALOSGMSYFRNFVNSCLQKIPQDRPTSEVLKHFVLRERPPYIMLIQCTKA 300  
 DB 241 ESPALOSGMSYFRNFVNSCLQKIPQDRPTSEVLKHFVLRERPPYIMLIQCTKA 300  
 QY 301 VVELDLQYRKMKKILFOEAPNGGAEAPDEEAEAPYHNRAGTILSLSSHSVPMSIS 360  
 DB 301 VVELDLQYRKMKKILFOEAPNGGAEAPDEEAEAPYHNRAGTILSLSSHSVPMSIS 360  
 QY 361 ASSOSSVNSLADASDNEEEEEEEEGEPESREMAAMOGEGHTVSSHIIHR 420  
 DB 361 ASSOSSVNSLADASDNEEEEEEEEGEPESREMAAMOGEGHTVSSHIIHR 420  
 QY 421 LFGSDLYDDPYOPEMTPEPLPPAPPTSTSSSARRAYCRNRHFTITASLYVSO 480  
 DB 421 LFGSDLYDDPYOPEMTPEPLPPAPPTSTSSSARRAYCRNRHFTITASLYVSO 480  
 QY 481 IOEHEDSALRLQSGYKMRROHOKOLLALSRLGEEESGRLQRELEAORAGFGE 540  
 DB 481 IOEHEDSALRLQSGYKMRROHOKOLLALSRLGEEESGRLQRELEAORAGFGE 540  
 QY 541 AEKLARRHOAIGEKERAAQAEEERKFOOHILGQKKELALLAEOKRTYKLRKEQLKEEL 600  
 DB 541 AEKLARRHOAIGEKERAAQAEEERKFOOHILGQKKELALLAEOKRTYKLRKEQLKEEL 600  
 QY 601 QENPSTPRKEKAEWILLROKQEOLOQCAEEAGILRRORQYFELQCRQYRKMLARHSID 660  
 DB 601 QENPSTPRKEKAEWILLROKQEOLOQCAEEAGILRRORQYFELQCRQYRKMLARHSID 660  
 QY 661 ODLEREDLKKKOTOKDLECALLLRQHEATRELELRQIAOVORTRAELTLOHOTELGNOL 720  
 DB 661 ODLEREDLKKKOTOKDLECALLLRQHEATRELELRQIAOVORTRAELTLOHOTELGNOL 720

QY 721 EYNKRREDELROKHAQVROQPSLKVRAQOLPMGLPATGALPLSTGTLSEOPCSSSQ 780  
 DB 721 EYNKRREDELROKHAQVROQPSLKVRAQOLPMGLPATGALPLSTGTLSEOPCSSSQ 780  
 QY 781 EAILQORMLGEEEAPEPMIIGKESTTLEPEQORLQDEMKTFSSSPQKHSLYNEEDW 840  
 DB 781 EAILQORMLGEEEAPEPMIIGKESTTLEPEQORLQDEMKTFSSSPQKHSLYNEEDW 840  
 QY 841 DSKEMKESRVSLASQENIIGOEACAMNIMEKHGMLVMEERKLGAVQGPVLTPE 900  
 DB 841 DSKEMKESRVSLASQENIIGOEACAMNIMEKHGMLVMEERKLGAVQGPVLTPE 900  
 QY 901 EEEEEEEGADIGTPRDFGDCPSPDIPPEPPSHLRQYPASQLPGTUSHLGLSFA 960  
 DB 901 EEEEEEEGADIGTPRDFGDCPSPDIPPEPPSHLRQYPASQLPGTUSHLGLSFA 960  
 QY 961 VGSSGGLPLLLLLPLLPAPRWRMLAGSTAGP 993  
 DB 961 VGSSGGLPLLLLLPLLPAPRWRMLAGSTAGP 993

RESULT 2  
 AAB41663  
 ID AAB41663 standard: Protein; 1235 AA.  
 XX  
 XX AAB41663;  
 AC  
 XX  
 DT 08-FEB-2001 (first entry)  
 XX

Human ORF5 ORF1427 polypeptide sequence SEQ ID NO:2854.

Human: open reading frame; ORF; detection; cytosolic; hepatotropic;  
 vunerary; antiporlatic; antiparkinsonian; noctropic; neuroprotective;  
 anticonvulsant; osteopathic; antirheumatic; immunosuppressant; cardiant;  
 immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;  
 hypotensive; dermatological; immunosuppressive; antinflammatory;  
 antiviral; antibacterial; antifungal; antineumatic; antihypoid;  
 antianemic; gene therapy; cancer; proliferative disorder; hypertension;  
 neurodegenerative disorder; osteoarthritis; graft vs host disease;  
 cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;  
 cholesterol ester storage; systemic lupus erythematosus; infection;  
 severe combined immunodeficiency; malaria; autoimmune disorder; asthma;  
 allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;  
 bone damage; cartilage damage; antinflammatory disease; coagulation;  
 thrombosis; contraceptive.

Homo sapiens.

WO200058473-A2.

05-OCT-2000.

31-MAR-2000; 2000WO-US08621.

31-MAR-1999; 9905-0127607.

02-APR-1999; 9905-0127636.

05-APR-1999; 9905-0127728.

30-MAR-2000; 2000US-0540763.

(CURA-) CURAGEN CORP.

Shimkets RA, Leach M;

WPI; 2000-602362/57.

N-PSDB; AAC75872.

Novel nucleic acids and peptides derived from open reading frame X,  
 useful for treating e.g. cancers, proliferative disorders,  
 neurodegenerative disorders and cardiovascular disease -

Claim 11; Page 2092-2095; 5507pp; English.  
 AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,

CC which represent the human ORFX open reading frames 1 to 3161. The ORFX  
 CC sequences have activities such as: cytostatic; hepatotropic; vulnery;   
 CC antiproliferative; antiparkinsonian; nootropic; neuroprotective;   
 CC osteopathic; anticonvulsant; antiarthritic; immunosuppressive;   
 CC immunostimulant; cardiant; thrombolytic; coagulant; vasotrophic;   
 CC antidiabetic; hypotensive; dermatological; immunosuppressive;   
 CC antitumor; antineoplastic; antiviral; antifungal; antihemetic;   
 CC antihypertensive; antianemic. The sequences can be used for determining   
 CC the presence of or predisposition to, or preventing or treating   
 CC pathological conditions associated with an ORFX-associated disorder. The   
 CC nucleic acids can be used to express ORFX proteins in gene therapy   
 CC vectors. The proteins and nucleic acids may be used to treat cancers,   
 CC proliferative disorders, neurodegenerative disorders, osteoarthritis,   
 CC graft vs host disease, cardiovascular disease, diabetes mellitus,   
 CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus   
 CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,   
 CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,   
 CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,   
 CC nocturnal haemoglobinuria, anti-inflammatory disease; to enhance   
 CC coagulation; to inhibit thrombosis; and as a contraceptive.

XX Sequence 1235 AA:

Query Match 91.0%; Score 4676; DB 21; Length 1235;  
 Best Local Similarity 93.0%; Pred. No. 7.7e-289;  
 Matches 913; Conservative 23; Mismatches 40; Indels 6; Gaps 3;

QY 1 MPAGGAGSLKPDVALEFFKDDPEKLFSDLRIGSGGAYFARDVRNSEVAIKMS 60  
 DB 1 MPAGGAGSLKPDVALEFFKDDPEKLFSDLRIGSGGAYFARDVRNSEVAIKMS 60  
 QY 61 YSGKQNEKMODIKRHFVLRHPTIOYRGCTLRHPTAMVMEYICGSASDLLEVHK 120  
 DB 61 YSGKQNEKMODIKRHFVLRHPTIOYRGCTLRHPTAMVMEYICGSASDLLEVHK 120  
 QY 121 KPLQVEIAVTHGALQGLAYLHSHNMHRDVAGNILLSEPLVIGDGFSGASIMAPAN 180  
 DB 121 KPLQVEIAVTHGALQGLAYLHSHNMHRDVAGNILLSEPLVIGDGFSGASIMAPAN 180  
 QY 181 SPVGTYYMAPEVITLAMDQGDYGVWSLGTCTELAEKRPPLFNMAAMSLYHIAON 240  
 DB 181 SPVGTYYMAPEVITLAMDQGDYGVWSLGTCTELAEKRPPLFNMAAMSLYHIAON 240  
 QY 241 ESPALQSGHMFSEFRNFVSCLOKIPDRPTSEVLKHRVLERPPTYMDLIQRTKA 300  
 DB 241 ESPALQSGHMFSEFRNFVSCLOKIPDRPTSEVLKHRVLERPPTYMDLIQRTKA 300  
 QY 301 VRELDMLOYRKMKKILFOEAPNGGAEAEPEEEAEPPYMHRACTILTSLSHVSPTSIS 360  
 DB 301 VRELDMLOYRKMKKILFOEAPNGGAEAEPEEEAEPPYMHRACTILTSLSHVSPTSIS 360  
 QY 361 ASSQSSSVNSLADASNEEEEEEEEEEEEPESREMAAMQGEHTVTSHTSIHR 420  
 DB 361 ASSQSSSVNSLADASNEEEEEEEEEEEEPESREMAAMQGEHTVTSHTSIHR 420  
 QY 421 LRGSDNLVDDPPOEPTPGPLPPAPPTSTSSARRAYCNRHFNATIRASLVSRQ 480  
 DB 421 LRGSDNLVDDPPOEPTPGPLPPAPPTSTSSARRAYCNRHFNATIRASLVSRQ 480  
 QY 481 IOEHEDSALREOLSGYKMRROHQKOLALLESRLGEREHEHGRLORELEAORAGFTE 540  
 DB 481 IOEHEDSALREOLSGYKMRROHQKOLALLESRLGEREHEHGRLORELEAORAGFTE 540  
 QY 541 AEKLIARRHOAIGEKARAAQAEERKFOHITLGOQKELAALEAQRKYKLRKEOLKEEL 600  
 DB 541 AEKLIARRHOAIGEKARAAQAEERKFOHITLGOQKELAALEAQRKYKLRKEOLKEEL 600  
 QY 601 QEMPSTPKREKAMILLRQKQLOQCAEEBAGLLRRQROYFELQCYQYKRMILLASHSD 660  
 DB 601 QEMPSTPKREKAMILLRQKQLOQCAEEBAGLLRRQROYFELQCYQYKRMILLASHSD 660  
 QY 661 ODLLREDLNNKQTKQKDECALLRQHEATRELELROLAQVORTRAELTRLOHTEGNOL 720  
 DB 661 ODLLREDLNNKQTKQKDECALLRQHEATRELELROLAQVORTRAELTRLOHTEGNOL 720

DB 659 ODLLREDLNNKQTKQKDECALLRQHEATRELELROLAQVORTRAELTRLOHTEGNOL 718  
 QY 721 EYKKRREQELROKHAQVQPKSLVVRAGQPMG--LRATAGLPLSTGTLSEBPCCS 778  
 DB 719 EYKKRREQELROKHAQVQPKSLVVRAGQPMG--LRATAGLPLSTGTLSEBPCCS 778  
 QY 779 GQPAVLDDRLMGLGEEAVRERMLTKEGTTLEPEEORILQEEGTSSSPORKRSIVNE 838  
 DB 779 GQPAVLDDRLMGLGEEAVRERMLTKEGTTLEPEEORILQEEGTSSSPORKRSIVNE 838  
 QY 839 DWDISKEMKSRVPSLASERNITGOEAGWNLWEKHEGNLVMKFKLGWVGPLYTPV 898  
 DB 839 DWDISKEMKSRVPSLASERNITGOEAGWNLWEKHEGNLVMKFKLGWVGPLYTPV 898  
 QY 899 PEEDEEEER--GAPIDTPRDPGDCSPDIPPPPSHLRQYRASOLPGLSHGLLAGIS 956  
 DB 899 PEEDEEEER--GAPIDTPRDPGDCSPDIPPPPSHLRQYRASOLPGLSHGLLAGIS 956  
 QY 959 FAVGSSGILLPLLLPLLA 980  
 DB 957 FAVGSSGILLPLLLPLLA 978

RESULT 3  
 AAE04366  
 ID AAE04366 standard; Protein: 1049 AA.

XX AAE04366;  
 XX 04-SEP-2001 (first entry)  
 XX  
 DE Human kinase (PKIN)-7.  
 XX  
 KW Human kinase; PKIN-7; therapy; immune disorder; Addison's disease; AIDS;  
 KW acquired immune deficiency syndrome; growth and developmental disorder;  
 KW arteriosclerosis; mixed connective tissue disease; MCTD; adenocarcinoma;  
 KW leukaemia; cardiovascular disease; myocardial infarction; hypertension;  
 KW lipid disorder; cancer; fatty liver; cholestasis; transgenic animal;  
 KW gene therapy; antiallergic; antiasthmatic; antihypertensive; dermatological;  
 KW antidiabetic; nephrotrophic; antitumor; antitubercular; antihemetic;  
 KW antiproliferative; neuroprotective; cytostatic; hepatotropic; osteopathic;  
 KW vasotropic; antitubercular; anorectic.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FH Domain 28..281  
 FT /note="Eukaryotic protein kinase domain"  
 FT Domain 30..269  
 FT /note="Protein kinase domain"  
 FT Region 147..158  
 FT /note="Protein kinase ST"  
 FT Region 618..777  
 FT /note="Serine/threonine protein kinase TAO1"  
 PN MO200146397-A2.  
 XX  
 PD 28-JUN-2001.  
 XX  
 PF 20-DEC-2000; 2000MO-US35304.  
 XX  
 PR 23-DEC-1999; 99US-0172066.  
 PR 14-JAN-2000; 2000US-0176107.  
 PR 21-JAN-2000; 2000US-0177731.  
 PR 28-JAN-2000; 2000US-0178573.  
 XX  
 PA (INCY-) INCYTE GENOMICS INC.  
 XX Yang J, Baugin MR, Burford N, Au-Young J, Lu DM, Reddy R, Yue H;  
 PI Yao MG, Lal P, Khan FA;  
 XX  
 DR WPI: 2001-418059/44.  
 DR N-PSDB; AAD08640.

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XX Novel human kinase proteins (PKIN) useful for diagnosing, treating,
PT preventing immune disorders, cardiovascular diseases and disorders
PT affecting growth and development associated with abnormal expression of
PT PKIN
XX
XX Claim 1: Page 111-113; 128pp: English.
XX
XX The invention relates to novel human kinase proteins (PKIN) and
CC nucleic acid molecules encoding them. PKIN is useful for identifying
CC compounds that modulates its activity. PKIN cDNA is useful for
CC assessing toxicity of a test compound. PKIN and its cDNA are useful
CC for diagnosis, prevention and treatment of immune disorders such as
CC acquired immune deficiency syndrome (AIDS), Addison's disease, anaemia,
CC adult respiratory distress syndrome, allergies, amyloidosis, psoriasis,
CC autoimmune haemolytic anaemia, autoimmune thyroiditis, multiple
CC sclerosis, asthma, osteoarthritis, osteoporosis, rheumatoid arthritis,
CC ulcerative colitis and diabetes mellitus; growth and developmental
CC disorders such as actinic keratosis, arteriosclerosis, atherosclerosis,
CC bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD),
CC and myelofibrosis; cancers such as adenocarcinoma and leukaemia,
CC cardiovascular diseases such as myocardial infarction and hypertension;
CC and lipid disorders such as fatty liver and cholestasis. PKIN cDNA is
CC useful to detect upstream sequences such as promoters and regulatory
CC elements, for creating knock in or knock out in humanised animals or
CC transgenic animals to model human disease and for somatic or germline
CC gene therapy for treating the above mentioned disorders. The present
CC sequence is human kinase (PKIN)-7.
XX
XX Sequence 1049 AA:
XX
XX Query Match 73.3%; Score 3769.5; DB 22; Length 1049;
XX Best Local Similarity 78.9%; Pred. No. 2.9e-231;
XX Matches 778; Conservative 36; Mismatches 112; Indels 60; Gaps 14;
XX
QY 1 MPAGGAGSLKDDVALEFFKDPPEKLFSDLRITGSGFAYFANDVNSEVAIAIKMS 60
DB 1 MPAGGAGSLKDDVALEFFKDPPEKLFSDLRITGSGFAYFANDVNSEVAIAIKMS 60
QY 61 YSGKQNEKMODIKREVFLOKLRHNTIOYRGCTLRHNTAMVMEYCSASDILEVHK 120
DB 61 YSGKQNEKMODIKREVFLOKLRHNTIOYRGCTLRHNTAMVMEYCSASDILEVHK 120
QY 121 KPLQVEIAVTHGALOGALYLHSHNMIRDVAGNILLSEPGIVKIGFGSASIMAPAN 180
DB 121 KPLQVEIAVTHGALOGALYLHSHNMIRDVAGNILLSEPGIVKIGFGSASIMAPAN 180
QY 181 SFVGTYYMAPEYIILAMDQGYDKVWVSLGITCIELERKRPPLFNMAAMSLYHIAON 240
DB 181 SFVGTYYMAPEYIILAMDQGYDKVWVSLGITCIELERKRPPLFNMAAMSLYHIAON 240
QY 241 ESPALQSGHMFSEFRNFVDSCLQIKIPDRPTSEVLKHNRFVLERPPTYIMDIQOTKA 300
DB 241 ESPALQSGHMFSEFRNFVDSCLQIKIPDRPTSEVLKHNRFVLERPPTYIMDIQOTKA 300
QY 301 VRELDMLOYRKMKILFOEAPNGGADEEEDAEPEYMHRAAGTLTSLSSHSVPMSIS 360
DB 301 VRELDMLOYRKMKILFOEAPNGGADEEEDAEPEYMHRAAGTLTSLSSHSVPMSIS 360
QY 361 ASSQSSSVNSLADASDNEEEEEEEEEEEEPESREMAAMOGCHTIVTSHSIIHR 420
DB 361 ASSQSSSVNSLADASDNEEEEEEEEEEEEPESREMAAMOGCHTIVTSHSIIHR 420
QY 421 LRGSDMLYDDPYQPEMTPGLOPPAPRPTSTSSSARRAYCANNRHAFITRASLYVHQ 480
DB 421 LRGSDMLYDDPYQPEMTPGLOPPAPRPTSTSSSARRAYCANNRHAFITRASLYVHQ 480
QY 481 IOEHEDSALREOLSGYKMMRROHOKOLALLESRLGEEESHGRLQRELEQORAFGTE 540
DB 479 IOEHEDSALREOLSGYKMMRROHOKOLALLESRLGEEESHGRLQRELEQORAFGTE 538
QY 541 AEKLARRHOALIGEKAARAAQAEERKFOOHIILGOQKELAALEAOKRTYKLRKEQLEEL 600
DB 541 AEKLARRHOALIGEKAARAAQAEERKFOOHIILGOQKELAALEAOKRTYKLRKEQLEEL 600

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DB 539 AEKLARRHOALIGEKAARAAQAEERKFOOHIILGOQKELAALEAOKRTYKLRKEQLEEL 598
QY 601 QENPSTPKREKAWMLRQKEOIQCOAESEAGILRRORQYFELQCHQYRKMLARHSID 660
DB 599 QENPSTPKREKAWMLRQKEOIQCOAESEAGILRRORQYFELQCHQYRKMLARHSID 658
QY 661 ODLLREDLNKKOTQKDIKCALILRQHEATRELEAOLQAVORTRAELTRLOHOTELGNOL 720
DB 659 QDLRLDNLKKQTKQKLECALLILRQHEATRELEAOLQAVORTRAELTRLOHOTELGNOL 718
QY 721 EYKREDELRQKHAQVROQPSKLVKRVAGOLPMGLPATGALGPLSTGLSEE--QPCSS 778
DB 719 EYKREDELRQKHAQVROQPSKLVKRVAGOLPMGLPATGALGPLSTGLSEE--QPCSS 778
QY 779 GOBALIGOMLGEPEEAVPEBMILGKE-----GTLPEDEQRI--LGE 819
DB 779 AOKSKLLKRL--KEQTKRLALILAEQYPOSISEMISALRLDETQEAEPALRQOOLQO 835
QY 820 EMQTFSSSPQK-----HRSIVNEEDMDIS--KEMKESRVPSS--LASOE-----RNI 861
DB 836 EELLMAYQSKIRITRESQHERELRELEQVRLRALLQGVAEELALQOTGSRKIRSL 895
QY 862 IGOEEGANNMEKEKGNLVDMFKLGWV-----QG-FVLIPVPEEEEEEEEGGA--- 911
DB 896 L-ERQAREIEAFDAESMRIGFSSMALGIPAEAAQGYPAAPPAPAPSPRYPVRSQAHWS 954
QY 912 ----PIGTPRDDPGCGSPDIPPEPP 933
DB 955 HGPPPPGMP-PPAWKOPSLAPPGBP 979
XX
XX RESULT 4
XX ID AAM97677 standard: Protein; 758 AA.
XX AC AAM97677:
XX DT 10-MAY-1999 (first entry)
XX DE Human KDS2 protein kinase.
XX KW KDS2: kinase domain related to Ste20; human; serine kinase;
XX KW threonine kinase; protein kinase; signal transduction.
XX OS Homo sapiens.
XX PN W09902699-A1.
XX PD 21-JAN-1999.
XX PF 07-JUL-1998; 98WO-US14231.
XX PR 08-JUL-1997; 97US-0889518.
XX PA (CADU-) CADUS PHARM CORP.
XX PI Johnson GL, Pleiman CM;
XX DR WPT: 1999-120900/10.
XX N-PSDB: AAX07075.
XX
XX New isolated vertebrate kinase - used to develop products for the
XX diagnosis and treatment of disorders involving cellular processes
XX such as signal transduction processes
XX
XX Claim 31: Page 85-88; 100pp: English.
XX
XX This polypeptide comprises human protein kinase KDS2, a novel
XX protein associated with signal transduction. KDS2 has a
XX kinase domain related to that of Ste20 (KDS1 = Kinase Domain
XX related to Ste20). KDS2 cDNA (see AAX07075) was isolated from a
XX human bone marrow cDNA library. A clone (see AAX07074) encoding the
XX highly homologous KDS1 (see AAM97676) was also obtained. Both KDS1

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CC and KDS2 have Glu/Gln-rich regions at their C-terminus (see also  
 CC AAW97678-79) suggesting an alpha-helical structure that may play a  
 CC role in covalently localising these proteins to a specific site  
 CC within the cells, which may be necessary for function. A method  
 CC for producing KDS polypeptides in host cells is provided. Since  
 CC KDS molecules have kinase activity, they are useful as modulating  
 CC agents in regulating a variety of cellular processes such as signal  
 CC transduction pathways. These pathways may regulate cytoskeleton,  
 CC secretion, growth, apoptosis, superoxide generation, and specific  
 CC gene transcription. KDS polypeptides and polynucleotides can be  
 CC used for treating disorders involving aberrant expression of  
 CC mammalian KDS genes. They can also be used for detection,  
 CC diagnosis and drug screening.

xx Sequence 758 AA:

Query Match 72.5%; Score 3728; DB 20; Length 758;  
 Best local Similarity 96.0%; Pred. No. 8.4e-229;  
 Matches 728; Conservative 10; Mismatches 18; Indels 2; Gaps 1;

QY 1 MPAGRAGSLKDPDAVELPFKDDPEKLFSDLRIGSGGAVYFARVRSVYATKKMS 60  
 DB 1 MPAGRAGSLKDPDAVELPFKDDPEKLFSDLRIGSGGAVYFARVRSVYATKKMS 60  
 QY 61 YSGKSNEMKMODIKKVEFLQKLRHPTIQRCYLRHPTAMVMEYCLGASDLEVHK 120  
 DB 61 YSGKSNEMKMODIKKVEFLQKLRHPTIQRCYLRHPTAMVMEYCLGASDLEVHK 120  
 QY 121 KPLQVEIAAVTHGALQGLAYLHSHNMHRDKAGNLLSEPLVYLGDFGSASIMAPAN 180  
 DB 121 KPLQVEIAAVTHGALQGLAYLHSHNMHRDKAGNLLSEPLVYLGDFGSASIMAPAN 180  
 QY 181 SFVGTYYMAAPVYILAMDSEQYDGKVDVMSLGTCTELARKRPPLRNMAASLYHTAQN 240  
 DB 181 SFVGTYYMAAPVYILAMDSEQYDGKVDVMSLGTCTELARKRPPLRNMAASLYHTAQN 240  
 QY 241 ESPALOSGHWSEYFRNFVDSCLKIPQDRPTSVLLKHFVLRERPTVIMDLIQRTKDA 300  
 DB 241 ESPALOSGHWSEYFRNFVDSCLKIPQDRPTSVLLKHFVLRERPTVIMDLIQRTKDA 300  
 QY 301 VRELDMNQYRKMKKILFOEAPNGPGAEAPPEEAEAPYMRAGTLVLSHSHVPSMSIS 360  
 DB 301 VRELDMNQYRKMKKILFOEAPNGPGAEAPPEEAEAPYMRAGTLVLSHSHVPSMSIS 360  
 QY 361 ASSQSSSVNSLADASDN--DEEEEBEEEEEEBEGPESRMMAMQCEHVTSHSSTIHR 420  
 DB 361 ASSQSSSVNSLADASDN--DEEEEBEEEEEEBEGPESRMMAMQCEHVTSHSSTIHR 420  
 QY 421 LPSGDMLYDDPYOPENTPGPLQPPAAPPTSTSSSARRRAYCNRNDFATIRTSLSVSRQ 480  
 DB 421 LPSGDMLYDDPYOPENTPGPLQPPAAPPTSTSSSARRRAYCNRNDFATIRTSLSVSRQ 480  
 QY 481 IOEHEDDSALREOLSGYKMRROHOKOLLALLESRLNGEREHSGLQRELEAQRAGTGE 540  
 DB 481 IOEHEDDSALREOLSGYKMRROHOKOLLALLESRLNGEREHSGLQRELEAQRAGTGE 540  
 QY 541 AEKLARHQAIGKKEARAQAEEERKFOQHTLGOOKKELALLAOKRTYTLRKREQLKEEL 600  
 DB 541 AEKLARHQAIGKKEARAQAEEERKFOQHTLGOOKKELALLAOKRTYTLRKREQLKEEL 600  
 QY 601 QENPSTPKREKAEWLLROKROLOCOAEEBAGLLRRQRYFELQCRQYRKMKLLARSLD 660  
 DB 601 QENPSTPKREKAEWLLROKROLOCOAEEBAGLLRRQRYFELQCRQYRKMKLLARSLD 660  
 QY 661 QDLRLDLNKKQTKQDLECALLRQHEATRELELRQLOAVQRTAELTRLOHOTEIGNQL 720  
 DB 661 QDLRLDLNKKQTKQDLECALLRQHEATRELELRQLOAVQRTAELTRLOHOTEIGNQL 720  
 QY 721 EYKRRROELROKHAANOVRQPKSLVYRAGQLMGLPA 758  
 DB 721 EYKRRROELROKHAANOVRQPKSLVYRAGQLMGLPA 758

RESULT 5  
 AAB40294  
 ID AAB40294 standard; Protein; 1062 AA.  
 AC AAB40294;  
 DT 08-FEB-2001 (first entry)

Human ORFX ORF58 polypeptide sequence SEQ ID NO:116.

Human: open reading frame; ORFX: detection; cytostatic; hepatotropic;  
 KW vulnery; antiproliferative; antiparkinsonian; neurotropic; neuroprotective;  
 KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;  
 KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;  
 KW hypotensive; dermatological; immunosuppressive; antineoplastic;  
 KW antiviral; antibacterial; antitumor; antineoplastic; antihypertensive;  
 KW antineoplastic; gene therapy; cancer; proliferative disorder; hypertension;  
 KW neurodegenerative disorder; osteoarthritis; graft vs host disease;  
 KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;  
 KW cholesterol ester storage; systemic lupus erythematosus; infection;  
 KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;  
 KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;  
 KW bone damage; cartilage damage; antiinflammatory disease; coagulation;  
 KW thrombosis; contraceptive.

OS Homo sapiens.

PN WO200058473-A2.

PD 05-OCT-2000.

PF 31-MAR-2000; 2000NC-US08621.

PR 31-MAR-1999; 9905-0127607.

PR 02-APR-1999; 9905-0127636.

PR 05-APR-1999; 9905-0127728.

PR 30-MAR-2000; 2000US-0540763.

PA (CURA-) CURAGEN CORP.

PI Shinkets RA, Leach M;

DR WPI: 2000-602362/57.

DR N-PSDB; AAC74503.

PS Novel nucleic acids and peptides derived from open reading frame X,

PT useful for treating e.g. cancers, proliferative disorders,

PT neurodegenerative disorders and cardiovascular disease -

Claim 11; Page 481-484; 5507pp; English.

AAC7446 to AAC7606 encode the proteins given in AAB40237 to AAB4397,  
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX  
 CC sequences have activities such as: cytostatic; hepatotropic; vulnery;  
 CC antiproliferative; antiparkinsonian; neurotropic; neuroprotective;  
 CC osteopathic; anticonvulsant; antiarthritic; immunosuppressant;  
 CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;  
 CC antidiabetic; hypotensive; dermatological; immunosuppressive;  
 CC antiinflammatory; antibacterial; antiviral; antifungal; antineoplastic;  
 CC antihypertensive; antineoplastic. The sequences can be used for determining  
 CC the presence of or predisposition to, or preventing or treating  
 CC pathological conditions associated with an ORFX-associated disorder. The  
 CC nucleic acids can be used to express ORFX proteins in gene therapy  
 CC vectors. The proteins and nucleic acids may be used to treat cancers,  
 CC proliferative disorders, neurodegenerative disorders, osteoarthritis,  
 CC graft vs host disease, cardiovascular disease, diabetes mellitus,  
 CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus  
 CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,  
 CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,  
 CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,  
 CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance  
 CC coagulation; to inhibit thrombosis; and as a contraceptive.

SQ	Sequence	1062 AA;
Query Match	68.7%;	Score 3530; DB 21; Length 1062;
Best Local Similarity	90.8%;	Pred No. 5e-216;
Matches	695; Conservative	24; Mismatches 40; Indels 6; Gaps 3;
QY	218 LAERKPPLENNMAMSAHYIAQNESPALOSGHMSEYFRNFVDSCLKIPQDRPTSEVLK 277	
DB	45 VAERKPPLENNMAMSAHYIAQNESPVLOSCHMSEYFRNFVDSCLKIPQDRPTSEVLK 104	
QY	278 HRFVLRERPPYIMDIQRTKDAVRELDMQYRKMKILFOEAPNPGAEAPREEEAPR 337	
DB	105 HRFVLRERPPYIMDIQRTKDAVRELDMQYRKMKILFOEAPNPGAEAPREEEAPR 164	
QY	338 YMHKGTLSLSSSHSVPMSTISASSOSSVNSLADASNEEESEEESEEESEEGPE 397	
DB	165 YMHKGTLSLSSSHSVPMSTISASSOSSVNSLADASN--EESEEESEEESEEGPE 222	
QY	398 SREMMAMQGEHTVTSHSIIHRLPGSDMLYDDPYOPEMTPGPLQPPAAPPTSTSSSAR 457	
DB	223 AREMMAMQGEHTVTSHSIIHRLPGSDMLYDDPYOPEITPSPLOPPAPAPTSTSSAR 282	
QY	458 RRAYCNRDHFATIRTSVLSROIQEHEDSALREOLSGTKRRRQHQOLALBSRLG 517	
DB	283 RRAYCNRDHFATIRTSVLSROIQEHEDSALREOLSGTKRRRQHQOLALBSRLG 342	
QY	518 EREHSGRLQRELEAQRAGEGTAEKTLARRHOAIGEKARAQAEEKRFQOHLGGQKKE 577	
DB	343 EREHSGRLQRELEAQRAGEGTAEKTLARRHOAIGEKARAQAEEKRFQOHLGGQKKE 402	
QY	578 LAALEAQRRTYKLRKEQLKEQLQENPSTPKREKAEMLLRQKQLOQCAEEBAGLLRQ 637	
DB	403 LAALEAQRRTYKLRKEQLKEQLQENPSTPKREKAEMLLRQKQLOQCAEEBAGLLRQ 462	
QY	638 RQYFELQCGQYRKRMLLARHSIDODLLREDLNKKQTKQLECHLLLRQEHARFELRLQ 697	
DB	463 RQYFELQCGQYRKRMLLARHSIDODLLREDLNKKQTKQLECHLLLRQEHARFELRLQ 522	
QY	698 QAVQRTAELTLRQHOTELGNQLEYNKRREOELRQKHAQVROOPKSLYRAGQLPMG-- 755	
DB	523 QAVQRTAELTLRQHOTELGNQLEYNKRREOELRQKHAQVROOPKSLYRAGQRPGLP 582	
QY	756 LPATGALGPLSTGTSEEQPCSSGQAILGQRMIGEENAVPERMLTKEGTTLEPEQR 815	
DB	583 LPATGALGPLSTGTSEEQPCSSGQAILGQRMIGEENAVPERMLTKEGTTLEPEQR 642	
QY	816 ILQEEGTSSSSQOKRSTVNEEDMDISKMKRSVPSLASQNRNITIGQEEAGNMLMKR 875	
DB	643 ILQEEGTSSSSQOKRSTVNEEDMDISKMKRSVPSLASQNRNITIGQEEAGNMLMKR 702	
QY	876 EHGNTLDMFEKLGWVGPLTVPEEEEEEEEGAPITGTPRPGGCGSPDIPPEPPS 935	
DB	703 EHGNTLDMFEKLGWVGPLTVPEEEEEEEEGAPITGTPRPGGCGSPDIPPEPPR 760	
QY	936 HURQYPAQLPGFLSHGLLTGLSFAVSSSGLPLLLLLLPLLA 980	
DB	761 HURQYPAQLPGFLSHGLLTGLSFAVSSSGLPLLLLLLPLLA 805	
RESULT 6	AA555942	
ID	AA555942 standard; Peptide; 1001 AA.	
XX	AA555942;	
AC	18-FEB-2000 (first entry)	
DT	Human/Murine SUL3 consensus protein sequence.	
DE	Antirheumatic; antiarthritic; antiinflammatory; antiallergic; osteopathic;	
XX	antipsoaratic; antiarteriosclerotic; antiaschmatic; immunosuppressive;	
KW	neuroprotective; cardiac; cerebroprotective; cytostatic; antidiabetic;	
KW	vulnery; STE20; protein kinase; STLK3; STLK4; STLK5; STLK6; STLK7;	

KW	ZC1; ZC2; ZC3; ZC4; KHS2; SUL01; SUL03; GEX2; PAK4; PAK5; antagonist;
KW	antibody; gene therapy; rheumatoid arthritis; artherosclerosis; asthma;
KW	inflammatory bowel disease; Crohn's disease; osteoarthritis; psoriasis;
KW	rthritis; autoimmunity; organ transplantation; multiple sclerosis;
KW	myocardial infarction; cardiovascular disease; stroke; renal failure;
KW	oxidative stress-related neurodegenerative disorder; Parkinson's disease;
KW	amyotrophic lateral sclerosis; Leigh syndrome; cancer; cardiomyopathy;
KW	ischemic disorder; inflammation; diabetes mellitus; fibrosis; mitosis;
KW	mesangial disorder; growth regulation; wound healing; T cell activation;
OS	immunosuppressant.
OS	Homo sapiens.
OS	Mus sp.
PN	WO9953036-A2.
PD	21-OCT-1999.
XX	13-APR-1999; 99WO-0508150.
PF	14-APR-1998; 98US-0081784.
PR	(SUGB-) SUGEN INC.
PA	Plowman G, Martinez R, Whyte D;
PI	WPI: 1999-611301/52.
DR	Novel kinase-related polypeptides used for the diagnosis and treatment
XX	of kinase-related diseases and disorders
PS	Claim 11: Page 312-315; 387pp; English.
XX	This sequence represents a consensus peptide sequence contained in novel
CC	STE20-related protein kinases. The invention relates to a nucleic acid
CC	molecule encoding a kinase polypeptide selected from STLK2, STLK3, STLK4,
CC	STLK5, STLK6, STLK7, ZC1, ZC2, ZC3, ZC4, KHS2, SUL01, SUL03, GEX2, PAK4
CC	and PAK5. The proteins are used to identify agonists and antagonists, and
CC	to raise antibodies. The polynucleotides are useful in gene therapy
CC	protocols. The polynucleotides, polypeptides, antibodies, antagonists and
CC	agonists may be used to treat diseases such as immune-related disorders
CC	and diseases (e.g. rheumatoid arthritis, artherosclerosis, chronic
CC	inflammatory bowel disease (e.g. Crohn's disease), asthma,
CC	osteoarthritis, psoriasis, atherosclerosis, rinitis, autoimmunity,
CC	and organ transplantation, chronic inflammatory pelvic disease, multiple
CC	sclerosis, organ transplantation, myocardial infarction, cardiovascular
CC	disease, stroke, renal failure, oxidative stress-related
CC	neurodegenerative disorders (e.g. amyotrophic lateral sclerosis,
CC	Parkinson's disease and Leigh syndrome), cancer, cardiomyopathies,
CC	ischemic disorders, inflammatory disorders, diabetes mellitus, fibrotic
CC	and mesangial disorders. The proteins may also be useful for cell growth
CC	regulation (e.g. in wound healing), T cell activation, mitosis control,
CC	and as immunosuppressants.
XX	
SQ	Sequence 1001 AA;
Query Match	54.7%; Score 2812.5; DB 20; Length 1001;
Best Local Similarity	59.5%; Pred. No. 2e-170;
Matches	590; Conservative 104; Mismatches 197; Indels 101; Gaps 15;
QY	1 MPAGRAGSLKDPVALEFFKDDPEKLSDLREIGHSGFAGAYFARDVNSSEVAIAKMS 60
DB	1 MPSTNRAGSLKDPETALFFKEDPEKLFDDLREIGHSGFAGAYFARDVNTNEVAIAKMS 60
QY	61 YSGKSNKEMKQDITKVRFLQKRNHTIOYRCCTVREHFAWVMYCYGSASDLLEVRK 120
DB	61 YSGKOSTERKQDITKVRFLQKRNHTIOYRCCTVREHFAWVMYCYGSASDLLEVRK 120
QY	121 KPLQVEIAAVTHGALQGLAYLHSHMIRHDYKAGNILLSEPLVLRGFGSASIMAPAN 180
DB	121 KPLQVEIAAVTHGALQGLAYLHSHMIRHDYKAGNILLTEPQVYLRGFGSASIMAPAN 180
QY	181 SFVGTPIYMAPEVILAMDEGQYDGKDVVWSLGTICIELAERKPPLENNMAMSAHYIAQN 240



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Db 181 SFVGTPTWMAPEVILAMDEGOYDGKVDVWSLGTICIELAEKRPPLFMNMMASALYHIAQN 240
QY 241 ESPALQSGHSEYFRNVDSCLOKIPDRPTSEVILKHNRYLRRPPTVIMDLQRTKDA 300
Db 241 ESPALQSGHSEYFRNVDSCLOKIPDRPTSEVILKHNRYLRRPPTVIMDLQRTKDA 300
QY 301 VRELDNIQYRKMKILFQEAHPNGGAPEEEAEFPYMRAGLTLSLSSHVSPTSIS 360
Db 301 VRELDNIQYRKMKILFQEAHPNGGAPEEEAEFPYMRAGLTLSLSSHVSPTSIS 360
QY 361 ASSQSSSVNSIADASDNEEEEEEEEEEEEEEPESREKAMMOQSEHTVTSHTSIHR 420
Db 361 ASSQSSSVNSIADASDNEEEEEEEEEEEEEEPESREKAMMOQSEHTVTSHTSIHR 420
QY 421 LPQSDNIYDPPYQPEMTPGP-LQPPAAPPTSTSSSARRAYCNRNHFATIRASLVS 479
Db 421 LPQSDNIYDPPYQPEMTPGP-LQPPAAPPTSTSSSARRAYCNRNHFATIRASLVS 479
QY 480 QIOEHEDSALREQLSGYKRMROHOKOLLALRESLGEREEHSGRLQRELEAQRAGEGT 539
Db 480 QIOEHEDSALREQLSGYKRMROHOKOLLALRESLGEREEHSGRLQRELEAQRAGEGT 539
QY 540 QMOEHEDSELREQMSGYKRMROHOKOLMTLENKILAEHDEHRLDKDLETOYRNFAA 509
Db 540 QMOEHEDSELREQMSGYKRMROHOKOLMTLENKILAEHDEHRLDKDLETOYRNFAA 509
QY 550 EAEKLARRHOAIGEKARAAQAEERKFOHILGQOKKELALLAEQKRYKLRKEQLKEE 599
Db 550 EAEKLARRHOAIGEKARAAQAEERKFOHILGQOKKELALLAEQKRYKLRKEQLKEE 599
QY 560 LOENPSTPRKREKAWLLRQKQEOLOCAQAEBAGLLRQROYFELQCRQYKRMILANSL 659
Db 560 LOENPSTPRKREKAWLLRQKQEOLOCAQAEBAGLLRQROYFELQCRQYKRMILANSL 659
QY 660 DQDLRLDKLKKOTQKLECALILRQEHATRELRQLOAVQRTAFELTQHOTETLGNQ 719
Db 660 DQDLRLDKLKKOTQKLECALILRQEHATRELRQLOAVQRTAFELTQHOTETLGNQ 719
QY 720 LEYKRRREOELRQKNAQVROQPKSLKVRAGOLPMGLPATGALGP-----LSTGT 769
Db 720 LEYKRRREOELRQKNAQVROQPKSLKVRAGOLPMGLPATGALGP-----LSTGT 769
QY 770 LSE-----EOPSSGOEAILGQM-LGEEBAVPE--RMILKEG 806
Db 770 LSE-----EOPSSGOEAILGQM-LGEEBAVPE--RMILKEG 806
QY 807 TLEPERQRILOE-----EMGTFSSSPQKHSLVNEEDMDISKEM-----KESVPS 853
Db 807 TLEPERQRILOE-----EMGTFSSSPQKHSLVNEEDMDISKEM-----KESVPS 853
QY 854 LASQERNIIQOEAGANILMEKEH--GNLYDMERK-----LGWVGQPVLLPYPEEEEE 905
Db 854 LASQERNIIQOEAGANILMEKEH--GNLYDMERK-----LGWVGQPVLLPYPEEEEE 905
QY 906 EEBGAPIGTPRPD---PDGQCSRPDIPTREPP 933
Db 906 EEBGAPIGTPRPD---PDGQCSRPDIPTREPP 933
QY 921 -HMGHPRMGGRPQAWGHPMOGGRPQWGNHPSGR 950
Db 921 -HMGHPRMGGRPQAWGHPMOGGRPQWGNHPSGR 950

RESULT 7
ABR97326
ID ABR97326 standard; Protein; 1001 AA.
AC ABR97326;
XX
XX 27-JUN-2002 (first entry)
XX
XX Novel human protein SEQ ID NO: 594.
XX
XX Human; anti-naemic; vulnerary; anti-inflammatory; immunomodulator;
XX anti-fertility; cerebroprotective; cytoskeletal; rheumatic; gene therapy;
XX neuroprotective; anti-parkinsonian; protein therapy; EST;
XX expressed sequence tag.
XX
XX Homo sapiens.
XX
```

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PN WO200222660-A2.
XX
XX 21-MAR-2002.
PD
XX 10-SEP-2001; 2001WO-US26015.
PF
XX 11-SEP-2000; 2000US-0659671.
PR
XX (HYSE-) HYSEQ INC.
PA
XX Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
XX Pi Xue AJ, Yang Y, Wehrman T, Drmanac RT;
XX DR WPT: 2002-292408/33.
XX DR N-PSDB; ABR97326.
XX
XX An isolated polynucleotide for treating diseases associated with its
XX encoded polypeptide such as cancer and multiple sclerosis -
XX
XX Example 2; SEQ ID NO 594; 509pp; English.
XX
XX The present invention provides the protein and coding sequences of 444
XX novel human proteins. These were isolated from expressed sequences tags
XX (ESTs). They can be used to stimulate cell growth, to regulate
XX haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth
XX e.g. in burn treatment, to regulate the immune system e.g. to treat
XX multiple sclerosis, to regulate activin or inhibin e.g. to treat
XX infertility, to regulate haemostasis or thrombolysis e.g. to treat
XX stroke and cancer, to screen for drugs, to treat inflammatory conditions
XX e.g. rheumatoid arthritis, and to treat nervous system disorders e.g.
XX Parkinson's disease. The present sequence is a protein of the invention.
XX
XX Sequence 1001 AA:
SQ
Query Match 54.7%; Score 2812.5; DB 23; Length 1001;
Best local Similarity 59.5%; Pred. No. 2e-170;
Matches 590; Conservative 104; Mismatches 197; Indels 101; Gaps 15;
QY 1 MPAGRGASLKDPRVALFLFKRDPKLFSDIRELGHSFGAVYFARVRSNVEVAIKMS 60
Db 1 MPSTNRAGSLKDPRIALFLFKRDEPKLFTDLRELGHSFGAVYFARVRSNVEVAIKMS 60
QY 61 YSGKSNKEMODITKEVRFLOKLRNPTIOYRCGYLRPHNAMLVMEYCLASASDLLLVHK 120
Db 61 YSGKOSTEKMODITKEVRFLOKLRNPTIOYRCGYLRPHNAMLVMEYCLASASDLLLVHK 120
QY 121 KPLQEVETIAVTHGALGGLAYLHSHNMIHRDVKAGNILLSPEGLYKLGDFGSASIMAPAN 180
Db 121 KPLQEVETIAVTHGALGGLAYLHSHNMIHRDVKAGNILLSPEGLYKLGDFGSASIMAPAN 180
QY 181 SFVGTPTWMAPEVILAMDEGOYDGKVDVWSLGTICIELAEKRPPLFMNMMASALYHIAQN 240
Db 181 SFVGTPTWMAPEVILAMDEGOYDGKVDVWSLGTICIELAEKRPPLFMNMMASALYHIAQN 240
QY 241 ESPALQSGHSEYFRNVDSCLOKIPDRPTSEVILKHNRYLRRPPTVIMDLQRTKDA 300
Db 241 ESPALQSGHSEYFRNVDSCLOKIPDRPTSEVILKHNRYLRRPPTVIMDLQRTKDA 300
QY 301 VRELDNIQYRKMKILFQEAHPNGGAPEEEAEFPYMRAGLTLSLSSHVSPTSIS 360
Db 301 VRELDNIQYRKMKILFQEAHPNGGAPEEEAEFPYMRAGLTLSLSSHVSPTSIS 360
QY 361 ASSQSSSVNSIADASDNEEEEEEEEEEEEEEPESREKAMMOQSEHTVTSHTSIHR 420
Db 361 ASSQSSSVNSIADASDNEEEEEEEEEEEEEEPESREKAMMOQSEHTVTSHTSIHR 420
QY 421 LPQSDNIYDPPYQPEMTPGP-LQPPAAPPTSTSSSARRAYCNRNHFATIRASLVS 479
Db 421 LPQSDNIYDPPYQPEMTPGP-LQPPAAPPTSTSSSARRAYCNRNHFATIRASLVS 479
QY 480 QIOEHEDSALREQLSGYKRMROHOKOLLALRESLGEREEHSGRLQRELEAQRAGEGT 539
Db 480 QIOEHEDSALREQLSGYKRMROHOKOLLALRESLGEREEHSGRLQRELEAQRAGEGT 539
QY 540 QMOEHEDSELREQMSGYKRMROHOKOLMTLENKILAEHDEHRLDKDLETOYRNFAA 509
Db 540 QMOEHEDSELREQMSGYKRMROHOKOLMTLENKILAEHDEHRLDKDLETOYRNFAA 509
```

OY	540	EAEKARRHQAIIGEKARAAQAEEERPOOHITLQOQKEALALLAEOAKRYTKLRREOLKEE	599
Db	510	EHEKLKKHQAAMEKAQKAWNSNEKKFOQHIOAQOKKELNFSLESOKREYKLRKEOLOKEE	569
OY	600	LOENSTPRKEAKEMWLLRKOEOLOGOOAEBAGLLRPROGYFELOSCROYKRKMILLARSL	659
Db	570	LWNOSTPKKEOEMLSKQENIQHQAEEEAHLRRORUYLEECRKFRMRMLGRHNL	629
OY	660	DODLLREDINKROTQKDLSCALLRLROHEATRELELROLAQVORTABETRLQHOTELGNQ	719
Db	630	EODLVVEELNKROTQKDLEHAMLLRHESMQELEFRILNTIQMKRCBLIRLOHOTELTNQ	689
OY	720	LVTNNRREDEBLOKNAAOVRQOPKSILVKRAGOLRMGIRPAGALSPP-----LSTGT	769
Db	690	LEYNNRREBELRRKHVWEVQRQPSLSKSELQIKKOFQDTCKITQTRUKALRNHLLETTP	749
OY	770	LSE-----EOPCSSGOEAILLGORM-LGEEEEAUPE--RMILGKEG	806
Db	750	KSEHNKAVLKRIKEEQTRKLIILAEOQDHSTINEMLSYDALRDENOERBCOYLKNQLODEL	809
OY	807	TTLEREORILQE-----EMGTSSSPQKHSRLVNEEDMDISKEN-----KESRVPS	853
Db	810	ELLNVAQSQIKKQAEQAHDRELRELEQRYVSLRRALLLEOK---LEEEMIALONERTERRIS	866
OY	854	LASOERNIIIGOEAGAWMNLMKEHH--GNLYDMEFK-----LGMVGQPVLTLPVEEEEE	905
Db	867	LIERQAREIEDARDSESRLGFSGMVLNLSPEAFSHSYPGASGSWHNPQTGGCP-----	920
OY	906	EEEGGARPIGTIPRD----PGDGCSPPDIPEPP	933
Db	921	--HWGHMGSGRPQAMGHNRMOGGSRQPMGHRPSGP	950
RESULT 8			
ID	AAY49896		
AC	AAY49896 standard; Protein; 1001 AA.		
XX	AAY49896;		
XX	27-JAN-2000 (first entry)		
DI	Rat TA01 kinase.		
DE			
XX	TA01; TAO2; MEK3; mitogen activated protein kinase; phosphorylation;		
KM	p38; protein kinase; cancer; inflammation; autoimmune disease;		
KM	degeneration; insulin-resistant diabetes; metabolic disorder;		
KM	neurodegeneration; MAP kinase; MAP/ERK kinase.		
XX			
OS	Rattus sp.		
XX			
PN	WO9953076-A1.		
PD	21-OCT-1999.		
XX			
PF	14-APR-1999; 99WO-US08165.		
XX			
PR	14-APR-1998; 98US-0060410.		
XX			
PA	(TEXA ) UNITV TEXAS SYSTEM.		
XX			
PI	Cobb M, Hutchison M, Chen Z, Berman K;		
XX			
DR	MP1: 1999-633831/54.		
XX	N-PsDB; AA232435.		
XX			
PT	New polypeptides that phosphorylate kinase, used to screen for		
XX	modulators for treating e.g. cancer or inflammation		
PS	Claim 1; Fig 1; 95pp; English.		
CC	The present sequence represents rat TA01 protein kinase, which is capable		
CC	of phosphorylating MEK3 (a MAP/ERK kinase). TAO kinases, and related		

Query Match	Best Local Similarity	Score	DB	Length
Matches 596; Conservative 108; Mismatches 225; Indels 103; Gaps 16;	57.8%;	2805.5;	20;	1001;
1 MPAGRAGSLKDPDYAELEFKDDPEKLSDLREIGHSGFAYFARDVNSVEVAIKKMS 60				
1 MSSTRAGSLKDPETALIELEFKDDPEKLSDLREIGHSGFAYFARDVNTNVEVAIKKMS 60				
61 YSGKSNEMKWDITKEVRLQKLRHPTQVGCYLRHTAFLVMEYCGSASDLEVHK 120				
61 YSGKSTEWKWDITKEVRLQKLRHPTQVGCYLRHTAFLVMEYCGSASDLEVHK 120				
121 KPLQVEIYALVHAGLQGLATYLDHSHNMHTRDVACNITLSEFGLVKLQFGSASIMAPAN 180				
121 KPLQVEIYALVHAGLQGLATYLDHSHNMHTRDVACNITLSEFGLVKLQFGSASIMAPAN 180				
181 SFVGTPIYMAPEVILAMDEGQYDGKVDVSLGITGIELAEKRPPLFNMNMSALYHIAON 240				
181 SFVGTPIYMAPEVILAMDEGQYDGKVDVSLGITGIELAEKRPPLFNMNMSALYHIAON 240				
241 ESPALQSGHMSYTFNPNVDSCLQKTPDRPTSEVILKHFVLRERPPVYIMLLQRTKDA 300				
241 ESPALQSGHMSYTFNPNVDSCLQKTPDRPTSEVILKHFVLRERPPVYIMLLQRTKDA 300				
301 VVELDNLQYRRKKKLTLPQAPNGPAAEPAREEESAEAPYHRAQTSLTSSHSVPMSIS 360				
301 VVELDNLQYRRKKKLTLPQAPNGPAAEPAREEESAEAPYHRAQTSLTSSHSVPMSIS 360				
361 ASSQSSSVNSLADASDNEEEEEEESBEEBESPEKREMAOMEGETVYVSSHSTIHR 420				
361 ASSQSSSVNSLADASDNEEEEEEESBEEBESPEKREMAOMEGETVYVSSHSTIHR 420				
421 LFGSNLIVDDPQPEMTPEP-LQPPAAPPTSSSSSARRACRRNRDHPATIRTSLSYR 479				
421 LFGSNLIVDDPQPEMTPEP-LQPPAAPPTSSSSSARRACRRNRDHPATIRTSLSYR 479				
480 QIOEHODSALKEQSLSGYKRMRRQOKOLYALRESLRGCEHRSQRLQRELAQAGAGFT 539				
480 QIOEHODSALKEQSLSGYKRMRRQOKOLYALRESLRGCEHRSQRLQRELAQAGAGFT 539				
510 EMEKLTIKKHQASMEKAEKAYMANEEKFOHIOAQOKELNSPLESQQKREYKLRKQDLEE 569				
510 EMEKLTIKKHQASMEKAEKAYMANEEKFOHIOAQOKELNSPLESQQKREYKLRKQDLEE 569				
600 LQENSTPKRREAEVLLKROKEDLOOCQAEFEAGLLRRQRYTELOCRQYKKMLARHSL 659				
600 LQENSTPKRREAEVLLKROKEDLOOCQAEFEAGLLRRQRYTELOCRQYKKMLARHSL 659				
660 DODLLREDLNKQOKQDLEACALLNQHENTRTELROLQAVQRTAEVLTRLQHOTELNQ 719				
660 DODLLREDLNKQOKQDLEACALLNQHENTRTELROLQAVQRTAEVLTRLQHOTELNQ 719				
720 LEYNKRRQEDLEKQKAAAOVROOPKSLKYVAGOLPMGLPATGALGP-----LSTGT 769				
720 LEYNKRRQEDLEKQKAAAOVROOPKSLKYVAGOLPMGLPATGALGP-----LSTGT 769				
770 LSE-----EQPCSSGOEAILGQRM-LGEEBAVPE--RMILGEG 806				

Db 750 KSEHKAVLKRLKEEQTRKLLALAEQYHSHINEMLSTQALRLDEAOEACQVLKMQLOQEL 809  
 QY 807 TYLEPEORILDE-----EMQTFSSPOKHSRLVNEEDMDISKEM-----KESRVP 853  
 Db 810 ELLINAVOSIKKQAOEAOHRELEFORSLRRALLEOK---IEEMLALONERTERINS 866  
 QY 854 LASQERNITGOEBAQAMNLMKEKH--GNLVDMEFK-----LGMVOGPV-----L 895  
 Db 867 LERQAREIEAFQSESMRLGFSNMVLNLSPEAFSHSYPGASWSMNPFGGSGPHMGHM 926  
 QY 896 TYPPEEEEEEBCGAPRTGPRDPCGCC-SPDIPPEPPSHLROYRPAQLPGLSHGL 954  
 Db 927 GGPQAMGHMGGPQPMGHPGSGPMQGVPRGSGIGVRNSFOALRRFASG---GRTEQGMS 983  
 QY 955 TGLSFAVGSSSG 966  
 Db 984 RSTSVTSQISNG 995

RESULT 9  
 AAY55938  
 ID AAY55938 standard; Protein; 748 AA.  
 XX -AAY55938;  
 AC  
 XX  
 DT 18-FEB-2000 (first entry)  
 XX  
 DE Murine SUTU3 protein.  
 XX  
 XX Antirheumatic; antiarthritic; antiinflammatory; antiallergic; osteopathic;  
 XX antipsoriatic; antiarteriosclerotic; antiasthmatic; immunosuppressive;  
 XX neuroprotective; cardiact; cerebroprotective; cytostatic; antidiabetic;  
 XX vulnery; STE20; protein kinase; STK2; STK3; STK4; STK5; STK6; STK7;  
 XX ZC1; ZC2; ZC3; ZC4; KHS2; SUTU3; SUTU3; GSK2; PAK4; PAK5; antagonists;  
 XX antibody; gene therapy; rheumatoid arthritis; artherosclerosis; asthma;  
 XX inflammatory bowel disease; Crohn's disease; osteoarthritis; psoriasis;  
 XX rhinitis; autoimmunity; organ transplantation; multiple sclerosis;  
 XX myocardial infarction; cardiovascular disease; stroke; renal failure;  
 XX oxidative stress-related neurodegenerative disorder; Parkinson's disease;  
 XX amyotrophic lateral sclerosis; Leigh syndrome; cancer; cardiomyopathy;  
 XX ischemic disorder; inflammation; diabetes mellitus; fibrosis; mitosis;  
 XX mesangial disorder; growth regulation; wound healing; T cell activation;  
 XX immunosuppressant.  
 XX  
 OS Mus sp.  
 XX  
 PN WO9553036-A2.  
 PD 21-OCT-1999.  
 XX  
 PF 13-APR-1999; 99WO-US08150.  
 XX  
 PR 14-APR-1998; 98US-0081784.  
 XX  
 PA (SUGEN-) SUGEN INC.  
 XX  
 PI Plowman G, Martinez R, Whyte D;  
 DR WPI; 1999-611301/52.  
 DR N-PSDB; AA240490.  
 XX  
 PT Novel kinase-related polypeptides used for the diagnosis and treatment  
 of kinase-related diseases and disorders  
 XX  
 XX Claim 11; Page 299-301; 387pp; English.  
 PS  
 CC This sequence represents a novel STE20-related protein kinase. The  
 CC invention relates to nucleic acid molecule encoding a kinase polypeptide  
 CC selected from STK2, STK3, STK4, STK5, STK6, STK7, ZC1, ZC2, ZC3,  
 CC ZC4, KHS2, SUTU3, SUTU3, GSK2, PAK4 and PAK5. The proteins are used to  
 CC identify agonists and antagonists, and to raise antibodies. The  
 CC polynucleotides are useful in gene therapy protocols. The polynucleotides,  
 CC polypeptides, antibodies, antagonists and agonists may be used to treat

CC diseases such as immune-related disorders and diseases (e.g. rheumatoid  
 CC arthritis, atherosclerosis, chronic inflammatory bowel disease (e.g.  
 CC Crohn's disease), asthma, osteoarthritis, psoriasis, atherosclerosis,  
 CC rhinitis, autoimmunity, and organ transplantation, chronic inflammatory  
 CC pelvic disease, multiple sclerosis, organ transplantation, myocardial  
 CC infarction, cardiovascular disease, stroke, renal failure, oxidative  
 CC stress-related neurodegenerative disorders (e.g. amyotrophic lateral  
 CC sclerosis, Parkinson's disease and Leigh syndrome), cancer,  
 CC cardiomyopathies, ischemic disorders, inflammatory disorders, diabetes  
 CC mellitus, fibrotic and mesangial disorders. The proteins may also be  
 CC useful for cell growth regulation (e.g. in wound healing), T cell  
 CC activation, mitosis control, and as immunosuppressants.  
 XX  
 SQ Sequence 748 AA;  
 Query Match 53.4%; Score 2743; DB 20; Length 748;  
 Best Local Similarity 71.3%; Pred. No. 3.7e-166;  
 Matches 537; Conservative 78; Mismatches 98; Indels 40; Gaps 5;  
 QY 1 MPAGRAGSLKDDPVAFLEPKDDPEKLFSDPREIGHSGGAVYFARDVNRSEVATKKMS 60  
 Db 1 MPSTNRAGSLKDPEIALELFKEDEPKLFTDLREIGHSGGAVYFARDVNRSEVATKKMS 60  
 QY 61 YSGKQSEKWKODIIRKVFLOKLRHPNTIQRCYUREHTAMLVMEYCLGASADLLEVHK 120  
 Db 61 YSGKQSEKWKODIIRKVFLOKLRHPNTIQRCYUREHTAMLVMEYCLGASADLLEVHK 120  
 QY 121 KPLQVEEIAAVTHGALQGLAVYLSHNMHRDVKAGNILLSEPLVRLGDFGSASIMAPAN 180  
 Db 121 KPLQVEEIAAVTHGALQGLAVYLSHNMHRDVKAGNILLSEPLVRLGDFGSASIMAPAN 180  
 QY 181 SPFGTGYMAPEYITLMDGQYGVKDVWSLGTICIELAEKRPPLNNMAMSLYHIAQN 240  
 Db 181 SPFGTGYMAPEYITLMDGQYGVKDVWSLGTICIELAEKRPPLNNMAMSLYHIAQN 240  
 QY 241 ESPALSGHSEYFRNFVNSLOKIPQDPRTSVYLKHNRPVLYREPPVYMDIQRTKDA 300  
 Db 241 ESPALSGHSEYFRNFVNSLOKIPQDPRTSVYLKHNRPVLYREPPVYMDIQRTKDA 300  
 QY 241 ESTPTLOS-----NMNSCLOKIKIDRPTSELLKHNFLREYVILDLQRTKDA 292  
 Db 241 ESTPTLOS-----NMNSCLOKIKIDRPTSELLKHNFLREYVILDLQRTKDA 292  
 QY 301 VRELNDLQYRKMKKILFOEAPNGSGADPEEAEAPYHNRAGTLTSSSHSVPSMSIS 360  
 Db 301 VRELNDLQYRKMKKILFOEAPNGSGADPEEAEAPYHNRAGTLTSSSHSVPSMSIS 360  
 QY 293 VRELNDLQYRKMKKILFOEAPNGSGADPEEAEAPYHNRAGTLTSSSHSVPSMSIS 352  
 Db 293 VRELNDLQYRKMKKILFOEAPNGSGADPEEAEAPYHNRAGTLTSSSHSVPSMSIS 352  
 QY 361 ASSQSSSVNSLADSNNEEEEEEDEEESGESRMAMOGCEHTVNSHSITIR 420  
 Db 361 ASSQSSSVNSLADSNNEEEEEEDEEESGESRMAMOGCEHTVNSHSITIR 420  
 QY 353 ASSQSSSVNSLADSNNEEEEEEDEEESGESRMAMOGCEHTVNSHSITIR 391  
 Db 353 ASSQSSSVNSLADSNNEEEEEEDEEESGESRMAMOGCEHTVNSHSITIR 391  
 QY 421 LPGSDNLVDDPYQPEMTGCP-LQPAAPPTSTSSSARRRAYCRNDRHATITATSLVSR 479  
 Db 421 LPGSDNLVDDPYQPEMTGCP-LQPAAPPTSTSSSARRRAYCRNDRHATITATSLVSR 479  
 QY 392 KPEEEN-----YQEBDDPRTIRADPQSP-----QYSRKHSYRNRNDEHATITATSLVSR 441  
 Db 392 KPEEEN-----YQEBDDPRTIRADPQSP-----QYSRKHSYRNRNDEHATITATSLVSR 441  
 QY 480 QIQEHQDSALRQSLGKYKMRROHOKOLLALLESRLRGEREESHGRLQRELEAQRAGFGT 539  
 Db 480 QIQEHQDSALRQSLGKYKMRROHOKOLLALLESRLRGEREESHGRLQRELEAQRAGFGT 539  
 QY 442 QMOEHQDSALRQSLGKYKMRROHOKOLLALLESRLRGEREESHGRLQRELEAQRAGFGT 501  
 Db 442 QMOEHQDSALRQSLGKYKMRROHOKOLLALLESRLRGEREESHGRLQRELEAQRAGFGT 501  
 QY 540 EAEKILARRHQDAGEKARARAAAEERKFOQHILGQKKELALLAEAKRYTKLKEQKEE 599  
 Db 540 EAEKILARRHQDAGEKARARAAAEERKFOQHILGQKKELALLAEAKRYTKLKEQKEE 599  
 QY 502 EMEKILARRHQDAGEKARARAAAEERKFOQHILGQKKELALLAEAKRYTKLKEQKEE 561  
 Db 502 EMEKILARRHQDAGEKARARAAAEERKFOQHILGQKKELALLAEAKRYTKLKEQKEE 561  
 QY 600 LOENPSTPKREAEWLLRQEOLOQOAOEAEALRORQYFELQCRQYKRYKMLLRHSI 659  
 Db 600 LOENPSTPKREAEWLLRQEOLOQOAOEAEALRORQYFELQCRQYKRYKMLLRHSI 659  
 QY 562 LNNQOSTPKREAEWLLRQEOLOQOAOEAEALRORQYFELQCRQYKRYKMLLRHSI 621  
 Db 562 LNNQOSTPKREAEWLLRQEOLOQOAOEAEALRORQYFELQCRQYKRYKMLLRHSI 621  
 QY 720 LEYNNRQEOLEKHAQYRQOPKSLKVRAGOL 752  
 Db 682 LEYNNRQEOLEKHAQYRQOPKSLKVRAGOL 714

RESULT 10





Qy	606	TPPEKXEMLLROKQEDLOOQOAAEEEGGLLRQOYQYELQOQYQYKRMMLLRHSJLDDLLR	665
Db	573	TPPEKQORISKHNENLOHTPOABEEBLLFTPOOLYIDKCKRFFKRYIMKREVEQONIR	632
Qy	666	EDLKKQOTOKDLECCALLRQHEATRELELNOLQAVORTAEFTRLQHOTELGNOLEYNKR	725
Db	633	ELNKKKFKQEMENHMLIRHDESTRRELEYROLHTLOKLMDELRIHQHOTELGNOLEYNKR	692
Qy	726	REOELROKHAQVOOQKSLKXVABOGLPMLPATGALGSL	766
Db	693	REBELHKKHWELELOQYKRNKAMQOIKQFOOTCAVOTCKQYKALKKNLOEVTPNNEKHT	752
Qy	767	TGTLSEBOPSSQGEAILQORMLGEEBEAVPERMILGEGTTLDEEQRITLOEEMGTF	824
Db	753	ILKTLKDEQ--TRKLIIIAEYOYEOSINEMMASQALRLDEABEAOALRLOLOQEMELL	809
Qy	825	S-----SSPKHSL-----VNEDDISKESKESVPISLQOE	858
Db	810	NAVOSKIKMQTEAOHELELOKLEORSVSLRANHEQKIEBELLALQKRESEKIKNLEQOE	869
Qy	859	RNITGOEBAGAMNLMKEHGNLYDMEF	885
Db	870	REI-----ETEDMESIRMGFGNLYTLDF	892

RESULT 12	
AAV55936	
ID	AAV55936 standard; Protein; 898 AA.
XX	
AC	AAV55936;
XX	
DT	18-FEB-2000 (first entry)
XX	
DE	Human SUG1 protein.
XX	
KW	Antiinflammatory; antiinflammatory; antifibrotic; osteopathic;
KW	antiproliferative; antineoplastic; antineoplastic; immunosuppressive;
KW	neuroprotective; cardiant; cerebroprotective; cytosolic; antidiabetic;
KW	vulneray; SRE20, protein kinase; STK2; STK3; STK4; STK5; STK6; STK7;
KW	ZC1; ZC2; ZC3; ZC4; KHS2; SUG1; SUG2; GSK3; PAK4; PAK5; antagonist;
KW	antibody; gene therapy; rheumatoid arthritis; atherosclerosis; asthma;
KW	inflammatory bowel disease; Crohn's disease; osteoarthritis; psoriasis;
KW	rthritis; autoimmunity; organ transplantation; multiple sclerosis;
KW	myocardial infarction; cardiovascular disease; stroke; renal failure;
KW	oxidative stress-related neurodegenerative disorder; Parkinson's disease;
KW	amyloidotic lateral sclerosis; Leigh syndrome; cancer; cardiomyopathy;
KW	ischemic disorder; inflammation; diabetes mellitus; fibrosis; mitosis;
KW	measial disorder; growth regulation; wound healing; T cell activation;
XX	immunosuppressant.
XX	
OS	Homo sapiens.
XX	
PN	W09953036-A2.
XX	
PD	21-OCT-1999.
XX	
PF	13-APR-1999; 99MO-US08150.
XX	
PR	14-APR-1998; 9805-0081784.
XX	
PA	(SUG1-) SUGEN INC.
XX	
PI	Plowman G, Martinez R, Whyte D;
XX	
DR	WPI; 1999-611301/52.
XX	
PT	N-PSDB; AAZ40488.
XX	
PR	Novel kinase-related polypeptides used for the diagnosis and treatment
XX	of kinase-related diseases and disorders -
XX	
PS	Claim 11; Page 293-296; 387pp; English.
CC	This sequence represents a novel SRE20-related protein kinase. The

invented relates to nucleic acid molecule encoding a kinase polypeptide selected from SPMK2, SPMK3, SPMK4, SPMK5, SPMK6, SPMK7, ZC1, ZC2, ZC3, ZC4, KMS2, SNU01, SNU03, GEX2, PAK4 and PAK5. The proteins are used to identify agonists and antagonists, and to raise antibodies. The polynucleotides are useful in gene therapy protocols. The polynucleotides, polypeptides, antibodies, antagonists and agonists may be used to treat diseases such as immune-related disorders and diseases (e.g. rheumatoid arthritis, atherosclerosis, chronic inflammatory bowel disease (e.g. Crohn's disease), asthma, osteoarthritis, psoriasis, atherosclerosis, rheitis, autoimmunity, and organ transplantation, chronic inflammatory polyic disease, multiple sclerosis, organ transplantation, myocardial infarction, cardiovascular disease, stroke, renal failure, oxidative stress-related neurodegenerative disorders (e.g. amyotrophic lateral sclerosis, Parkinson's disease and Leigh syndrome), cancer, cardiomyopathies, ischemic disorders, inflammatory disorders, diabetes mellitus, fibrotic and mesangial disorders. The proteins may also be useful for cell growth regulation (e.g. in wound healing), T cell activation, mitosis control, and as immunosuppressants.

AA	Sequence	898	AA;
SQ			

Query Match	47.38;	Score 2432.5;	DB 20;	Length 898;
-------------	--------	---------------	--------	-------------

```

Best Local Similarity 34.3%, Freq. NO. 2.7/e 140,
Matches 503; Conservative 129; Mismatches 212; Indels 83; Gaps 10;

```

0Y 6 BAGSIKDPPVAEIEFKDDPEKI.FSDI.BEIGHGSEGAYFEABDVBNSEVAIKKMSYSGKO 65

QY	6	RAGSLKDPVNALEFPKDPDEKFLFSDLREIGHSGFAYVARYADRVNBEVVAIKKMSYSGO	65
Dd	2	RGVGLKDPEDIDLFPKDDPEELFIGHJHEGHSGFAYVATNANTHEVAIKKMSYSGO	61
QY	66	SNEKMODIKKEVRFLOKLEHPNTIOYRGCYLRHRTMVLWMEYCLGSASDLLEVHKRPLOE	125
Dd	62	THEKMODILEKVEFLRQLKHNPNTIEYKGCYLTENTMVLWMEYCLGSASDLLEVHKRPLOE	121
QY	126	VEIAATVTHGALOGFLAYLHSHNMIHRDVKAGNILLSEPLGVKLGDFGSSASIMAPANSFVGT	185
Dd	122	VEIAATHTHGLHGLAYLHSHALHHRDKAGNILLTEPQGVKIADFGSASMASPANSFVGT	181
QY	186	PYVMAPEVILLADEGOYDKVDYWSIGTICIELAEKRPPLFNNNANASALYHIAONSPL	245
Dd	182	PYVMAPEVILLADEGOYDKVDIWSIGTICIELAEKRPPLFNNNANASALYHIAONSPTL	241
QY	246	QSGHSEYFRNVDSCLQIKIPDRPISEVLLKHFRFLRREPRPVINDLIQRTKDAVRELD	305
Dd	242	QSEWMTDSFRRRVYDCLQIKIPDRPISEVLLKHFRFLRREPRPVINDLIQRTKDAVRELD	301
QY	306	NIQYRKMKKILFQEBADNGCAERDEEBEADEPYMHAQTLLTSIESHSVPMSISASOS	365
Dd	302	NIQYRKMKKILFQETENGGLNBSODEBDESEHTSILNREDSIGSNHSPMSVSGSOS	361
QY	366	SSVNSIADSDJNEEEEEEEEEEEBEGPRESEMAWMOEGEHTVTSIIHRLPGSD	425
Dd	362	SSVNSIQEWMDE-----SSSELYMMHDEDSITNSSSVYHK--KD	399
QY	426	NIYDDPYOPEMTGPILOPAPRAPPTSSSSARRRAYCRRNDHAPATIRIASLVRSQIOEHE	485
Dd	400	HYFT--RDEAGHGDRPRPRPTQSVQSOA---LHYRRREPRATIKSASLVYRQIHEHE	452
QY	486	QDSALREQISGKYKRRNRQOKOLLAELESYRGREESHSGRIQELAEQAFGTEDAKLA	545
Dd	453	QENELREQSGYKRRNRQOKOLLAELENTIKAEMDHRYLQLOEYVTNHNSSIELEKLA	512
QY	546	RHHOAIKEGEAAAOAEEKRFQOHIIGOOKKELAAOLAKRYLQIARKBEQLEEDQES	605
Dd	513	KQOVALITEEAAYAAADEKKFOOIIAQQOKDLTTLLESQOKQYKICKKEIKKEEMEDHS	572
QY	606	TKRREKAEMYLROKEDLOOAOAEEBAGLLRORQYFELQOYKRRMLLARHSLDODLRL	665
Dd	573	TKRREKQERISNKENULQTOQAEEBAHLLTQOGLYUDDKORNFKQIKIMIRHVEEONIR	632
QY	666	EDLNKQOTQDEBACALLLRQNEATRELELYROLOAOVOTRAELTRLOHOTELEGQOLEYNR	725
Dd	633	EBLNKRTQKEMEHAMILRHDSDETRELELYROHTELTQOKLRMDLIRLOHOTELENOLEYNKR	692









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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 22, 2002, 12:18:20 ; Search time 6.448 Seconds  
(without alignments)  
2675.892 Million cell updates/sec

Title: US-09-686-346a-4\_COPY\_1\_416  
Perfect score: 2161  
Sequence: 1 MPAGRAGSLKDPVLAELFF.....ESREMANMQEGEHTVTSRSS 416

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues  
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1032.5	47.8	982	1	SOUU_CAEEL
2	610.5	28.3	487	1	STR4_HUMAN
3	597.5	27.6	426	1	STR25_MOUSE
4	595.5	27.6	491	1	STR3_HUMAN
5	594	27.5	443	1	STR25_HUMAN
6	591	27.3	426	1	STR25_HUMAN
7	515.5	23.9	968	1	ST10_HUMAN
8	511.5	23.7	966	1	ST10_MOUSE
9	510	23.6	544	1	PAK1_RAT
10	508	23.5	545	1	PAK1_HUMAN
11	508	23.5	545	1	PAK1_MOUSE
12	505	23.4	544	1	PAK3_RAT
13	504	23.3	544	1	PAK3_HUMAN
14	500	23.1	544	1	PAK3_MOUSE
15	499	23.1	490	1	SPS1_YEAST
16	491	22.7	524	1	PAK2_HUMAN
17	491	22.7	524	1	PAK2_RABIT
18	489	22.6	524	1	PAK2_RAT
19	480	22.2	1080	1	NKX1_YEAST
20	463	21.4	1062	1	CC7_SCHPO
21	454.5	21.0	1080	1	M15_CAEEL
22	450.5	20.8	1230	1	ST20_CANAL
23	450	20.8	553	1	SPAK_RAT
24	449	20.8	558	1	PAK1_SCHPO
25	447	20.7	939	1	ST20_YEAST
26	445.5	20.6	547	1	SPAK_HUMAN
27	443	20.3	556	1	SPAK_MOUSE
28	438.5	20.3	591	1	PAK4_HUMAN
29	438	20.3	589	1	SHK2_SCHPO
30	431	19.9	971	1	CLA4_CANAL
31	430	19.9	719	1	PAK7_HUMAN
32	418.5	19.4	974	1	CC15_YEAST
33	418	19.3	655	1	SKM1_YEAST

34	415	19.2	842	1	CLA4_YEAST
35	407	18.8	1401	1	WIS4_SCHPO
36	394.5	18.3	626	1	M3K3_HUMAN
37	393.5	18.2	1501	1	NINC_DROME
38	388.5	18.0	626	1	M3K3_MOUSE
39	382	17.7	1478	1	BCK1_YEAST
40	373.5	17.3	618	1	M3K2_HUMAN
41	372.5	17.2	619	1	M3K2_MOUSE
42	365.5	16.9	506	1	NEK3_HUMAN
43	347	16.1	1493	1	M3K1_RAT
44	347	16.1	1495	1	M3K1_HUMAN
45	346	16.0	1493	1	M3K1_MOUSE

## ALIGNMENTS

RESULT 1  
SOUU\_CAEEL STANDARD; PRT; 982 AA.  
AC P46549;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Serine/threonine-protein kinase SOUU (EC 2.7.1.-).  
GN KIN-18 OR SOUU OR T17E9.1.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2.  
RA Du Z.;  
RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Bristol N2.  
RA Cope M.J.T.V., Kendrick-Jones A.;  
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.  
RI -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
-----  
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-----  
CC EMBL: 011280; AAA19437.1; -  
DR EMBL: 032275; AAA75370.1; -  
DR WormPep: T17E9.1; CE01405.  
DR InterPro: IPR000719; Euk\_pkinase.  
DR InterPro: IPR002290; Ser\_thr\_pkinase.  
DR Pfam: PF00069; pkinase; 1.  
DR ProDom: PD000001; Euk\_pkinase; 1.  
DR SMART: SM00220; S\_TKC; 1.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE: PS0011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; FALSE\_NEG.  
KW Transferase; Serine/threonine-protein kinase; ATP-binding.  
FT DOMAIN 30 289  
FT NP\_BIND 36 44 ATP (BY SIMILARITY).  
FT BINDING 59 59 ATP (BY SIMILARITY).  
FT ACT\_SITE 153 153 BY SIMILARITY.  
SO SEQUENCE 982 AA; 112870 MW; 745CE1E2E890977D CRC64;  
  
Query Match 47.8%; Score 1032.5; DB 1; Length 982;  
Best local Similarity 47.2%; Pred. No. 2e-54;  
Matches 204; Conservative 67; Mismatches 140; Indels 21; Gaps 3;  
  
QY 6 RAGSLNDPVAELFFKDPDEKLFSDLRKIGSGSFGAVYFARDVRNSEVVAIKMSTSGKQ 65

[illegible]

RESULT 2			
STK4_HUMAN			
ID	STK4_HUMAN	STANDARD;	PRT; 487 AA.
AC	Q13043; Q15802; Q9N7Z4;		
DT	16-OCT-2001 (Rel. 40, Created)		
DT	16-OCT-2001 (Rel. 40, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Serine/threonine protein kinase 4 (EC 2.7.1.37) (STE20-like kinase MS1) (MST-1) (Mammalian STE20-like protein kinase 1)		
DE	(Serine/threonine protein kinase Krs-2).		
GN	STK4 OR MST1.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=95394929; PubMed=7665586;		
RA	Cresay C.L., Chernoff J.;		
RT	"Cloning and characterization of a human protein kinase with homology		
RT	to Ste20.";		
RL	J. Biol. Chem. 270:21695-21700(1995).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=96413604; PubMed=8816758;		
RA	Taylor L.K., Wang H.C., Erikson R.L.;		
RT	"Newly identified stress-responsive protein kinases, Krs-1 and Krs-		
RT	2.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 93:10099-10104(1996).		
RN	[3]		
RP	SEQUENCE OF 1-435 FROM N.A.		
RA	Laird G.;		
RL	Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.		
CC	-1 CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.		
CC	-1 ENZYME REGULATION: THE C-TERMINAL NON-CATALYTIC REGION INHIBITS		
CC	THE KINASE ACTIVITY.		
CC	-1 SUBCELLULAR LOCATION: Cytoplasmic (By similarity).		
CC	-1 TISSUE SPECIFICITY: UBICUOUSLY EXPRESSED.		
CC	-1 PTM: AUTOPHOSPHORYLATED ON SERINE AND THREONINE RESIDUES.		
CC	-1 SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.		
CC	STE20 SUBFAMILY.		

```

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CC -----
CC
CC EMBL; U18297; AAA83254.1; -.
CC DR EMBL; U60207; AAB17262.1; -.
CC DR EMBL; AL109839; CAB89421.1; -.
CC DR HSSP; P24941; IHCL.
CC DR Genew; HGNC:11408; STR4.
CC MIM; 604965; -.
CC DR InterPro; IPR000719; Euk_pkinase.
CC DR InterPro; IPR002290; Ser_thr_pkinase.
CC DR InterPro; IPR001245; Tyr_pkinase.
CC DR Pfam; PF00069; pkinase; 1.
CC DR PRINTS; PR00109; TYRKINASE.
CC DR ProDom; PD000001; Euk_pkinase; 1.
CC DR SMART; SM00220; S_TKC; 1.
CC DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC DR PROSITE; PS00108; PROTEIN_KINASE_ST; FALSE_NEG.
CC DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
CC DR Transferase; Serine/threonine-protein kinase; ATP-binding.
CC
CC DOMAIN 30 281 PROTEIN KINASE.
CC FT NP_BIND 36 44 ATP (BY SIMILARITY).
CC FT BINDING 59 59 ATP (BY SIMILARITY).
CC FT ACT_SITE 149 149 BY SIMILARITY.
CC FT DOMAIN 373 378 POLY-GU.
CC FT CONFLICT 222 222 P -> R (IN REF. 1).
CC FT CONFLICT 312 312 V -> M (IN REF. 1).
CC Q SEQUENCE 487 AA; 35630 MW; 150758BCE5F77DC CRC64;

```

Query Match	28.3%	Score 610.5	DB 1	Length 487
Best Local Similarity	34.0%	Pred. No. 1,2e-29		
Matches 147	Conservative	71	Mismatches 159	Indels 55
				Gaps 9
QY	10	LKDPVAVLFFKDD-----PEKLFSDLRKREIGHSGFGAVYFARADYRNSEVAIKKMSYSG	63	
	1			
	2			
Db	6	LRRNPRLRLKRLDEDSLTROPEEVEVDYLEKLEGGSYGKAIHKEGTGIVAIKKQPV--	63	
	1			
	2			
QY	64	KOSNKMODITKEVRFLOKLRHPNTIOYRGCTLRBHTAVLWYEC-LGSASDLLEVHKRP	122	
	1			
	2			
Db	64	---EEDLOEITKEISIMQOCDSPHVYKKTIGSFKNTDLMIVWETGAGSYSDITLRNKT	120	
	1			
	2			
QY	123	LOEVEIAAVTGCALOGYLAHSHNMHHDVYKAGNTLLSEPGVLKLDGSA---SINAP	178	
	1			
	2			
Db	121	LTEDIAITLLIYSTKLGLEYLHMRKIHHDIRKGNITLLTEGHAKLADGVAQLDVTMAK	180	
	1			
	2			
QY	179	ANSFPGFTYMAAPETILAMDEGOYGVKDWVSLGTICIEIARPKRPLFMMNMSALYNHA	238	
	1			
	2			
Db	181	RNTVYGTFFMAAPEYI---QELGYCVADIMSLGITALIEMAGKRPYADIHMRALFMIP	237	
	1			
	2			
QY	239	QNESPALOSGH-WSEYFKNFVDSCLKIPDRPTSEVLKRNHFLVLRERPPVIMDLIORT	297	
	1			
	2			
Db	238	TNPPTFFKPELMSDNFTDVFQKCYLSPQGRATATOLLDFHFVSAKGVSTLRDLINEA	297	
	1			
	2			
QY	298	KDAVRELNDLQYRKKKKLLFQEARPGFALEAREEERAEYHNA-----	342	
	1			
	2			
Db	298	MDVVKLRQESQOREVDQ-----DDEENSEBDEMDSGTWRAVAVGDEMGTVRAVASTWT	348	
	1			
	2			
QY	343	-GTLTLESSHSVPMSIASASSQSSVNSLADASNEDEEEEEEDEEEDEEGPESRPM	401	
	1			
	2			
Db	349	DGANTMIEHDTLP-----SQLGTVYINADDEDEEGTMRKRDEFTMQAPKSFLEY	398	
	1			
	2			
QY	402	AMMOGEHTVTS	413	
	1			
	2			
Db	399	FEQEKERENJNS	410	
	1			
	2			

### RESULT 3

```

ST25_MOUSE
ID ST25_MOUSE STANDARD; PRT; 426 AA.
AC 09Z2M1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Serine/threonine protein kinase 25 (EC 2.7.1.37) (Sterile 20/oxidant
DE stress-response kinase 1) (Ste20/oxidant stress response kinase-1)
DE (SOK-1) (Ste20-like kinase).
GN STK25 OR SOK1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Melnick M.B.;
RT "Genetic mapping of human and mouse PAK genes.";
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: OXIDANT STRESS-ACTIVATED SERINE/THREONINE KINASE THAT
CC MAY PLAY A ROLE IN THE RESPONSE TO ENVIRONMENTAL STRESS (BY
CC SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- ENZYME REGULATION: ACTIVATED BY PHOSPHORYLATION, PROBABLY
CC AUTOPHOSPHORYLATION. THE C-TERMINAL NON-CATALYTIC REGION INHIBITS
CC THE KINASE ACTIVITY (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC STE20 SUBFAMILY.
-----
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-----
DR EMBL: AF004934; AAD01208.1; -.
DR MGD: MGI:1891699; Stk25
DR InterPro: IPR000719; Euk-kinase.
DR InterPro: IPR002290; Ser_thr-kinase.
DR InterPro: IPR001245; Tyr-kinase.
DR Pfam: PF00069; kinase.1.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD000001; Euk-kinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; FALSE_NEG.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00101; PROTEIN_KINASE_DOM; 1.
DR Transfaser: Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.
FT DOMAIN 20 270 PROTEIN KINASE.
FT NP_BIND 26 34 ATP (BY SIMILARITY).
FT BINDING 49 49 ATP (BY SIMILARITY).
FT ACT_SITE 140 140 BY SIMILARITY.
FT SEQUENCE 426 AA; 48175 MW; 6A01916034E26362 CRC64;
SO QUERY MATCH
Best local Similarity 27.6%; Score 597.5; DB 1; Length 426;
Matches 159; Conservative 68; Mismatches 135; Indels 73; Gaps 17;
QY 23 DEPKLSDLEIGHGSGAVFYFADVANSFVAIKKMSYSGKSNEMWQILKEVRLOK 82
DB 15 DPDELFTKIDRIGKSGEYKGDINDHTKEVVAIKIIDL--EEAEEDIEDIQEITVLSQ 72
QY 83 LRHPNTIYRGCYLREHTALVMEYC-LGSASDLEVHKRPLOEVEIAATGALQGIAY 141
DB 73 CDSPIYTRYGSLKSKLMIIMEYLGSGSALDLK--PPPLEETVYATILREILKLDY 130
QY 142 LHSNNMHRVYKAGNILLSPGLVKLGDFGSASTADP-----NSFVGTPYMAPEVILAM 197

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DB 131 LHSERKTHRIDIKANVLLSOGDYKMADFGVAGQLDFTQIKRNTFVGTPEWMAPEVI --- 187
QY 198 DEQYDQKVDVWSIGITCIELAEKRPPLFNMNMSALYHTAIONESPALQSGHMYEPNF 257
DB 188 KQSAVDKPAIWSIGITAIELACGEPNSDLHPRVYFLPKNNPFLF-GHNSKPKRF 246
QY 258 VDSCLQKIPQDRPTSEVILKRPVLR-ERPPYIMDLIOFTKCAVRELMDLYRKMKIL 316
DB 247 VEACLNDPFRFPYAKELKKHFTFRYTKKTSFLETIDR-----YKRKMS-- 292
QY 317 FQENPNPGADAPPEER---EAE-----PY--MIRAGTILSLSES 353
DB 293 ----EGHGESESDSDIDGEADGEGPITWTFPTIRSPHKLHG--TALHSOK 344
QY 354 VPSMSISASSOSSSVNSLADSDNEEEEEE-----EEEE-----EEEGPESREM 401
DB 345 -PAEPIKRPQRSQCLSTLVPRVGELEKHKQSGSGVGALEENAFSLAESCPGISDK 403
QY 402 AMMOGEHYVT-SHS 415
DB 404 LNVHLVERVQRFSS 418
RESULT 4
STK3_HUMAN
ID STK3_HUMAN STANDARD; PRT; 491 AA.
AC 013188; 015801; 015445;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Serine/threonine protein kinase 3 (EC 2.7.1.37) (STE20-1like kinase
DE MST2) (MST-2) (Mammalian STE20-1like protein kinase 2)
DE (Serine/threonine protein kinase Krs-1).
GN STK3 OR MST2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96144292; PubMed=8566796;
RA Creasy C.L., Chernoff J.;
RT "Cloning and characterization of a member of the MST subfamily of
RT Ste20-1like kinases.";
RL Gene 167:303-306(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96413604; PubMed=8816758;
RA Taylor L.K., Wang H.C., Erikson R.L.;
RT "Newly identified stress-responsive protein kinases, Krs-1 and Krs-
RT 2.",
RL Proc. Natl. Acad. Sci. U.S.A. 93:10099-10104(1996).
RN [3]
RP SEQUENCE OF 96-203 FROM N.A.
RX MEDLINE=94100173; PubMed=8274451;
RA Schultz S.J., Nigg E.A.;
RT "Identification of 21 novel human protein kinases, including 3 members
RT of a family related to the cell cycle regulator nimA of Aspergillus
RT nidulans.";
RL Cell Growth Differ. 4:821-830(1993).
CC -1- FUNCTION: OXIDANT STRESS-ACTIVATED SERINE/THREONINE KINASE THAT
CC MAY PLAY A ROLE IN THE RESPONSE TO ENVIRONMENTAL STRESS (BY
CC SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN ADULT KIDNEY,
CC SKELETAL AND PLACENTA TISSUES AND AT VERY LOW LEVELS IN ADULT
CC HEART, LUNG AND BRAIN TISSUES.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC STE20 SUBFAMILY.
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL: U26424; AAC50386.1; -  
DR EMBL: U60206; AAB17261.1; -  
DR EMBL: Z25422; CAAB0909.1; -  
DR HSP: P24941; 1HCL.  
DR Genew: HGNC:11406; STK3.  
DR MIM: 605030; -  
DR InterPro: IPR000719; Euk\_pkinase.  
DR InterPro: IPR002290; Ser\_thr\_pkinase.  
DR Pfam: PF000069; pkinase; 1.  
DR ProDom: PD000001; Euk\_pkinase; 1.  
DR SMART: SM00220; S\_TKC; 1.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; FALSE\_NEG.  
DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR Transferrase: Serine/threonine-protein kinase; ATP-binding.  
FT DOMAIN 27 278 PROTEIN KINASE.  
FT NP\_BIND 33 41 ATP (BY SIMILARITY).  
FT BINDING 56 56 ATP (BY SIMILARITY).  
FT ACT\_SITE 146 146 BY SIMILARITY.  
FT DOMAIN 308 314 POLY-GLU.  
FT DOMAIN 370 375 POLY-GLU.  
FT CONFLICT 96 98 WTG -> YLX (IN REF. 3).  
FT CONFLICT 121 121 D -> Y (IN REF. 3).  
FT CONFLICT 203 203 D -> G (IN REF. 3).  
FT CONFLICT 303 303 D -> E (IN REF. 2).  
FT CONFLICT 332 334 GEC -> EGV (IN REF. 2).  
FT CONFLICT 332 334 GEC -> EGV (IN REF. 2).  
SQ SEQUENCE 491 AA; 56261 MW; 9CA3B0644FC14A9 CRC64;

Query Match 27.6%; Score 595.5; DB 1; Length 491;  
Best Local Similarity 34.4%; Pred. No. 9.8e-29;  
Matches 137; Conservative 68; Mismatches 144; Indels 49; Gaps 8;

QY 24 PEKLFSDLEIGHSGFAYFARDVNSSEVVALKKMSYSGQSNEMKMODIRKREPLQKL 83  
DB 23 PEVFPVLYLKGSGSYGKFAIKHKGQVVALKQYV-----ESDQLQELIKRISIMQC 77  
QY 84 RHPNTIQYRGCYLREHTAMLYMEYC-LGSASDLEVHKRPLOEVEIAAATGALQGLAYL 142  
DB 78 DSYVYVKKYGYSPKNDMLVMEYCGAGSYDILRLNKTLLDELTATILKTLKGLEYL 137  
QY 143 HSNMTHRYKAGNILLSEGLYKLDFFGA-----SIMAPNSFVGPYMAPEVLLAD 198  
DB 138 HEMRK1HRDIKAGNILLNEGAKLADFGVAGQLTDTMKRNRTVIGTPFMAPEVLT--Q 194  
QY 199 EGYDGVKVVWVSLGTCIELAEKRPPLFMNMAVSALYHIAONSPALQSGH-WSEYFRNF 257  
DB 195 ELIGNCVADIVMSIGTISTEAEKRPYADIHPRKALFMTPTNPPFRKPELMSDFTDF 254  
QY 258 VDSCLQIKQDRPTSEVLKHKREPLRPPVYIMDLIORTKDAVRELDNLYRKMKILF 317  
DB 255 VKKCLVKNQEQRTATQQLQHPRTKNAKPVSLRLDITEAMEIKARHDEQCELE--- 311  
QY 318 QEPNPGCAAPPEEEAEAPRYMRACLTLSLESHVPSKMSISASSOSSVNSLAASDN 377  
DB 312 -----EEENSDEDEL-----DSHTMVTYSVECGCTMATRTSTMSGAQT 349  
QY 378 EEEEEEEEEE-----EEEEEGEPSEEMAMQ 405  
DB 350 MIEHNSTMLESLDGLTWVINSDEDEEDGTMKRNATSPQ 387

RESULT 5  
ST24\_HUMAN  
AC Q916E0; O14840; STANDARD; PRT; 443 AA.  
DT 16-OCT-2001 (Rel. 40, Created)  
FT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Serine/threonine protein kinase 24 (EC 2.7.1.37) (STE20-like kinase  
DE MST3) (MST-3) (Mammalian STE20-like protein kinase 3).  
GN STK24 OR MST3 OR STK3.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM A).  
RX MEDLINE=98019249; PubMed=9353338;  
RA Schikmann K., Blenis J.;  
RT "Cloning and characterization of a human STE20-like protein kinase  
RT with unusual cofactor requirements.";  
RL J. Biol. Chem. 272:28695-28703(1997).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM B), AND MUTAGENESIS OF THR-18.  
RC TISSUE=Brain;  
RX MEDLINE=20112612; PubMed=10644707;  
RA Zhou T.-H., Ling K., Guo J., Zhou H., Wu Y.-L., Jing Q., Ma L.,  
RA Pei G.;  
RT "Identification of a human brain-specific isoform of mammalian  
RT STE20-like kinase 3 that is regulated by cAMP-dependent protein  
RT kinase.";  
RL J. Biol. Chem. 275:2513-2519(2000).  
CC -1- FUNCTION: PROTEIN KINASE THAT ACT ON BOTH SERINE AND THREONINE  
CC RESIDUES.  
CC -1- CATALYTIC ACTIVITY: ATP + a protein -> ADP + a phosphoprotein.  
CC -1- COFACTOR: ISOFORM A REQUIRES MANGANESE FOR ITS ACTIVITY.  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A AND B (SHOWN HERE); ARE  
CC PRODUCED BY ALTERNATIVE SPLICING.  
CC -1- TISSUE SPECIFICITY: ISOFORM A IS UBQUITOUS. ISOFORM B IS  
CC EXPRESSED IN BRAIN WITH HIGH EXPRESSION IN HIPPOCAMPUS AND  
CC CEREBRAL CORTEX.  
CC -1- PTM: AUTOPHOSPHORYLATED. ISOFORM B IS ACTIVATED BY PHOSPHORYLATION  
CC BY PKA.  
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
CC STE20 SUBFAMILY.  
CC -----  
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DR EMBL: AF024636; AAB82560.1; -  
DR EMBL: AF083420; AAD42039.1; -  
DR HSP: P24941; 1CRP.  
DR Genew: HGNC:11403; STK24.  
DR MIM: 604984; -  
DR InterPro: IPR000719; Euk\_pkinase.  
DR InterPro: IPR002290; Ser\_thr\_pkinase.  
DR InterPro: IPR001245; Tyr\_pkinase.  
DR Pfam: PF000069; pkinase; 1.  
DR PRINTS: PR00109; TYRKINASE.  
DR ProDom: PD000001; Euk\_pkinase; 1.  
DR SMART: SM00220; S\_TKC; 1.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; FALSE\_NEG.  
DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR Transferrase: Serine/threonine-protein kinase; ATP-binding;  
KW Phosphorylation; Alternative splicing.  
KW DOMAIN 36 286 PROTEIN KINASE.  
FT NP\_BIND 42 50 ATP (BY SIMILARITY).  
FT BINDING 65 65 ATP (BY SIMILARITY).  
FT ACT\_SITE 156 156 BY SIMILARITY.  
FT MOD\_RES 18 18 PHOSPHORYLATION (BY PKA).  
FT VARSPPLIC 1 26 MDSRAQWLGLAANKRRATLPHRGSGT -> MAHSPVQGLP  
FT FT  
FT MUTAGEN 18 18 T->A: LOSS OF PHOSPHORYLATION BY PKA.

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FT CONFLICT 414 414 A -> V (IN REF. 2).
SQ SEQUENCE 443 AA; 49307 MM; 4A9FF16B6A8A97 CRC64;
Query Match 27.5%; Score 594; DB 1; Length 443;
Best Local Similarity 45.8%; Pred. No. 1,1e-28;
Matches 130; Conservative 48; Mismatches 92; Indels 14; Gaps 7;

OY 21 KDDPEKLFSDLRBIGHGSGFAYVFARDVNSEVAIKKMSYSGKSNKMODIIEKREPL 80
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 29 KADPEELFTKLEKKGSGEYFKGIDNRQKVAIKIIDL--EAEDEIEDIQOETVL 86
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 81 QKLRHNTIOYRGCYLRHTAWLMEYC-IGSADLLEVHKRPLEVEAATVHGALOG 139
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 87 SQCDSPYVKKYGYSLKDKRMIMEXLGGGSALDLE--PGPLDETQIATILREILKGL 144
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 140 AYHSHNMTHRDYKAGNILLSEPLVKLGDFGSASIMAPA---NSVGTPTPMAPREVIL 195
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 145 DYHSEKTHRDYKAGNILLSEPLVKLGDFGSASIMAPA---NSVGTPTPMAPREVIL 203
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 196 AMDEGOYDGVVWVSLGTCIEIAERKPLPFNNMAMSAHYHIAONESPALOGSHSEYFR 255
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 204 --KQSAVDKADIMSLGITAIELARGEPRHSELPKMKVLFILKKNPPTLE-GNYSKPLK 260
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 256 NEVDCLQKIPDPTSEVLLKHFVLRERPP-VIMDLIQRTK 298
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 261 EFEVACLINKEPSFRPTAKELKHKRFLIRNAKTSYLTFLIDRYK 304
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 6
ST75_HUMAN STANDARD; PRT; 426 AA.
ID ST75_HUMAN 000506; Q15522;
AC 000506; Q15522;
DT 16-OCT-2001 (rel. 40, Created)
DT 16-OCT-2001 (rel. 40, Last sequence update)
DE 16-OCT-2001 (rel. 40, Last annotation update)
DE Serine/threonine protein kinase 25 (Ec 2.7.1.37) (sterile 20/oxidant stress/threonine kinase 1) (Ste20/oxidant stress response kinase-1) (SOK-1) (Ste20-like kinase).
GN STK25 OR SOK1 OR YSK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-97042345; PubMed=8887545;
RA Pomo C.M., Bonventre J.V., Molnar A., Kyriakis J., Force T.;
RT "Activation of a human Ste20-like kinase by oxidant stress defines a novel stress response pathway.";
RL EMBO J. 15:4537-4546(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-97304522; PubMed=9160885;
RA Osada S.-I., Izawa M., Saito R., Mizuno K., Suzuki A., Hirai S.-I., Ohno S.;
RT "YSK1, a novel mammalian protein kinase structurally related to Ste20 and SPK1, but is not involved in the known MAPK pathways.";
RL Oncogene 14:2047-2057(1997).
CC -1- FUNCTION: OXIDANT STRESS-ACTIVATED SERINE/THREONINE KINASE THAT MAY PLAY A ROLE IN THE RESPONSE TO ENVIRONMENTAL STRESS.
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- ENZYME REGULATION: ACTIVATED BY PHOSPHORYLATION, PROBABLY AUTOPHOSPHORYLATION. THE C-TERMINAL NON-CATALYTIC REGION INHIBITS THE KINASE ACTIVITY.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: UBQUITOUSLY EXPRESSED. HIGHEST LEVELS ARE FOUND IN TESTIS, LARGE INTESTINE, BRAIN AND STOMACH FOLLOWED BY HEART AND LUNG.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC STE20 SUBFAMILY.
CC -----
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CC -----
DR EMBL; X93925; CAA67700.1; -
DR EMBL; D63780; BAA20420.1; -
DR HSSP; P12931; 1FMK.
DR Genew; HGNC:11404; STK25.
DR MIM; 602255; -
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR Prodom; PP000001; Euk_pkinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; FALSE_NEG.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00011; PROTEIN_KINASE_DOM; 1.
DR Transferase; Serine/threonine-protein kinase; ATP-binding; phosphorylation.
KW DOMAIN. 270
FT NP_BIND 26 34 ATP (BY SIMILARITY).
FT BINDING 49 49 ATP (BY SIMILARITY).
FT ACT_SITE 140 140 BY SIMILARITY.
FT CONFLICT 347 348 EP -> DA (IN REF. 1).
SQ SEQUENCE 426 AA; 4811 MM; 183CE5700CEA716 CRC64;

Query Match 27.3%; Score 591; DB 1; Length 426;
Best Local Similarity 36.4%; Pred. No. 1,5e-28;
Matches 154; Conservative 68; Mismatches 129; Indels 72; Gaps 16;

OY 23 DPKLISDLREIGHGSGFAYVFARDVNSEVAIKKMSYSGKSNKMODIIEKREPLQK 82
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 15 DPELFTKIDRIKIGSGEYKGIIDNHTKEVAIKIIDL--EAEDEIEDIQOETVL 72
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 83 LRHPNTIOYRGCYLRHTAWLMEYC-IGSADLLEVHKRPLEVEAATVHGALOG 141
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 73 CDSPIYTRRGYSGLSKTKMLIMEYLGGSALDLK--PEPLEETIATILREILKGLDY 130
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 142 LHSNMIHRDYKAGNILLSEPLVKLGDFGSASIMAPA---NSVGTPTPMAPREVILAM 197
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 131 LHSERKTHRDYKAGNILLSEPLVKLGDFGSASIMAPA---NSVGTPTPMAPREVIL 187
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 198 DEGOYDGVVWVSLGTCIEIAERKPLPFNNMAMSAHYHIAONESPALOGSHSEYFRNF 257
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 188 KQSAVDFKADIMSLGITAIELARGEPRHSELPKMKVLFILKKNPPTLE-GNYSKPLK 246
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 258 VDSCLOKIPDPTSEVLLKHFVLR-ERPPVIMDLIQRTKDAVRELNLQYRKMKKIL 316
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 247 VEACLNKDPFRPTAKELKHKRFLIRNAKTSYLTFLIDR-----YKRWKS-- 292
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 317 FOEAPNGPGAEAEDEE--EAE-----PY--MHRAGTLTLESSHS 353
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 293 -----EGHGESESSSDSIDGEAEDEEQGIWTFPTIRSPSKLHG--TALHSSOK 344
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 354 VPMSSISASSQSSVNSLADASNEEEEEE-----EEEE-----EEGSPESREM 401
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 345 -PAEPVAKRPSQCLSTLVAPVFEELKHKHKGSGSGVGALELENAFSALESCPGISDK 403
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 402 AMM 404
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 404 LMV 406
|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

RESULT 7
ST10_HUMAN STANDARD; PRT; 968 AA.
ID ST10_HUMAN 094804; O94104;
AC 094804; O94104;
DT 16-OCT-2001 (rel. 40, Created)
DT 16-OCT-2001 (rel. 40, Last sequence update)
DT 16-OCT-2001 (rel. 40, Last annotation update)
DE Serine/threonine-protein kinase 10 (Ec 2.7.1.37) (lymphocyte-oriented

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DE kinase).
GN STK10 OR LOK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99216434; PubMed=10199912;
RA Kurumochi S., Matsuda Y., Okamoto M., Kitamura F., Yonekawa H.,
RA Karasuyama H.;
RT "Molecular cloning of the human gene STK10 encoding lymphocyte-
RT oriented kinase, and comparative chromosomal mapping of the human,
RT mouse, and rat homologues."
RN [2]
RP Immunogenetics 49:369-375(1999).
RN
RP SEQUENCE OF 814-968 FROM N.A.
RC TISSUE-Testis;
RA Bloecher H., Boecher M., Brandt P., Mewes H.-W., Gassenhuber J.,
RA Wiemann S.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: CAN ACT ON SUBSTRATES SUCH AS MYELIN BASIC PROTEIN AND
CC HISTONE H1A ON SERINE AND THREONINE RESIDUES (BY SIMILARITY).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN LYMPHOID ORGANS.
CC -!- PTM: AUTOPHOSPHORYLATED (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC STE20 SUBFAMILY.
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-----
DR EMBL: AB015718; BAA35073.1; -
DR EMBL: AL133081; CAB61400.1; -
DR HSSP: P24941; 1CKP.
DR Genew: HGNC:11388; STK10.
DR MIM: 603919; -
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; pkinase.1
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD000001; Euk_pkinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
KM Transferrase; Serine/threonine-protein kinase; ATP-binding;
KM Phosphorylation; Coiled coil.
KW
FT DOMAIN 36 294 PROTEIN KINASE.
FT DOMAIN 573 947 COILED COIL (POTENTIAL).
FT DOMAIN 750 884 GIN-RICH.
FT NP_BIND 42 50 ATP (BY SIMILARITY).
FT BINDING 65 65 ATP (BY SIMILARITY).
FT ACT_SITE 157 157 BY SIMILARITY.
SQ SEQUENCE 968 AA; 112134 MW; 15E245193ECC53D CRC64;

```

Query Match 23.9%; Score 515.5; DB 1; Length 968;  
 Best Local Similarity 33.6%; Pred. No. 1.3e-23;  
 Matches 125; Conservative 65; Mismatches 145; Indels 37; Gaps 9;

```

QY 23 DPEKLFSDREIHSFGAVYFARDVRNSEVAIKKMSYSGKSNKMODIKVEFLQK 82
DB 31 DNEWEIYVIGELGDGAFGVYKA---KNKETGALAAAKYIEKSELEDDYIEIILAT 87
QY 83 LRHPNTIYQRCYLRHETAWLMEVCLGSASD--LLEVHKRPLOEVEIAVTHGALOGIA 140
DB 88 CHPPIYVKLLGAYYHDKGLMIMIEFCPGAGVADIMLEL-DRGITEPQIQVNCROMLEALN 146

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QY 141 YLHSHNMHRDVKAGNIIISPGLVKGDFG----SASIMADANSPVGTPLYMAPEVIL- 195
DB 147 FLHSKRTHRDKAGVNLTLTGDRILADFGVSAKULKTLQKRDSFTIGPIYMAPEVYVC 206
QY 196 -AMDEQYDGRKDVWSLGTICIEIAERKPPFLFNMMASALYHIAONESPALOS-GHWSEY 253
DB 207 EIMKDPYDKADIMSLGTLIEMAQIEPPHHELNMRVLKIAKSDPTLLTPSKWSVE 266
QY 254 FRNFVDSCLQKIPQDRPISVILKRFVLRERPPYIMDLIORTDAVEELNLOYRKMK 313
DB 267 FRDFKLIALDKNPEKPSAOLLEHPFVSSITSNKALRELVAEARAEVVE----- 316
QY 314 KILFQAPNGPAEAPEEEEEAPEYHRAQT----TSLSSHSVSPMSISASSQSSVNS 370
DB 317 -----ETEDG-----RDGEEDAVDAASTLENHTQNSSEVSFSLNDRKPLESPSTP 365
QY 371 LADASDNEEEEE 382
DB 366 LAPSQSDSVNE 377

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RESULT 8
ID ST10_MOUSE STANDARD: PRT; 966 AA.
AC 055098;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Serine/threonine-protein kinase 10 (Ec 2.7.1.37) (Lymphocyte-oriented
DE kinase).
GN STK10 OR LOK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Thymus;
RX MEDLINE=97426413; PubMed=9278426;
RA Kurumochi S., Moriguchi T., Kuida K., Endo J., Semba K., Nishida E.,
RA Karasuyama H.;
RT "LOK is a novel mouse STE20-like protein kinase that is expressed
RT predominantly in lymphocytes."
RL J. Biol. Chem. 272:22679-22684(1997).
CC -!- FUNCTION: CAN ACT ON SUBSTRATES SUCH AS MYELIN BASIC PROTEIN AND
CC HISTONE H1A ON SERINE AND THREONINE RESIDUES.
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN LYMPHOID ORGANS
CC SUCH AS SPLEEN, THYMUS, AND BONE MARROW.
CC -!- PTM: AUTOPHOSPHORYLATED.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC STE20 SUBFAMILY.
-----
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CC or send an email to license@isb-sib.ch).
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DR EMBL: D89728; BAA24073.1; -
DR HSSP: P24941; 1CKP.
DR MGD: MGI:1099439; STK10.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase.1.
DR ProDom: PD000001; Euk_pkinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.

```



KW Transferase; Serine/threonine-protein kinase; ATP-binding;  
 KM Phosphorylation; Coiled coil.  
 FT DOMAIN 36 294 PROTEIN KINASE.  
 FT DOMAIN 588 936 COILED COIL (POTENTIAL).  
 FT DOMAIN 749 883 GIN-RICH.  
 FT NP\_BIND 42 50 ATP (BY SIMILARITY).  
 FT BINDING 65 65 ATP (BY SIMILARITY).  
 FT ACT\_SITE 157 157 BY SIMILARITY.  
 SQ SEQUENCE 966 AA; 111992 MW; 7115EAC01032BF94 CRC64;

Query Match 23.7%; Score 511.5; DB 1; Length 966;  
 Best Local Similarity 26.5%; Pred. No. 2.2e-23;  
 Matches 146; Conservative 77; Mismatches 160; Indels 167; Gaps 12;

QY 23 DPEKLFSDREIGHSGFGAYFADVNSVVAIKKMSYSGKSNKWKODIIEKVEFLQK 82  
 DB 31 DPEVDVEIYGLDGFAGFYKKA---KNETGLAAKAYETSESELEIYIEIELIAT 87  
 QY 83 LRHPNTIQYRGCYLRHTAMLVMEYCLGSASD--LLEVHKRPLQEVETIAVTHGALQGLA 140  
 DB 88 CDHPYIVKLLGAYYYDGKLMIMEFPCPGAVDAIMLEL-DRGLEPDQIQVVCQMLALN 146  
 QY 141 YLASHMIRHDVAGNILLSEPLVKGDPG---SASIMAPANSYVGYPMMAPEVYL- 195  
 DB 147 FLHGKRRIHRDLKAGNVLMLEEDIRLADFGVSAKMLKTLQKRDSEFIPYKMAPEVYLC 206  
 QY 196 -AMDEGOYDQKVDVMSIGITICIELAEKRPFLFNNMNSALYHTAONSPALOS-GHWSEY 253  
 DB 207 EYMKDAPYQKADIMSLGITLIMAOIEPHEHNLNPRVYLITAKSDPPLLTPSKMSVE 266  
 QY 254 FRNEVDSCLOKIPQDRPTSEVLLKRRFVLERPPYIMDLQRTK----- 298  
 DB 267 FRDFLKALDKNETRPSAQLQHFVSVTSNKALRELVAKAEVMEIEDRGDE 326  
 QY 299 ---DAVEILDN----- 306  
 DB 327 EEDAVAVAPVPLVNHQTDSANVTQPSLDSNKLLODSSPTLPPOPEPVNGPCSQPSGDP 386  
 QY 307 -----LQYRKMKKILFOBAPGPAEPEE 332  
 DB 387 LQTTSPADGSKNDNDLKVPLRKSRPLSMARIOMDEKQIPDDDENSPAAKSQKA 446  
 QY 333 EEAEPYHRACTL-----TSLESSHVSPTSISASSQSSSVN---SL-ADAS 375  
 DB 447 NQSRPNSSALETLGEGALTEGELPSSVTPSHSKRASDCSNLSTPSMDYGTSLSDLS 506  
 QY 376 DNEEE-----EEEEEEEEEEEGEPESR 399  
 DB 507 LNKETGSLSGSKLHNKTLKTRTRRVVDGVEVSTTSKLIISDEKKEDEMRLRQELR 566  
 QY 400 EMAMQEGEH 409  
 DB 567 ELRLQKEEH 576

RESULT 9  
 ID PAKL\_RAT STANDARD; PRT; 544 AA.  
 AC P35465; Q62934; 01-JUN-1994 (Rel. 29, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Serine/threonine-protein kinase PAK 1 (EC 2.7.1.-) (p21-activated kinase 1) (PAK-1) (P68-PAK) (Alpha-PAK) (Protein kinase MUK2).  
 GN PAK1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=94150588; PubMed=8107774;

RA Manser E., Leung T., Salihuddin H., Zhao Z.-S., Lim L.;  
 RT "A brain serine/threonine protein kinase activated by Cdc42 and Rac1."  
 RL Nature 367:40-46(1994).  
 RN [2]  
 RP REVISIONS.  
 RA Zhao Z.-S.;  
 RL Submitted (JAN-1998) to the EMBL/Genbank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Osada S.-I., Izawa M., Saito R., Mizuno K., Suzuki A., Hirai S.-I.,  
 RA Ohno S.;  
 RL Submitted (JUL-1996) to the EMBL/Genbank/DBJ databases.  
 RN [4]  
 RP TISSUE SPECIFICITY.  
 RX MEDLINE=96027610; PubMed=7559638;  
 RA Manser E., Chong C., Zhao Z.-S., Leung T., Michael G., Hall C.,  
 RA Lim L.;  
 RT "Molecular cloning of a new member of the p21-Cdc42/Rac-activated kinase (PAK) family."  
 RL J. Biol. Chem. 270:25070-25078(1995).

CC -1- FUNCTION: THE ACTIVATED KINASE ACTS ON A VARIETY OF TARGETS. LIKELY TO BE THE GTPASE EFFECTOR THAT LINKS THE RHO-RELATED GTPASES TO THE JNK MAP KINASE PATHWAY.  
 CC -1- SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND CDC42/P21 AND RAC1 (BY SIMILARITY).  
 CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN THE BRAIN, WITH HIGHER EXPRESSION IN NEURONAL GROUPS ASSOCIATED WITH MOTOR FUNCTION, AND AT LOWER LEVELS IN THE SPLEEN.  
 CC -1- DEVELOPMENTAL STAGE: FOUND IN THE EMBRYONIC CNS WITH LITTLE EXPRESSION ELSEWHERE.  
 CC -1- PTM: AUTOPHOSPHORYLATED WHEN ACTIVATED BY CDC42/P21.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC -1- SIMILARITY: CONTAINS 1 CRIB DOMAIN.

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CC EMBL: U23443; AAB95646.1; -  
 DR EMBL: U49953; AAB61533.1; -  
 DR PIR: S40482; S40482.  
 DR HSSP: P24941; 1CRP.  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR000095; PAKbox/RhoBinding.  
 DR InterPro: IPR002290; Ser\_thr\_pkinase.  
 DR Pfam: PF00069; pkinase; 1.  
 DR Pfam: PF00786; PBD; 1.  
 DR ProDom: PD000001; Euk\_pkinase; 1.  
 DR SMART: SM00285; PBD; 1.  
 DR ProDom: SM00220; S\_TKc; 1.  
 DR PROSITE: PS50108; CRIB; 1.  
 DR PROSITE: PS50107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW Transferase; Serine/threonine-protein kinase; ATP-binding;  
 KM Phosphorylation.  
 FT DOMAIN 75 88 CRIB.  
 FT DOMAIN 134 268 LINKER.  
 FT DOMAIN 269 520 PROTEIN KINASE.  
 FT NP\_BIND 275 283 ATP (BY SIMILARITY).  
 FT BINDING 298 298 ATP (BY SIMILARITY).  
 FT ACT\_SITE 388 388 BY SIMILARITY.  
 SQ SEQUENCE 544 AA; 60577 MW; 93BE32D8222F5B7B CRC64;

Query Match 23.6%; Score 510; DB 1; Length 544;  
 Best Local Similarity 40.9%; Pred. No. 1.4e-23;  
 Matches 117; Conservative 52; Mismatches 103; Indels 14; Gaps 6;

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OY 23 DPEKLESDIREIGHGSGFAYFARDYRNSEVAIKKMSYSGKSNKKWDIIEKVEFLQK 82
DB 264 DPKKKTREKIGQSGAGVYTMADVATGQEVAIKQMNL---QQQPKKELIINEILVIRE 320
OY 83 LRHPNTIOYRGCLREHTAMLVMEYCL-GSASDLLEVHKPKLOEVEIAVTHGALOGLAY 141
DB 321 NKNPNIVNTLSDVLDVDELMVMEYLAGSLIDV--VTETCMDEGOIAVACRECLQALEF 378
OY 142 LHSNMIHRDVAKGNILLSEPLVKLGDFGSASIMAPANS---FVGTPTYMAPEVILAM 197
DB 379 LHSNOYIHRDIKSDNILLGMDGSVKLTDFGCAQITPEQSKSTMTGTPYMAPEV--- 435
OY 198 DEQGYDKVDWSLGTICIELAEKRPPLFNMAASALYHIAQNESPALOSGH-WSEYFRN 256
DB 436 TRKAYGPKVDWSLGTICIELAEKRPPLFNMAASALYHIAQNESPALOSGH-WSEYFRN 495
OY 257 FVDSCLQKIPDRPTSEVLKHFVLRERPPVYIMDLQRTDAVR 302
DB 496 FLNRCLMDVEKRGSAKELLOHOFKIAKPLSLTPLIAAKEATK 541

RESULT 10
PAK1_HUMAN
ID PAK1_HUMAN STANDARD; PRT; 545 AA.
AC Q13153; Q13567;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Serine/threonine-protein kinase PAK 1 (EC 2.7.1.-) (p21-activated
kinase 1) (PAK-1) (P65-PAK) (Alpha-PAK).
GN PAK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBL_Taxid=9606;
RN [1]
RP MEDLINE=97199447; PubMed=9395435;
RA Sells M.A., Klaus U.G., Bagrodia S., Ambrose D.M., Bokoch G.M.,
Chernoff J.;
RT "Human p21-activated kinase (PAK1) regulates actin organization in
mammalian cells."
RL Curr. Biol. 7:202-210(1997).
[2]
RP SEQUENCE FROM N.A.
RC TISSUE=placenta;
RX MEDLINE=96398842; PubMed=8805275;
RA Brown J.L., Stowers L., Baer M., Trejo J., Coughlin S., Chant J.;
RT "Human Ste20 homologue hPAK1 links GTPases to the JNK MAP kinase
pathway."
RL Curr. Biol. 6:598-605(1996).
CC -1- FUNCTION: THE ACTIVATED KINASE ACTS ON A VARIETY OF TARGETS.
LIKELY TO BE THE GTPASE EFFECTOR THAT LINKS THE RHO-RELATED
GTPASES TO THE JNK MAP KINASE PATHWAY.
CC -1- SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND
CDC42/P21 AND RAC1.
CC -1- PTM: AUTOPHOSPHORYLATED WHEN ACTIVATED BY CDC42/P21.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
ST20 SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 1 CRIB DOMAIN.
-----
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-----
CC EMBL: U24152; AA65441.1; -.
DR EMBL: U51120; AAC50590.1; -.
DR HSP: P24941; ICKP.

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DR Genew; HGNC:8590; PAK1.
DR MIM: 602590; -.
DR InterPro: IPR000719; Euk.pkinase.
DR InterPro: IPR000095; PAKbox/Rhoindng.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00786; PBD; 1.
DR ProDom: PD000001; Euk.pkinase; 1.
DR SMART: SM00285; PBD; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS50108; CRIB; 1.
DR PROSITE: PS50107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation.
FT DOMAIN 75 88
FT DOMAIN 134 269
FT 521 LINKER.
FT 521 PROTEIN_KINASE.
FT NP_BIND 270 521 ATP (BY SIMILARITY).
FT BINDING 276 284 ATP (BY SIMILARITY).
FT BINDING 299 299 ATP (BY SIMILARITY).
FT ACT_SITE 389 389 BY SIMILARITY.
FT MOTIF 107 107 L->F: CONSTITUTIVELY ACTIVE.
FT CONFLICT 26 26 V->A (IN REF. 2).
FT CONFLICT 237 237 R->L (IN REF. 2).
FT CONFLICT 379 379 F->S (IN REF. 2).
FT CONFLICT 503 503 D->E (IN REF. 2).
SQ SEQUENCE 545 AA; 60661 MW; 14A1E70E6480CD7E CRC64;

Query Match 23.5%; Score 508; DB 1; Length 545;
Best Local Similarity 40.9%; Pred. No. 1.8e-23;
Matches 117; Conservative 51; Mismatches 104; Indels 14; Gaps 6;

OY 23 DPEKLESDIREIGHGSGFAYFARDYRNSEVAIKKMSYSGKSNKKWDIIEKVEFLQK 82
DB 264 DPKKKTREKIGQSGAGVYTMADVATGQEVAIKQMNL---QQQPKKELIINEILVIRE 321
OY 83 LRHPNTIOYRGCLREHTAMLVMEYCL-GSASDLLEVHKPKLOEVEIAVTHGALOGLAY 141
DB 321 NKNPNIVNTLSDVLDVDELMVMEYLAGSLIDV--VTETCMDEGOIAVACRECLQALEF 379
OY 142 LHSNMIHRDVAKGNILLSEPLVKLGDFGSASIMAPANS---FVGTPTYMAPEVILAM 197
DB 379 LHSNOYIHRDIKSDNILLGMDGSVKLTDFGCAQITPEQSKSTMTGTPYMAPEV--- 436
OY 198 DEQGYDKVDWSLGTICIELAEKRPPLFNMAASALYHIAQNESPALOSGH-WSEYFRN 256
DB 437 TRKAYGPKVDWSLGTICIELAEKRPPLFNMAASALYHIAQNESPALOSGH-WSEYFRN 496
OY 257 FVDSCLQKIPDRPTSEVLKHFVLRERPPVYIMDLQRTDAVR 302
DB 497 FLNRCLMDVEKRGSAKELLOHOFKIAKPLSLTPLIAAKEATK 542

RESULT 11
PAK1_MOUSE
ID PAK1_MOUSE STANDARD; PRT; 545 AA.
AC O88643;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Serine/threonine-protein kinase PAK 1 (EC 2.7.1.-) (p21-activated
kinase 1) (PAK-1) (P65-PAK) (Alpha-PAK) (CDC42/RAC effector kinase
PAK-A).
GN PAK1 OR PAKA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBL_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=99282526; PubMed=10352232;
RA Burbelo P.D., Kozak C.A., Finegold A.A., Hall A., Pirone D.M.;

```

RT "Cloning, central nervous system expression and chromosomal mapping of  
RT the mouse PAK-1 and PAK-3 genes." ;  
RL Gene 232:209-215(1999).  
CC -1- FUNCTION: THE ACTIVATED KINASE ACTS ON A VARIETY OF TARGETS.  
CC LIKELY TO BE THE GTPASE EFFECTOR THAT LINKS THE RHO-RELATED  
CC GTPASES TO THE JNK MAP KINASE PATHWAY (BY SIMILARITY).  
CC -1- SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND  
CC CDC42/P21 AND RAC1 (BY SIMILARITY).  
CC -1- PTM: AUTOPHOSPHORYLATED WHEN ACTIVATED BY CDC42/P21 (BY  
CC SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
CC STE20 SUBFAMILY.  
CC -1- SIMILARITY: CONTAINS 1 CRIB DOMAIN.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: AF082077; AAC32375.1; -.  
DR HSSP: P24941; 1CKP.  
DR MGD: MGI:135975; Pak1.  
DR InterPro: IPR000719; Euk\_pkinase.  
DR InterPro: IPR000095; PAKbox/Rhodung.  
DR InterPro: IPR002290; Ser\_thr\_pkinase.  
DR Pfam: PF00069; pkinase; 1.  
DR Pfam: PF00786; PBD; 1.  
DR ProDom: PD000001; Euk\_pkinase; 1.  
DR SMART: SM00285; PBD; 1.  
DR SMART: SM00220; S\_TKC; 1.  
DR PROSITE: PSS0108; CRIB; 1.  
DR PROSITE: PSS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE: PSS00108; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: PSS00101; PROTEIN\_KINASE\_DOM; 1.  
DR TRANSFERASE: Serine/threonine-protein kinase; ATP-binding;  
KW Phosphorylation.  
FT DOMAIN 75 88 CRIB.  
FT DOMAIN 134 267 LINKER.  
FT DOMAIN 270 521 PROTEIN\_KINASE.  
FT NP\_BIND 276 284 ATP (BY SIMILARITY).  
FT BINDING 299 299 ATP (BY SIMILARITY).  
FT ACT\_SITE 389 389 BY SIMILARITY.  
SQ SEQUENCE 545 AA; 60737 MW; A4861289534C3819 CRC64;  
  
Query Match 23.5%; Score 508; DB 1; Length 545;  
Best Local Similarity 40.6%; Pred. No. 1.8e-23;  
Matches 116; Conservative 52; Mismatches 104; Indels 14; Gaps 6;

PAK3\_RAT  
ID PAK3\_RAT STANDARD; PRT; 544 AA.  
AC 062829;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Serine/threonine-protein kinase PAK 3 (EC 2.7.1.1-) (p21-activated  
DE kinase 3) (PAK-3) (Beta-PAK) (p65-PAK).  
GN PAK3.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE OF 37-56.  
RC TISSUE=Brain;  
RX MEDLINE=96027610; Pubmed=7559638;  
RA Manser E., Chong C., Zhao Z.-S., Leung T., Michael G., Hall C.,  
RA Lim E.;  
RT "Molecular cloning of a new member of the p21-Cdc42/Rac-activated  
RT kinase (PAK) family." ;  
RL J Biol Chem. 270:25070-25078(1995).  
CC -1- FUNCTION: THE ACTIVATED KINASE ACTS ON A VARIETY OF TARGETS.  
CC -1- SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND  
CC CDC42/P21 AND RAC1. SHOWS HIGHLY SPECIFIC BINDING TO THE SH3  
CC DOMAINS OF PHOSPHOLIPASE C-GAMMA AND OF ADAPTER PROTEIN NCK (BY  
CC SIMILARITY).  
CC -1- TISSUE SPECIFICITY: DETECTED AT HIGH LEVELS IN THE BRAIN AND AT  
CC LOW LEVELS IN THE TESTIS.  
CC -1- DEVELOPMENTAL STAGE: FOUND IN THE EMBRYONIC CNS WITH LITTLE  
CC EXPRESSION ELSEWHERE.  
CC -1- PTM: AUTOPHOSPHORYLATED WHEN ACTIVATED BY CDC42/P21.  
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
CC STE20 SUBFAMILY.  
CC -1- SIMILARITY: CONTAINS 1 CRIB DOMAIN.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL: U33314; AAC52268.1; -.  
DR HSSP: P24941; 1CKP.  
DR InterPro: IPR000719; Euk\_pkinase.  
DR InterPro: IPR000095; PAKbox/Rhodung.  
DR InterPro: IPR002290; Ser\_thr\_pkinase.  
DR Pfam: PF00069; pkinase; 1.  
DR Pfam: PF00786; PBD; 1.  
DR ProDom: PD000001; Euk\_pkinase; 1.  
DR SMART: SM00285; PBD; 1.  
DR SMART: SM00220; S\_TKC; 1.  
DR PROSITE: PSS0108; CRIB; 1.  
DR PROSITE: PSS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE: PSS00108; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: PSS00101; PROTEIN\_KINASE\_DOM; 1.  
DR TRANSFERASE: Serine/threonine-protein kinase; ATP-binding;  
KW Phosphorylation.  
FT DOMAIN 70 83 CRIB.  
FT DOMAIN 129 267 LINKER.  
FT DOMAIN 268 519 PROTEIN\_KINASE.  
FT NP\_BIND 274 282 ATP (BY SIMILARITY).  
FT BINDING 297 297 ATP (BY SIMILARITY).  
FT ACT\_SITE 387 387 BY SIMILARITY.  
SQ SEQUENCE 544 AA; 78940FC2042B48B CRC64;  
  
Query Match 23.4%; Score 505; DB 1; Length 544;  
Best Local Similarity 40.6%; Pred. No. 2.7e-23;  
Matches 116; Conservative 52; Mismatches 104; Indels 14; Gaps 6;

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Db      263 DPKKKTREKIGOGASGYVYTLADIATGGEVAIKOMNL---QQQPKKEIINEIIVME 319
OY      83 LRHPNTIYRGCYLRREHTAMLVMEYCL-GSASDLLEVHKRPLOEVEIAAHTGALGLAY 141
Db      320 NKNPNIVNTLDSYLVDELWVMEYLAGSLTDV--VTEFCMDEGOIAACRECLQALDF 377
OY      142 LHSNNMHRDVKAGNILLSEPLVKLGDFGSASIMAPANS---FVGTYPMAPEVILAM 197
Db      378 LHSNOYIHRDIKSDNILLGMDGSVKLDFGFCQIITPEQSKRSTWGTYPMAPEVY--- 434
OY      198 DEQGYGKYDWSLGTITCIELEAKRPPLFNMMASALYHIAONESPALOS-GHWSEYFRN 256
Db      435 TRKAYGPKVDIVSLGIMALEMVEGPEPPYINENPLRALYLATNGTELPQLNPERLSAVFRD 494
OY      257 FVDSCLQKIPQDRPTSEVILKHFVLRERPPYIMDLQRTDAVR 302
Db      495 FLNRKCLEMDVDRGSAKELLQHFLEKLAKPLSLTPLLIAAKEAIK 540

```

## RESULT 13

```

PAK3_HUMAN          STANDARD;          PRT;          544 AA.
ID      PAK3_HUMAN          STANDARD;          PRT;          544 AA.
AC      075914;
DT      15-DEC-1998 (Rel. 37, Created)
DT      15-DEC-1998 (Rel. 37, Last sequence update)
DT      15-JUN-2002 (Rel. 41, Last annotation update)
DE      Serine/threonine-protein kinase PAK 3 (EC 2.7.1.-) (p21-activated
GN      kinase 3) (PAK-3) (Beta-PAK) (oligophrenin-3).
OS      PAK3 OR OPHN3.
OC      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=98400251; PubMed=9731525;
RA      Allen R.M., Gleeson J.G., Bagrodia S., Partington M.W.,
RA      Macmillan J.C., Cerione R.A., Mulley J.C., Walsh C.A.;
RT      "PAK3 mutation in nonsyndromic x-linked mental retardation.";
RL      Nat. Genet. 20:25-30(1998).

```

```

CC      -|- FUNCTION: THE ACTIVATED KINASE ACTS ON A VARIETY OF TARGETS.
CC      -|- SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND
CC      CDC42/P21 AND RAC1. SHOWS HIGHLY SPECIFIC BINDING TO THE SH3
CC      DOMAIN OF PHOSPHOLIPASE C-GAMMA AND OF ADAPTER PROTEIN NCK.
CC      -|- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN POSTMITOTIC NEURONS OF THE
CC      DEVELOPING AND POSTNATAL CEREBRAL CORTEX AND HIPPOCAMPUS.
CC      -|- PTM: AUTOPHOSPHORYLATED WHEN ACTIVATED BY CDC42/P21.
CC      -|- DISEASE: DEFECTS IN PAK3 ARE A CAUSE OF AN X-LINKED FORM OF
CC      NONSYNDROMIC MENTAL RETARDATION (MRX30).
CC      -|- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC      STE20 SUBFAMILY.
CC      -|- SIMILARITY: CONTAINS 1 CRIB DOMAIN.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AF068864; AAC36097.1; -.
DR      HSSP; P24941; ICKP.
DR      Genew; HGNC:8592; PAK3.
DR      MIM; 300142; -.
DR      InterPro; IPR000719; Pak_pkinase.
DR      InterPro; IPR000095; Pakbox/RhoGndy.
DR      InterPro; IPR002290; Ser_thr_pkinase.
DR      Pfam; PF00069; pkinase; 1.
DR      Pfam; PF00786; PBD; 1.
DR      ProDom; PD000001; Euk_pkinase; 1.
DR      SMART; SM00285; PBD; 1.

```

```

DR      SMART; SM00220; S_TKC; 1.
DR      PROSITE; PS50108; CRIB; 1.
DR      PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR      PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR      PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW      Transferase; Serine/threonine-protein kinase; ATP-binding;
KW      SH3-binding; Phosphorylation.
FT      DOMAIN 129 267 LINKER.
FT      DOMAIN 268 519 PROTEIN_KINASE.
FT      NP_BIND 274 282 ATP (BY SIMILARITY).
FT      BINDING 297 297 ATP (BY SIMILARITY).
FT      ACT_SITE 387 387 BY SIMILARITY.
SQ      SEQUENCE 544 AA; 60692 MW; 230AF6952CB049E2 CRC64;

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Query Match 23.3%; Score 504; DB 1; Length 544;  
 Best Local Similarity 40.6%; Pred. No. 3; le-23;  
 Matches 116; Conservative 52; Mismatches 104; Indels 14; Gaps 6;

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OY      23 DPEKLESDIREIGHGSFGAVYFARVDRNSEVVAIKKMSYSGKSNKEMODIIEKVEFLQK 82
Db      263 DPKKKTREKIGOGASGYVYTLADIATGGEVAIKOMNL---QQQPKKEIINEIIVME 319
OY      83 LRHPNTIYRGCYLRREHTAMLVMEYCL-GSASDLLEVHKRPLOEVEIAAHTGALGLAY 141
Db      320 NKNPNIVNTLDSYLVDELWVMEYLAGSLTDV--VTEFCMDEGOIAACRECLQALDF 377
OY      142 LHSNNMHRDVKAGNILLSEPLVKLGDFGSASIMAPANS---FVGTYPMAPEVILAM 197
Db      378 LHSNOYIHRDIKSDNILLGMDGSVKLDFGFCQIITPEQSKRSTWGTYPMAPEVY--- 434
OY      198 DEQGYGKYDWSLGTITCIELEAKRPPLFNMMASALYHIAONESPALOS-GHWSEYFRN 256
Db      435 TRKAYGPKVDIVSLGIMALEMVEGPEPPYINENPLRALYLATNGTELPQLNPERLSAVFRD 494
OY      257 FVDSCLQKIPQDRPTSEVILKHFVLRERPPYIMDLQRTDAVR 302
Db      495 FLNRKCLEMDVDRGSAKELLQHFLEKLAKPLSLTPLLIAAKEAIK 540

```

## RESULT 14

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PAK3_MOUSE          STANDARD;          PRT;          544 AA.
ID      PAK3_MOUSE          STANDARD;          PRT;          544 AA.
AC      Q61036; 088645;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      15-JUN-2002 (Rel. 41, Last annotation update)
DE      Serine/threonine-protein kinase PAK 3 (EC 2.7.1.-) (p21-activated
GN      kinase 3) (PAK-3) (Beta-PAK) (CDC42/RAC effector kinase PAK-B).
GN      PAK3 OR PAK-3 OR STK4 OR PAKB.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=99282526; PubMed=10352232;
RA      Bagrodia S., Taylor S.J., Creasy C.L., Chernoff J., Cerione R.A.;
RT      "Identification of a mouse p21cdc42/Rac activated kinase.";
RL      J. Biol. Chem. 270:22731-22737(1995).

```

```

CC      -|- FUNCTION: THE ACTIVATED KINASE ACTS ON A VARIETY OF TARGETS.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AF068864; AAC36097.1; -.
DR      HSSP; P24941; ICKP.
DR      Genew; HGNC:8592; PAK3.
DR      MIM; 300142; -.
DR      InterPro; IPR000719; Pak_pkinase.
DR      InterPro; IPR000095; Pakbox/RhoGndy.
DR      InterPro; IPR002290; Ser_thr_pkinase.
DR      Pfam; PF00069; pkinase; 1.
DR      Pfam; PF00786; PBD; 1.
DR      ProDom; PD000001; Euk_pkinase; 1.
DR      SMART; SM00285; PBD; 1.

```

```

CC -1- SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND
CC CDC42/P21 AND RAC1. SHOWS HIGHLY SPECIFIC BINDING TO THE SH3
CC DOMAINS OF PHOSPHOLIPASE C-GAMMA AND OF ADAPTER PROTEIN NCK.
CC -1- PFM: AUTOPHOSPHORYLATED WHEN ACTIVATED BY CDC42/P21.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC STE20 SUBFAMILY.
CC -1- SIMILARITY: CONTAINS 1 CRIB DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U39738; AAC52354.1; -
CC EMBL: AF082297; AAC31969.1; -
CC HSSP: P24941; ICKP.
CC MGD: MGI:1339656; Pak3.
CC InterPro: IPR000719; Pakbox/Rhodung.
CC InterPro: IPR000095; Pakbox/Rhodung.
CC InterPro: IPR002290; Ser_thr_pkinase.
CC Pfam: PF00069; pkinase; 1.
CC Pfam: PF00786; PBD; 1.
CC ProDom: PD000001; Euk_pkinase; 1.
CC SMART: SM00285; PBD; 1.
CC SMART: SM00220; S_TKc; 1.
CC PROSITE: PS50107; CRIB; 1.
CC PROSITE: PS50107; PROTEIN_KINASE_ATP; 1.
CC PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
CC PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
CC Transfaser: Serine/threonine-protein kinase; ATP-binding;
CC SH3-binding; Phosphorylation.
CC KW SH3-binding; Phosphorylation.
CC FT DOMAIN 70 83
CC FT DOMAIN 129 267
CC FT NP_BIND 268 519
CC FT NP_BIND 274 282
CC FT BINDING 297 387
CC FT ACT_SITE 361 361
CC FT CONFLICT 161 161
CC FT CONFLICT 361 361
CC FT CONFLICT 493 493
CC FT CONFLICT 525 525
CC FT CONFLICT 525 525
CC SEQUENCE 544 AA; 60683 MW; C4AEB71DD33E6988 CRC64;

Query Match 23.1%; Score 500; DB 1; Length 544;
Best Local Similarity 40.2%; Pred. No. 5.4e-23;
Matches 115; Conservative 52; Mismatches 105; Indels 14; Gaps 6;

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ID SP51_YEAST STANDARD; PRT; 490 AA.
AC P08458;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Sporulation-specific protein 1 (EC 2.7.1.-).
GN SP51 OR YDR523C OR D9719.27.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Friesen H., Lunz R., Doyle S., Segall J.;
RA Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Dietrich F.S., Mulligan J., Allen E., Araujo R., Aviles E.,
RA Berne A., Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M.,
RA Hunnicke-Smith S., Hyman R., Komp C., Lashkari D., Lew H., Lin D.,
RA Mosedale D., Nakahara K., Namath A., Oefner F., Oh C., Petel F.X.,
RA Roberts D., Schramm S., Schroeder M., Shogren T., Shroff N.,
RA Winant A., Yelton M., Botstein D., Davis R.W.;
RA Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 396-490 FROM N.A.
RX MEDLINE=87064542; PubMed=3023934;
RA Percival-Smith A., Segall J.;
RT "Characterization and mutational analysis of a cluster of three genes
RT expressed preferentially during sporulation of Saccharomyces
RT cerevisiae."
RL Mol. Cell. Biol. 6:2443-2451(1986).
CC -1- FUNCTION: SERINE/THREONINE PROTEIN KINASE REQUIRED FOR SPORE WALL
CC DEVELOPMENT.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC STE20 SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U13018; AAA64833.1; -
CC EMBL: U33057; AAB64963.1; -
CC EMBL: M13629; AAA35079.1; -
CC PIR: B25376; B25376.
CC SCD: S0002931; SP51.
CC InterPro: IPR000719; Euk_pkinase.
CC InterPro: IPR002290; Ser_thr_pkinase.
CC Pfam: PF00069; pkinase; 1.
CC ProDom: PD000001; Euk_pkinase; 1.
CC SMART: SM00220; S_TKc; 1.
CC PROSITE: PS50107; PROTEIN_KINASE_ATP; 1.
CC PROSITE: PS50108; PROTEIN_KINASE_ST; FALSE_NEG.
CC PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
CC Transfaser: Serine/threonine-protein kinase; ATP-binding;
CC Sporulation; Meiosis.
CC KW Sporulation; Meiosis.
CC FT DOMAIN 18 272
CC FT NP_BIND 24 32
CC FT BINDING 47 47
CC FT ACT_SITE 141 141
CC FT CONFLICT 454 454
CC FT CONFLICT 469 469
CC FT CONFLICT 469 469
CC SEQUENCE 490 AA; 55704 MW; 614305585BAFAFF CRC64;

Query Match 23.1%; Score 499; DB 1; Length 490;
Best Local Similarity 36.4%; Pred. No. 5.5e-23;
Matches 135; Conservative 67; Mismatches 129; Indels 40; Gaps 14;

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Db      14 PSKLYSIGSCYGRGNGFVGUYKAVDROVTOEIAIVLVNL--EHSODEIELLAQELFFIAEL 71
QY      84 RHPNTIOYRGCYLREHRTAMWMEYC-LGSADLLE-VHKRPLOEVEIAVTHGALOGLAY 141
Db      72 KSPLTINYATMLIEDVSMWIMEYECGGGSCSDLLKRSYVNGLPREKVSFIITHEVTGLKY 131
QY      142 LHSNHHMHRDYKAGNILLSEPGVLYKLDGFC-SASIMA--PANSVVGPIPMAREVILIAMD 198
Db      132 LHEORKIHRDIKANILLINEGMVKLDFGVSGHIRSTLKRDFEFGPYMMAREEVUCEV 191
QY      199 EGYDQKVDVMSLGIITCELEAKRPRLEFNMMASALYHIIONESPALQSGHSEYFNFEV 258
Db      192 DG-YNEKADIMSLGIIITYELKGLRPLSKYDPMKVMNLPKRKPKLQ--GPFSDAADFV 249
QY      259 DSCLOKITQODRPTSEVLLKHFFVLERPPYI-----MDLIQRKDAVRELDNIQYKKM 313
Db      250 AGCELVKTPPADRPSAYNMLSEFEV---KNITITMLKSDVDLTIKOKK--VQE-----RTKVP 300
QY      314 KI-----LFOEAPRPGAE-----APEEEEAEPYIMRAGTLT--SLESMSHVS 356
Db      301 KYPLONRITKXNSNTRVKGKEWNEPESTRLSITQISKEELSPITDOSPSSLNMESPYLLHG 360
QY      357 MSIASOSSS 367
Db      361 QVTVPITNPSS 371

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Search completed: November 22, 2002, 12:24:17  
Job time : 9.448 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: November 22, 2002, 12:20:50 ; Search time 23.088 Seconds  
(without alignments)  
3712.561 Million cell updates/sec

Title: US-09-686-346a-4\_COPY\_1\_416

Perfect score: 2161

Sequence: 1 MPAGRAGSLKDPVAELFF.....ESREMMMQEGEHTVTSRSS 416

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL\_21:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phase:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rv1rus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2161	100.0	1235	11	Q9JLS3
2	2133	98.7	1049	4	Q94957
3	2133	98.7	1235	4	Q94957
4	1728.5	80.0	1001	11	Q94954
5	1726.5	79.5	1005	4	Q94954
6	1718.5	79.5	1001	4	Q94954
7	1540.5	71.3	898	4	Q94954
8	1538.5	71.2	898	13	Q94954
9	1537.5	71.1	898	4	Q94954
10	1531.5	70.9	898	4	Q94954
11	1480.5	68.5	898	4	Q94954
12	1300	60.2	1039	5	Q94954
13	987	45.7	1062	4	Q94954
14	902.5	41.8	398	4	Q94954
15	677	31.3	842	10	Q94954
16	646	29.9	836	10	Q94954

17	639	29.6	1120	10	Q9JLS3	Q9JLS3
18	634.5	29.4	445	11	Q60877	Q60877
19	634.5	29.4	497	11	Q9J110	Q9J110
20	625.5	28.9	809	10	Q8YVCL	Q8YVCL
21	623	28.8	825	10	Q8SAE1	Q8SAE1
22	618.5	28.6	825	10	Q9ARL7	Q9ARL7
23	615.5	28.5	487	11	Q9J111	Q9J111
24	605	28.0	1268	4	Q9UKD8	Q9UKD8
25	605	28.0	1276	4	Q9UKD1	Q9UKD1
26	605	28.0	1307	4	Q9UKD9	Q9UKD9
27	605	28.0	1305	4	Q9UKD3	Q9UKD3
28	605	28.0	1333	4	Q9UKD0	Q9UKD0
29	605	28.0	1331	4	Q9UKD4	Q9UKD4
30	605	28.0	1352	4	Q9UKD2	Q9UKD2
31	605	28.0	1360	4	Q9UKD5	Q9UKD5
32	600.5	27.8	461	5	Q61125	Q61125
33	598	27.7	491	4	Q96FM6	Q96FM6
34	596	27.6	431	11	Q96R88	Q96R88
35	595	27.5	426	4	Q96BA2	Q96BA2
36	594	27.5	478	5	Q62571	Q62571
37	592.5	27.4	669	5	Q8T0S6	Q8T0S6
38	587.5	27.2	491	11	Q54748	Q54748
39	587	27.2	596	5	Q9V8W4	Q9V8W4
40	576.5	26.7	416	11	Q9JMT2	Q9JMT2
41	572.5	26.5	1300	11	Q9JMT9	Q9JMT9
42	572.5	26.5	1308	11	Q9JMT5	Q9JMT5
43	571	26.4	416	4	Q9P289	Q9P289
44	570.5	26.4	1295	4	Q9P2R8	Q9P2R8
45	570.5	26.4	1303	4	Q9P1X1	Q9P1X1

## ALIGNMENTS

RESULT 1  
ID Q9JLS3 PRELIMINARY; PRT; 1235 AA.

AC Q9JLS3:  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
DE Serine/threonine protein kinase TAO2.  
GN TAO2.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-99428563; PubMed-10497253;  
RA Chen Z., Hutchison M., Cobb M.H.;  
RT "Isolation of the protein kinase TAO2 and identification of its  
RT mitogen-activated protein kinase/extracellular signal-regulated kinase  
RT kinase binding domain."  
RL J. Biol. Chem. 274:28803-28807(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Chen Z., Hutchison M., Cobb M.;  
RA Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
DR EMBL: A0140556; A0139480.2; -  
DR HSSP: P24941; 1B38.  
DR InterPro: IPR000719; Euk\_pkinase.  
DR InterPro: IPR001899; Gram\_pos\_anchor.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR002290; Ser\_thr\_pkinase.  
DR InterPro: IPR001245; Tyr\_pkinase.  
DR Pfam: PF00069; pkinase; I.  
DR PRINTS: PR00109; TYRKINASE.  
DR ProDom: PD000001; Euk\_pkinase; 1.  
DR SMART: SM00220; S\_TKc; 1.  
DR PROSITE: PS00343; GRAM\_POS\_ANCHORING; UNKNOWN\_1.  
DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_1.

DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
 SQ SEQUENCE 1235 AA; 138750 MM; 426960DD812518AD CRC64;

Query Match 100.0%; Score 2161; DB 11; Length 1235;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-158;  
 Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAGRAGSLKPDVAELFFKDDPEKLFSDLRIGSGFGAYFPADVNSSEVAIAKKMS 60  
 DB 1 MPAGRAGSLKPDVAELFFKDDPEKLFSDLRIGSGFGAYFPADVNSSEVAIAKKMS 60  
 QY 61 YSGKSNEMKMODIIKEVRFLQKLRHPTIYRGCYLREHTAMLVMEYCLGSASDLLEVHK 120  
 DB 61 YSGKSNEMKMODIIKEVRFLQKLRHPTIYRGCYLREHTAMLVMEYCLGSASDLLEVHK 120  
 QY 121 KPLQVEIATAVTHGALQGLAYLHSHNMIRDYKAGNILLSEGLYKLGDFGSASIAWAPAN 180  
 DB 121 KPLQVEIATAVTHGALQGLAYLHSHNMIRDYKAGNILLSEGLYKLGDFGSASIAWAPAN 180  
 QY 181 SVVGTPYMAPEVILLAMDGOYDKVDVSLGITCTELAEKRPPLFNMMASALYHIAON 240  
 DB 181 SVVGTPYMAPEVILLAMDGOYDKVDVSLGITCTELAEKRPPLFNMMASALYHIAON 240  
 QY 241 ESPALQSGHMSSEYFRNFVDSCLQKIPQDRPTSEVLKHFVLRERPTVIMDLIQRTKA 300  
 DB 241 ESPALQSGHMSSEYFRNFVDSCLQKIPQDRPTSEVLKHFVLRERPTVIMDLIQRTKA 300  
 QY 301 VRELNLQYRKMKKILFOEAPNGPGAEPDEEAPYHNRAGTILTSLSHSPMSIS 360  
 DB 301 VRELNLQYRKMKKILFOEAPNGPGAEPDEEAPYHNRAGTILTSLSHSPMSIS 360  
 QY 361 ASSOSSVNSLADASDNEEEEEEEEEEEBEGPESREMMAMOGCHTVSHSS 416  
 DB 361 ASSOSSVNSLADASDNEEEEEEEEEEEBEGPESREMMAMOGCHTVSHSS 416

## RESULT 2

Q94957 PRELIMINARY; PRT; 1049 AA.

AC 094957;  
 DT 01-MAY-1999 (TREMBLrel. 10, Created)  
 DT 01-MAY-1999 (TREMBLrel. 10, last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)  
 DE KIA0881 protein (STE20-like kinase).  
 GN KIA0881.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=BRIN;  
 RC MEDLINE=99156230; PubMed=10048485;  
 RA Nagase T., Ishikawa K., Suyama M., Kikuno R., Hirosewa M.,  
 RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;  
 RT "Prediction of the coding sequences of unidentified human genes. XII.  
 RT The complete sequences of 100 new cDNA clones from brain which code  
 RT for large proteins in vitro.";  
 RL DNA Res. 5:355-364(1998).  
 RP SEQUENCE FROM N.A.  
 RA Yuste J.T., Robinson D., Templeton D.J., Kung H.-J.;  
 RT "Characterization of a Subfamily of Human STE20-like Kinases that  
 RT Selectively Activate p38 Through MK3 and are Regulated via a p38A-  
 RT dependent Mechanism.";  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC EMBL; AB020688; BA74904.1; -;  
 CC EMBL; AF263313; AAG38503.1; -;  
 DR HSP; P24941; 1B38.

DR InterPro; IPR000719; Euk\_pkinase.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR Pfam; PF00069; pkinase; 1.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR PRODOM; PD000001; Euk\_pkinase; 1.  
 DR SMART; SM00220; S\_TKc; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
 SQ SEQUENCE 1049 AA; 119280 MM; D6C5062EF47794030 CRC64;

Query Match 98.7%; Score 2133; DB 4; Length 1049;  
 Best Local Similarity 99.0%; Pred. No. 3.4e-156;  
 Matches 412; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

QY 1 MPAGRAGSLKPDVAELFFKDDPEKLFSDLRIGSGFGAYFPADVNSSEVAIAKKMS 60  
 DB 1 MPAGRAGSLKPDVAELFFKDDPEKLFSDLRIGSGFGAYFPADVNSSEVAIAKKMS 60  
 QY 61 YSGKSNEMKMODIIKEVRFLQKLRHPTIYRGCYLREHTAMLVMEYCLGSASDLLEVHK 120  
 DB 61 YSGKSNEMKMODIIKEVRFLQKLRHPTIYRGCYLREHTAMLVMEYCLGSASDLLEVHK 120  
 QY 121 KPLQVEIATAVTHGALQGLAYLHSHNMIRDYKAGNILLSEGLYKLGDFGSASIAWAPAN 180  
 DB 121 KPLQVEIATAVTHGALQGLAYLHSHNMIRDYKAGNILLSEGLYKLGDFGSASIAWAPAN 180  
 QY 181 SVVGTPYMAPEVILLAMDGOYDKVDVSLGITCTELAEKRPPLFNMMASALYHIAON 240  
 DB 181 SVVGTPYMAPEVILLAMDGOYDKVDVSLGITCTELAEKRPPLFNMMASALYHIAON 240  
 QY 241 ESPALQSGHMSSEYFRNFVDSCLQKIPQDRPTSEVLKHFVLRERPTVIMDLIQRTKA 300  
 DB 241 ESPALQSGHMSSEYFRNFVDSCLQKIPQDRPTSEVLKHFVLRERPTVIMDLIQRTKA 300  
 QY 301 VRELNLQYRKMKKILFOEAPNGPGAEPDEEAPYHNRAGTILTSLSHSPMSIS 360  
 DB 301 VRELNLQYRKMKKILFOEAPNGPGAEPDEEAPYHNRAGTILTSLSHSPMSIS 360  
 QY 361 ASSOSSVNSLADASDNEEEEEEEEEEEBEGPESREMMAMOGCHTVSHSS 416  
 DB 361 ASSOSSVNSLADASDN--EEEEEEEEEEEEBEGPESREMMAMOGCHTVSHSS 414

## RESULT 3

Q90L54 PRELIMINARY; PRT; 1235 AA.

AC Q90L54;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)  
 DE Prostate derived STE20-like kinase PSK.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxId=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=BREAST CARCINOMA;  
 RC MEDLINE=20127920; PubMed=10660600;  
 RA Moore T.M., Garg R., Johnson C., Copiccoat M.J., Ridley A.J.,  
 RA Morris J.D.H.;  
 RT "PSK, a novel STE20-like kinase derived from prostatic carcinoma that  
 RT activates the JNK MAPK pathway and regulates actin cytoskeletal  
 RT organization.";  
 RL J. Biol. Chem. 275:4311-4322(2000).  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC EMBL; AF061943; AAD45616.1; -;  
 DR HSP; P24941; 1B38.  
 DR InterPro; IPR000719; Euk\_pkinase.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.



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DR InterPro: IPR001245; Tyr-kinase.
DR Pfam: PF00069; kinase: 1.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD000001; Euk-kinase: 1.
DR SMART: SM00220; S_TKc: 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding: Kinase; Serine/threonine/protein kinase; Transferase.
SQ SEQUENCE 1235 AA; 138232 MW; 3AB9EBE690934307 CRC64;

Query Match          98.7%; Score 2133; DB 4; Length 1235;
Best Local Similarity 99.0%; Pred. No. 4,3e-156;
Matches 412; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

QY 1 MPAGGAGSGSLKDDVALELFKDDPEKLFSDLRREIGHSGFGAVYFARDVRNSEVVAIKKMS 60
   |||||||
DB 1 MPAGGAGSGSLKDDVALELFKDDPEKLFSDLRREIGHSGFGAVYFARDVRNSEVVAIKKMS 60

QY 61 YSGKSNSEKMODIIKEVRFLOKLRHPNTIOYRGCYLREHTAMLVMEYCLGSASDLEVHK 120
   |||||||
DB 61 YSGKSNSEKMODIIKEVRFLOKLRHPNTIOYRGCYLREHTAMLVMEYCLGSASDLEVHK 120

QY 121 KPIQVEIIAAVTHGALQGLAYLHSHNMHRDVAKAGNILLSEPGIVKLGDFGSASIMAPAN 180
   |||||||
DB 121 KPIQVEIIAAVTHGALQGLAYLHSHNMHRDVAKAGNILLSEPGIVKLGDFGSASIMAPAN 180

QY 181 SFVGTPTWMAPEVILAMDEQYDGKDVWSLGTCTIEFLARKRPPLFNMMASALYHTAQN 240
   |||||||
DB 181 SFVGTPTWMAPEVILAMDEQYDGKDVWSLGTCTIEFLARKRPPLFNMMASALYHTAQN 240

QY 241 ESPALSGHSEYFRNFVDSCLQIPODRPTSEVLKHFRLRERPTVIMDLIQRTKDA 300
   |||||||
DB 241 ESPALSGHSEYFRNFVDSCLQIPODRPTSEVLKHFRLRERPTVIMDLIQRTKDA 300

QY 301 VRELDNLQYRKMKKILFQEAHPNGGAPEPEEAEPEYMRAGTITLSLSHSPSKSIS 360
   |||||||
DB 301 VRELDNLQYRKMKKILFQEAHPNGGAPEPEEAEPEYMRAGTITLSLSHSPSKSIS 360

QY 361 ASSOSSSVNSLADASDNEEEEEEEEEEEEGPESRMMAMQGEHTVTSHSS 416
   |||||||
DB 361 ASSOSSSVNSLADASDNEEEEEEEEEEEEGPESRMMAMQGEHTVTSHSS 416

RESULT 4
088664 PRELIMINARY; PRT; 1001 AA.
AC 088664;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, last annotation update)
DE Serine/threonine protein kinase TA01.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99003202; PubMed=9786855;
RA Hutchison M., Berman K.S., Cobb M.H.;
RT "Isolation of TA01, a protein kinase that activates MEKs in stress-
   activated protein kinase cascades.";
RT J. Biol. Chem. 273:28625-28632(1998).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
EMBL: AF084205; AAC71014.1; -.
DR HSSP: P24941; 1B38.
DR InterPro: IPR000719; Euk-kinase.
DR InterPro: IPR002290; Ser_thr-kinase.
DR Pfam: PF000069; kinase: 1.
DR ProDom: PD000001; Euk-kinase: 1.
DR SMART: SM00220; S_TKc: 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_DOM; 1.
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DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding: Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 1001 AA; 115952 MW; 85511B62DBD2FCC CRC64;

Query Match          80.0%; Score 1728.5; DB 11; Length 1001;
Best Local Similarity 79.6%; Pred. No. 6e-125;
Matches 331; Conservative 32; Mismatches 32; Indels 21; Gaps 1;

QY 1 MPAGGAGSGSLKDDVALELFKDDPEKLFSDLRREIGHSGFGAVYFARDVRNSEVVAIKKMS 60
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MPSTNRAGSLKDDPEIAELFFKDDPEKLFSDLRREIGHSGFGAVYFARDVRNSEVVAIKKMS 60

QY 61 YSGKSNSEKMODIIKEVRFLOKLRHPNTIOYRGCYLREHTAMLVMEYCLGSASDLEVHK 120
   |||||||
DB 61 YSGKSNSEKMODIIKEVRFLOKLRHPNTIOYRGCYLREHTAMLVMEYCLGSASDLEVHK 120

QY 121 KPIQVEIIAAVTHGALQGLAYLHSHNMHRDVAKAGNILLSEPGIVKLGDFGSASIMAPAN 180
   |||||||
DB 121 KPIQVEIIAAVTHGALQGLAYLHSHNMHRDVAKAGNILLSEPGIVKLGDFGSASIMAPAN 180

QY 181 SFVGTPTWMAPEVILAMDEQYDGKDVWSLGTCTIEFLARKRPPLFNMMASALYHTAQN 240
   |||||||
DB 181 SFVGTPTWMAPEVILAMDEQYDGKDVWSLGTCTIEFLARKRPPLFNMMASALYHTAQN 240

QY 241 ESPALSGHSEYFRNFVDSCLQIPODRPTSEVLKHFRLRERPTVIMDLIQRTKDA 300
   ||| ||| ||:|||||
DB 241 ESPALSGHSEYFRNFVDSCLQIPODRPTSEVLKHFRLRERPTVIMDLIQRTKDA 300

QY 301 VRELDNLQYRKMKKILFQEAHPNGGAPEPEEAEPEYMRAGTITLSLSHSPSKSIS 360
   |||||||
DB 301 VRELDNLQYRKMKKILFQEAHPNGGAPEPEEAEPEYMRAGTITLSLSHSPSKSIS 360

QY 361 ASSOSSSVNSLADASDNEEEEEEEEEEEEGPESRMMAMQGEHTVTSHSS 416
   |||||||
DB 361 ASSOSSSVNSLADASDSELD-----MMEGDHTVMNS 395

RESULT 5
09P216 PRELIMINARY; PRT; 1005 AA.
AC 09P216; Q96L75;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, last annotation update)
DE KIAA1361 protein (Serine/threonine kinase TA01) (Fragment).
GN KIAA1361.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE-BRAIN;
RC MEDLINE=20181126; PubMed=10718198;
RA Nagase T., Kikuno R., Ishikawa K., Hirose M., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes.XVI.
   The complete sequences of 150 new cDNA clones from brain which code
   for large proteins in vitro.";
RT DNA Res. 7:65-73(2000).
RN [2]
RP SEQUENCE OF 5-1005 FROM N.A.
RA Jenkins S.G., D'Andrea R.J., Gamble J.R., Vadas M.A.;
RT "Characterization of human TA01.";
RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
EMBL: AB037782; BAA92599.1; -.
DR EMBL: AY049015; AAL12217.1; -.
DR HSSP: P24941; 1B38.
DR InterPro: IPR000719; Euk-kinase.
DR InterPro: IPR002290; Ser_thr-kinase.
DR InterPro: IPR001245; Tyr-kinase.
DR Pfam: PF00069; kinase: 1.
DR PRINTS: PR00109; TYRKINASE.
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DR ProDom: PD000001: Euk_pkinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
KW NON_TER
SQ SEQUENCE 1 1005 AA; 116540 MW; A83BD4E53569BCB5 CRC64;

Query Match
Best Local Similarity 79.9%; Score 1726.5; DB 4; Length 1005;
Matches 330; Conservative 33; Mismatches 32; Indels 21; Gaps 1;

QY 1 MPAGRAGSLKPDVAVLFFKDDPEKLFSDLRREIGHSGFGAYVFARDVNNSEVAIAIKKS 60
DB 5 MSTNRAGSLKPDPELAEFFKEDPEKLFDTLRREIGHSGFGAYVFARDVNNSEVAIAIKKS 64

QY 61 YSGKSNEMKMODIKRVRFLQKLRHPTIQYRCYLRREHTAMLVMEYICGASADLLEVRK 120
DB 65 YSGKSTKEMODIKRVRFLQKLRHPTIQYRCYLRREHTAMLVMEYICGASADLLEVRK 124

QY 121 KPLQVEIAAVTHGALQGLAYLHSHNMIRHDYKAGNILLSEGLVYLGFGSASIMAPAN 180
DB 125 KPLQVEIAAITHGALQGLAYLHSHNMIRHDYKAGNILLTEPGQVYLGFGSASIMAPAN 184

QY 181 SFVGPYMAPEVYIAMDGGQYDGKDVWSLGTICIELAEKRPPLFNNMAMSLYHIAQN 240
DB 185 SFVGPYMAPEVYIAMDGGQYDGKDVWSLGTICIELAEKRPPLFNNMAMSLYHIAQN 244

QY 241 ESPALOSGHMSEYFRNFVDSCLQKIPQDRPTSEVLKLRFLVRRPPYIMDLIQRTKDA 300
DB 245 ESPTLQSNEMSDYFRNFVDSCLQKIPQDRPTSEVLKLRFLVRRPPYIMDLIQRTKDA 304

QY 301 VELDLMLQYRKMKKILFQAPNPGCAEAPDEEAPYMHRAAGTLTSLSSHSVPMSIS 360
DB 305 VELDLMLQYRKMKKILFQAHNPGPAVEAEDEEODHGGRGTIVNSVSNOSIPMSIS 364

QY 361 ASSQSSSVNSLADASDNEEEEEEDEEEDEEGPESREMANMOGERTVTSNHS 416
DB 365 ASSQSSSVNSLDPVSDKSELD-----MMGDHTVSNSS 399

RESULT 6
Q9H2K7 PRELIMINARY; PRT; 1001 AA.
AC Q9H2K7;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE STE20-like kinase (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Yustein J.T., Robinson D., Kung H.-J.;
RT "Characterization of a Subfamily of Human STE20-like kinases that
RT selectively activate p38 Through MK3 and are Regulated via a p22A-
RT dependent Mechanism";
RL Submitted (May-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF263312; AAC38302.1; -.
DR HSSP; P24941; 1B38.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; Tyrc; 1.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.

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KW Kinase.
FT NON_TER
SQ SEQUENCE 1001 AA; 115957 MW; 7F0E534D3E7E159E CRC64;

Query Match
Best Local Similarity 79.5%; Score 1718.5; DB 4; Length 1001;
Matches 329; Conservative 33; Mismatches 33; Indels 21; Gaps 1;

QY 1 MPAGRAGSLKPDVAVLFFKDDPEKLFSDLRREIGHSGFGAYVFARDVNNSEVAIAIKKS 60
DB 1 MSTNRAGSLKPDPELAEFFKEDPEKLFDTLRREIGHSGFGAYVFARDVNNSEVAIAIKKS 60

QY 61 YSGKSNEMKMODIKRVRFLQKLRHPTIQYRCYLRREHTAMLVMEYICGASADLLEVRK 120
DB 61 YSGKSTKEMODIKRVRFLQKLRHPTIQYRCYLRREHTAMLVMEYICGASADLLEVRK 120

QY 121 KPLQVEIAAVTHGALQGLAYLHSHNMIRHDYKAGNILLSEGLVYLGFGSASIMAPAN 180
DB 121 KPLQVEIAAITHGALQGLAYLHSHNMIRHDYKAGNILLTEPGQVYLGFGSASIMAPAN 180

QY 181 SFVGPYMAPEVYIAMDGGQYDGKDVWSLGTICIELAEKRPPLFNNMAMSLYHIAQN 240
DB 181 SFVGPYMAPEVYIAMDGGQYDGKDVWSLGTICIELAEKRPPLFNNMAMSLYHIAQN 240

QY 241 ESPALOSGHMSEYFRNFVDSCLQKIPQDRPTSEVLKLRFLVRRPPYIMDLIQRTKDA 300
DB 241 ESPTLQSNEMSDYFRNFVDSCLQKIPQDRPTSEVLKLRFLVRRPPYIMDLIQRTKDA 300

QY 301 VELDLMLQYRKMKKILFQAPNPGCAEAPDEEAPYMHRAAGTLTSLSSHSVPMSIS 360
DB 301 VELDLMLQYRKMKKILFQAHNPGPAVEAEDEEODHGGRGTIVNSVSNOSIPMSIS 360

QY 361 ASSQSSSVNSLADASDNEEEEEEDEEEDEEGPESREMANMOGERTVTSNHS 416
DB 361 ASSQSSSVNSLDPVSDKSELD-----MMGDHTVSNSS 395

RESULT 7
Q9HC79 PRELIMINARY; PRT; 898 AA.
AC Q9HC79;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Serine kinase (STE20-like kinase).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Zhang W., Chen T., Wan T., He L., Li N., Yuan Z., Cao X.;
RT "Cloning of DPK, a novel dendritic cell-derived protein kinase
RT activating the ERK1/ERK2 and JNK/SAPK pathways";
RL Biochem. Biophys. Res. Commun. 274:872-879(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RT Submitted (Feb-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF151518; AAC09131.1; -.
DR EMBL; BC002756; AAC02756.1; -.
DR HSSP; P24941; 1B38.
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR InterPro; IPR000130; Zn_Mpripdase.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00220; S_TKC; 1.
DR SMART; SM00219; Tyrc; 1.

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[illegible]

RESULT	10			
09H2K8				
ID	Q9H2K8	PRELIMINARY;	PRT;	898 AA.
AC	Q9H2K8;			
DT	01-MAR-2001	(TREMBLrel. 16, Created)		
DT	01-MAR-2001	(TREMBLrel. 16, Last sequence update)		
DT	01-JUN-2002	(TREMBLrel. 21, Last annotation update)		
DE	STE20-like kinase (Fragment).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
OX	NCBI_taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Yustein J.T., Robinson D., Kung H.-J.;			
RT	"Characterization of a Subfamily of Human STE20-like Kinases that			
RT	Selectively Activate p38 Through MKK3 and are Regulated via a PP2A-			
RT	dependent Mechanism.";			
RL	Submitted (MAY-2000) to the EMBL/Genbank/DBJ databases.			
DR	EMBL; AF263311; AAC38501.1; -			
DR	HSSP; P24941; 1838.			
DR	InterPro; IPR000719; Euk_kinase.			
DR	InterPro; IPR002290; Ser_thr_kinase.			
DR	InterPro; IPR001245; Tyr_kinase.			
DR	InterPro; IPR000130; Zn_MTPepdase.			
DR	Pfam; PF000069; pkinase; 1.			
DR	PRINTS; PR00109; TYRKINASE.			
DR	ProDom; PD000001; Euk_kinase; 1.			
DR	SMART; SM00220; S_TKC; 1.			
DR	SMART; SM00219; TYTKC; 1.			
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.			
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.			
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.			
DR	PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.			
KW	kinase.			
FT	NON-TER.			
SO	SEQUENCE	898 AA;	898 MW;	E52C5BFEDD67264E CRC64;
Query Match		70.9%;	Score 1531.5;	DR 4; Length 898;
Best Local Similarity		70.8%;	Pred. NO. 8.7e-110;	
Matches *291; Conservative		44;	Mismatches 57;	Indels 19; Gaps 1;

QY	6	RAGSLKDDVAELFKPKDDPELFSQRLREITGSGSGAYAFADVANSNVEYAIKKKXSGKQ	65
Db	2	RKGYLKDEIDLDFKDDPEELFGLHEITGSGSGAYAFATNAHTNEVAAIKKXSGKQ	61
QY	66	SNKKMODIKERFLPQKRHRHNTTIORCYCHREHTAMLVMEYCGSGASDLELVHKRPLOE	1252
Db	62	THEKKQDILKEVKEFLRQKHKHPNTLEYKCYLKEHTAMLVMEYCGSGASDLELVHKRPLOE	1222
QY	126	VEIAAVTHGALOGALYTHSHMHHRDVKAGNIIILSEPLVYKLGDFGSASIMAPANSVGT	1855
Db	122	VEIAAITGHALHGLYTHSHALHRDIAKGNIIILTEPOYKLAIDFGASAPRANSVGT	1818
QY	186	PYVMAPEVILMDEGOYGVKDVMSIGTICTELKERKPLFNMNMAISALVHIAQNESPAL	2455
Db	132	PYVMAPEVILMDEGOYGVKDVMSIGTICTELKERKPLFNMNMAISALVHIAQNDSPTL	2411
QY	246	QSGHNSSEYFRNFVDSCLQIKIPQDPTSEVLKHKRFVLEREPVYIMLIQRTKDAVELD	3059
Db	242	QSNEMTDSFRFRVYDCIQIKIPQERTSEVLLRHDFVYRDRPLRVLIIDLQRTKDAVELD	3018
QY	306	NLOYTKKKKKILFQEPAPNGPAGAPDEEBEAEAPVYHRAGTLSLESSSVDSMISASQOS	3655
Db	302	NLOYTKKKKKILFQETERNGPLNESODEEDSEHGTSILAREMDSIGSNHSISMSVSTGOS	3618
QY	366	SSVNSLADASNEBEEBEEBEEBEEBEGESKEMAMQDGEHTVYSHS	416
Db	362	SSVNSMOWEVD-----SSSELVYMHDESTINSSS	393

RESULT 11		
Q9UHG7	PRELIMINARY:	PRT: 898 AA.
ID Q9UHG7		
AC Q9UHG7;		
DT 01-MAY-2000 (TREMBLrel. 13, Created)		
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)		
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)		
DE STE20-like kinase.		
GN JIK.		
OS Homo sapiens (Human).		
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
OX NCBI_TaxID=9606;		
RN [1]		
SEQUENCE FROM N.A.		
RX MEDLINE=20026851; PubMed=10559204;		
RA Tassi E., Blesova Z., Di Fiore P., Gutkind J.S., Mong M.T.;		
"Human JIK, a novel member of the STE20 kinase family that inhibits		
RT JNK and is negatively regulated by epidermal growth factor.";		
RL J. Biol. Chem. 274:33287-33295(1999).		
-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.		
EMBL: AF179867; AAF14559.1; -		
CC HSSP: P24941; 1B38.		
DR HSSP: P24941; 1B38.		
DR InterPro: IPR000719; Euk_pkinase.		
DR InterPro: IPR002290; Ser_thr_pkinase.		
DR InterPro: IPR001245; Tyr_pkinase.		
DR InterPro: IPR000130; Zn_MTepidse.		
DR Pfam: PF00069; pkinase. 1.		
DR PRINTS: PR00109; TYRKINASE.		
DR ProDom: PD000001; Euk_pkinase. 1.		
DR SMART: SM00220; S_TKc. 1.		
DR PROSITE: PS00107; PROTEIN_KINASE_ATP. 1.		
DR PROSITE: PS50011; PROTEIN_KINASE_DOM. 1.		
DR PROSITE: PS00108; PROTEIN_KINASE_ST. 1.		
DR PROSITE: PS00142; ZINC_PROTEASE; UNKNOWN.1.		
DR ATP-binding_Kinase_Serine/threonine-protein_kinase; Transferase.		
KW SEQUENCE 898 AA; 10557 MW; 61F04628713EE6025 CRC64;		

Query Match	68.5%,	Score 1480.5,	DB 4,	Length 898;
Best Local Similarity	68.6%,	Pred. No. 7.6e-106;		
Matches 282;	Conservative 48;	Mismatches 62;	Indels 19;	Gaps 1;



RA Bloecker H., Boecker M., Brandt P., Nemes H.W., Gaassenhuber J.,  
RA Wiemann S.;  
RL Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases.  
DR EMBL: AL137701; CAB70882.1; -  
DR HSSP: P02649; INFO.  
DR InterPro: IPR000719; Euk\_pkinase.  
DR Pfam: PF00069; pkinase; 1.  
DR ProDom: PD000001; Euk\_pkinase; 1.  
KW ATP-binding; Hypothetical protein; Transferase.  
SQ SEQUENCE 1062 AA; 118780 MW; A4B2B359EBC9CAD CRC64;

Query Match 45.7%; Score 987; DB 4; Length 1062;  
Best Local Similarity 97.5%; Pred. No. 1.3e-67;  
Matches 194; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

QY 218 LAERKPLFNMMAMSAALYHIAQNESPALQSGHWFERNFVDSCLQKIPQDRPTSEVLK 277  
DB 45 VAEKRPFLFNMMAMSAALYHIAQNESPVLOSGHWFERNFVDSCLQKIPQDRPTSEVLK 104  
QY 278 HRFVLEREPPTVIMDLIQRTKDAVRELDNLQYRKMKILFOEAPNGPAGAEPEEEEAEP 337  
DB 105 HRFVLEREPPTVIMDLIQRTKDAVRELDNLQYRKMKILFOEAPNGPAGAEPEEEEAEP 164  
QY 338 YNHRAGTLTSLSSHSVPMSISASSQSSVNSLADASONEEEEEEEEEEEEGEP 397  
DB 165 YNHRAGTLTSLSSHSVPMSISASSQSSVNSLADASN--EEEEEEEEEEEEEGEP 222  
QY 398 SREMMAMQEGEHTVTSRSS 416  
DB 223 AREMMAMQEGEHTVTSRSS 241

## RESULT 14

Q9H7S5 PRELIMINARY; PRT; 398 AA.  
AC Q9H7S5.  
DT 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
DE CDNA FLJ1314 f1s, clone PLACE300350, weakly similar to  
DE serine/threonine-protein kinase SULKU (EC 2.7.1.-).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=PLACENTA;  
RA Tsogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,  
RA Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,  
RA Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,  
RA Arima M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,  
RA Wakematsu A., Nakamura Y., Nagahara K., Masuho Y., Oshima A.;  
RT "NEO human cDNA sequencing project."  
RL Submitted (AUG-2000) to the EMBL/Genbank/DBJ databases.  
DR EMBL: AK024376; BAB14901.1; -  
DR InterPro: IPR000719; Ser\_pkinase.  
DR InterPro: IPR002290; Ser\_thr\_pkinase.  
DR Pfam: PF00069; pkinase; 1.  
DR ProDom: PD000001; Euk\_pkinase; 1.  
DR SMART: SM00220; S\_TKc; 1.  
DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
KW ATP-binding; Transferase.  
SQ SEQUENCE 398 AA; 46177 MW; B1ADD4A5D46FA4 CRC64;

Query Match 41.8%; Score 902.5; DB 4; Length 398;  
Best Local Similarity 74.2%; Pred. No. 1.2e-61;  
Matches 178; Conservative 17; Mismatches 24; Indels 21; Gaps 1;

QY 177 AARNSVGTGYPMAPRYVILLAMDEGQYDGVVWSLGTITETLAERKPLFNMMAMSAALYH 236  
DB 3 SPANSVGTGYPMAPRYVILLAMDEGQYDGVVWSLGTITETLAERKPLFNMMAMSAALYH 62

QY 237 IAQNESPALQSGHWFERNFVDSCLQKIPQDRPTSEVLKRNFRVLEREPPTVIMDLIOR 296  
DB 63 IAQNESPTLQSNEMTDTYFRNFVDSCLQKIPQDRPTSEVLKRNFRVLEREPPTVIMDLIOR 122  
QY 297 TKDAVRELDNLQYRKMKILFOEAPNGPAGAEPEEEEAEPYHNRAGTLTSLSSHSVS 356  
DB 123 TKDAVRELDNLQYRKMKILFOEAPNGPAGAEPEEEEAEPYHNRAGTLTSLSSHSVS 182  
QY 357 MSISASSQSSVNSLADASONEEEEEEEEEEEEGEPESREMMAMQEGEHTVTSRSS 416  
DB 183 MSISASSQSSVNSLADASONEEEEEEEEEEEEGEPESREMMAMQEGEHTVTSRSS 221

## RESULT 15

Q9FNJ3 PRELIMINARY; PRT; 842 AA.  
AC Q9FNJ3.  
DT 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
DE 3615.3.  
OS Oryza sativa (Rice).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Eriaraloideae; Oryzaceae; Oryza.  
OX NCBI\_TaxID=4530;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV. NIPPOBARE; TRANSPOSOM-GAIGAN;  
RX MEDLINE=21140318; PubMed=11244114;  
RA Dubcovsky J., Ramakrishna W., SanMiguel P.J., Busso C.S., Yan L.,  
RA Shiloff B.A., Bennetzen J.L.;  
RT "Comparative sequence analysis of collinear barley and rice bacterial  
RT artificial chromosomes";  
RL Plant Physiol. 125:1342-1353(2001).  
DR EMBL: AY013245; AAG45491.1; -  
DR HSSP: O63450; 1A06.  
DR InterPro: IPR000719; Euk\_pkinase.  
DR InterPro: IPR002290; Ser\_thr\_pkinase.  
DR InterPro: IPR001245; Tyr\_pkinase.  
DR Pfam: PF00069; pkinase; 1.  
DR ProDom: PD000001; Euk\_pkinase; 1.  
DR SMART: SM00220; S\_TKc; 1.  
DR SMART: SM00219; TYKc; 1.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
KW ATP-binding; Transferase.  
SQ SEQUENCE 842 AA; 91646 MW; EBE222157E40558C CRC64;

Query Match 31.3%; Score 677; DB 10; Length 842;  
Best Local Similarity 33.3%; Pred. No. 9e-44;  
Matches 162; Conservative 86; Mismatches 151; Indels 88; Gaps 13;

QY 2 PAGGRAGSLKDP-----DVAELEFKDDPEKLFSDRLREIGHGSGF 40  
DB 214 PAVGQSEELRQALLVQOQHOOQNSRRKPSVSESVTRDPSTKYELHLHLEIGKSGY 273  
QY 41 AYYFARDVNSEVNAKKMSYSGKQSNKEMQDIKRYRRLQKLRHNTIYQGCYLRHFT 100  
DB 274 AYYKARDLFTQELVAIKIISLT--EGEEGYEDIKGIEMLQOCSHPNVVRYGSGYGEY 331  
QY 101 AMLVMEYC-LGSASDLLEVHKKRPLQVEIJAATYHGLAYLHSHMTIRPVKAGNILL 159  
DB 332 LMIIVMEYCGGGSVADLIGITEERPLDESQIAYICREALKGLATLHSTFKYHRDIKGNILL 391  
QY 160 SEGLVKLQDFGSAS---IMAPANSVGTGYPMAPRYVILLAMDEGQYDGVVWSLGTITC 215  
DB 392 TEOGEVKLQDFGVAAGLUTRTMSKRNTFICTPHMMPREV---QESRYDGVVWALGVSA 448  
QY 216 IELAERKPLFNMMAMSAALYHIAQNESPALQSGH-WSEFRNFVDSCLQKIPQDRPTSEV 274  
DB 449 IEMAEGMPRSTVHPRIVFMISSEPAFMLDEKESLTFHDFIAKCLTKRDLRPAASE 508



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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: November 22, 2002, 12:21:31 ; Search time 9.152 Seconds  
(without alignments)  
1337.406 Million cell updates/sec

Title: US-09-686-346a-4\_COPY\_1\_416

Perfect score: 2161

Sequence: 1 MPAGGRAGSLKDPDVAELF.....ESRENAHQEGHTVSHSS 416

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*

2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*

3: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*

4: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*

5: /cgn2\_6/ptodata/1/iaa/PTCTUS\_COMB.pep:\*

6: /cgn2\_6/ptodata/1/iaa/backfillsl.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2161	100.0	993	4	US-09-060-410-4
2	1728.5	80.0	1001	4	US-09-060-410-2
3	873.5	40.4	278	4	US-09-060-410-17
4	605.5	28.0	487	2	US-08-712-709-8
5	605.5	28.0	487	3	US-09-111-444-8
6	605.5	28.0	487	4	US-09-541-228-8
7	605	28.0	1360	4	US-09-393-569-2
8	594	27.5	431	2	US-09-211-930-5
9	594	27.5	431	3	US-09-340-993-5
10	594	27.5	431	4	US-09-152-406-3
11	594	27.5	431	4	US-09-468-442-5
12	592	27.4	426	2	US-08-852-743-2
13	592	27.4	426	2	US-09-211-930-4
14	592	27.4	426	3	US-09-340-993-4
15	592	27.4	426	3	US-09-185-370-2
16	592	27.4	426	4	US-09-152-406-4
17	592	27.4	426	4	US-09-468-442-4
18	576.5	26.7	416	2	US-09-211-930-11
19	576.5	26.7	416	2	US-09-340-993-11
20	576.5	26.7	416	4	US-09-468-442-11
21	571	26.4	416	3	US-09-211-930-3
22	571	26.4	416	3	US-09-340-993-3
23	571	26.4	416	4	US-09-468-442-3
24	560	25.9	403	2	US-08-712-709-3
25	560	25.9	403	3	US-09-111-444-3
26	560	25.9	403	4	US-09-541-228-3
27	555	25.7	270	2	US-08-852-743-5

28	555	25.7	270	3	US-09-185-370-5	Sequence 5, App11
29	516	23.9	276	2	US-08-852-743-7	Sequence 7, App11
30	516	23.9	276	3	US-09-185-370-7	Sequence 7, App11
31	505	23.4	545	2	US-08-935-760-4	Sequence 4, App11
32	503	23.3	465	2	US-08-114-555A-2	Sequence 2, App11
33	503	23.3	544	2	US-08-935-760-2	Sequence 2, App11
34	499	23.1	544	3	US-08-559-397A-2	Sequence 2, App11
35	497	23.0	544	3	US-08-559-397A-19	Sequence 19, App1
36	491	22.7	506	1	US-08-369-780-2	Sequence 2, App11
37	491	22.7	506	1	US-08-475-682-2	Sequence 2, App11
38	491	22.7	506	1	US-08-780-833-2	Sequence 2, App11
39	491	22.7	506	1	US-08-636-036-2	Sequence 2, App11
40	491	22.7	506	3	US-08-918-509-2	Sequence 2, App11
41	491	22.7	506	3	US-09-108-262-2	Sequence 2, App11
42	491	22.7	524	2	US-08-615-942A-2	Sequence 2, App11
43	489	22.6	268	2	US-08-852-743-3	Sequence 3, App11
44	489	22.6	268	3	US-09-185-370-3	Sequence 3, App11
45	487.5	22.6	272	2	US-08-852-743-6	Sequence 6, App11

## ALIGNMENTS

```
RESULT 1
US-09-060-410-4
; Sequence 4, Application US/09060410
; Patent No. 6165461
;
GENERAL INFORMATION:
; APPLICANT: Cobb, Melanie
; APPLICANT: Hutchinson, Michele
; APPLICANT: Chen, Zhu
; APPLICANT: Bertram, Kevin
; TITLE OF INVENTION: TAO PROTEIN KINASES AND METHODS OF USE
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; City: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
;
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/060,410
; FILING DATE: 14-Apr-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Makl, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 860098.421
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 682-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 993 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-060-410-4

Query Match 100.0%; Score 2161; DB 4; Length 993;
Best Local Similarity 100.0%; Pred. No. 2.1e-173; Indels 0; Gaps 0;
Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAGGRAGSLKDPDVAELFFKDPPEKLFSDLRIGHSFGAYVFARDVRNSEVAATKKMS 60
Db 1 MPAGGRAGSLKDPDVAELFFKDPPEKLFSDLRIGHSFGAYVFARDVRNSEVAATKKMS 60
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QY	61	YSGKSNKMODIIKEVREFLOKLIHNPNTIOYRGYILEHNTAMLYMEKCLASADLEVHK	120
Db	61	YSGKSNKMKMODIIKEVREFLOKLIHNPNTIOYRGYILEHNTAMLYMEKCLASADLEVHK	120
QY	121	KPLDEVELAANTHAGLOGLAYLHSHNMTHRDYKAGNILLSBPGVLKIGDFGSASIMAPAN	180
Db	121	KPLDEVELAANTHAGLOGLAYLHSHNMTHRDYKAGNILLSBPGVLKIGDFGSASIMAPAN	180
QY	181	SFVGTPYMAAEVILLADEGQYDCKVYVWSLGTICIELAEKRPFLFYMMNMSALYHNAON	240
Db	181	SFVGTPYMAAEVILLADEGQYDCKVYVWSLGTICIELAEKRPFLFYMMNMSALYHNAON	240
QY	241	ESPALQSHMSEYTRNFYDSCLOKIIPODRPTSEVLLKHFVLRERPRPTVIMDLIORTKDA	300
Db	241	ESPALQSHMSEYTRNFYDSCLOKIIPODRPTSEVLLKHFVLRERPRPTVIMDLIORTKDA	300
QY	301	VRELDNLOYRKMKKILFOEANGNGAELAEPEEEBAEYMRAGITLLESSHVPSKMSIS	360
Db	301	VRELDNLOYRKMKKILFOEANGNGAELAEPEEEBAEYMRAGITLLESSHVPSKMSIS	360
QY	361	ASSOSSSVNLSLAODSNDNEEEEEEEEBEEBEGPGRSREKAMMOGEENHTVTSHS	416
Db	361	ASSOSSSVNLSLAODSNDNEEEEEEEEBEEBEGPGRSREKAMMOGEENHTVTSHS	416

RESULT 2  
US-09-060-410-2  
; Sequence 2, Application US/09060410

```

GENERAL INFORMATION:
APPLICANT: Cobb, Melanie
APPLICANT: Hutchinson, Michele
APPLICANT: Chen, Zhu
APPLICANT: Berman, Kevin
TITLE OF INVENTION: TAO PROTEIN KINASES AND METHODS OF USE
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/060,410
FILING DATE: 14-APR-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Makl, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 860098.421
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1001 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
IS-09-060-410-2

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Query Match	80.0%;	Score 1728.5;	DB 4;	Length 1001;
Best Local Similarity	79.6%;	Pred. No. 5.1e-137;		
Matches 331;	Conservative 32;	Mismatches 32;	Indels 21;	Gaps 1

[illegible]

RESULT 3  
US-09-060-410-17  
; Sequence 17, Application US/09060410

GENERAL INFORMATION:  
APPLICANT: Cobb, Melanie  
APPLICANT: Hutchinson, Michele  
APPLICANT: Chen, Zhu  
APPLICANT: Berman, Kevin  
TITLE OF INVENTION: TAO PROTEIN KINASES AND METHODS OF USE  
TITLE OF INVENTION: THEREFOR  
NUMBER OF SEQUENCES: 26  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED and BERRY LLP  
STREET: 6300 Columbia Circle, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/060,410  
FILING DATE: 14 APR-1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Makl, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 860098.421  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 278 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
IS-09-060-410-17

Query Match 40.48; Score 873.5; DB 4; Length 278;

```

Best Local Similarity    59.1%; Pred. No. 7.4e-66; Indels      9; Gaps     2;
Matches   162; Conservative   47; Mismatches   56;

QY       6 RAGSLKEDVAVLEFKDDPEKLFSDLREIGHSGFAYVFARDVRNSEVAIKRMSYSQGQ 65
          : |::| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| 
Db        8 KPGVIKDSEISALFNKNDEPQ---DLREIGHGSFGAYVFADVKCKNEGVYAIKKMNFSGQ 64
QY       66 SNEKHODILKEVRFLOKRHPHTIOYRCGCIYLREHIAVLMEYCGLSASDLEVEHKPIQE 125
          ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| 
Db        65 AVEKMNDLIEKFSEFLNTVTVPRIHVPAIDYAKCFELKDTTCWLMVEYCIGLSADIYDLVKRGMR 124
QY       126 VEIIAIVTGALOGLAATLYSHNMTHRDVAKGNITLISEPGIYKLGDFGSAIMAPANSFYGT 185
          ||::| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| 
Db       125 VEIIAICQTLDALRYTLLSKRIHRDIKAGNITLSDHAIVKLADFSSASLVDPADPTLGT 184
QY       186 PYMAAPEVILIAMDECQYDKGYDVWSLTGITCIELAEERKPPLFMNNAMSALYHIQAENSEPAL 245
          ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| 
Db       185 PFEMAPEVILIAMDGEHYHDRAWDISLTGITCIELARRRPPLFEHMNASMLYHIQAONDPTLL 244
QY       246 -----QSCHMWSEFRNVDSCLQKITPDPRPSE 273
          : ||::| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| ::|| 

Db       245 SPIDTSEQEPEWSLEFPVOFDICKLRPAEEBMSAE 278

RESULT 4
US-08-712-709-8
; Sequence 8, Application US/08712709
; Patent No. 5863780
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Gegier, Karl J.
; APPLICANT: Hawkins, Phillip R.
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/712.709
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0118 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0535
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1117791
US-08-712-709-8

Query Match           28.0%; Score 605.5; DB 2; Length 487;
Best Local Similarity 34.0%; Pred. No. 5.5e-43;
Matches 147; Conservative 70; Mismatches 160; Indels 55; Gaps 9;

```

```

Db      6 LNNPRLKLLDESLTKQDEYFDVLEKLGSSYSYKAIHKETGQVIAKQVNV-- 63
OY      64 KQSNKEMODIKEYRFLOKTLHPPTIOYRGCYLREHTAMLVMEYC-LGSASDLELVHKRP 1222
Db      64 ---ESDLOEIIKEISIMQCCSPHVAVYYSYGFKNPTDMLVMEYCGAGSVSDIIRLNKT 120
OY      123 LQEVIAAIVHGALQGLAVLHSHNMHRDVKAGNILLSEPOLYKLGDFGSA---STMAP 178
Db      121 LTEDEIATIILOSTLKGLLEYLHFMRKIRHRDIAKGNILLNTEGHAKLAFVGAQLOTDPMK 180
OY      179 ANSFVGTPTMYNAPVYILAMDGCQYDGVKDVWVSLGTFITIELAEKRPPLFNMMASALYHIA 238
Db      181 RNVYIGTFPMMAPEYI---QEIQNCVADIMSLGITVIAEMAEGRPADIHMPKALFMP 237
OY      239 QNESPALDSGH-WSEYFNFNFVDSLOKIPODRPTSEVYLKHFPLRREPTVIMDLFORT 297
Db      238 TNPPTFFKPELMGDNFTDFYKQCLVSPERKATATQLOLHPYRSKAGVSIILRDLINEA 297
OY      298 KDVAVELDNIQYRKMKITLFGADNGPGAEAPDEEEEAPEYMHRA----- 342
Db      298 MDVKLRQESQQRMDQ-----DDEENSEDEMDSGTMVAVADEMGTVRVASTMT 348
OY      343 -GTLTSLSSHSVSMSTLSASSQSSVNSLADASDNEEEEEEEEEEEEEEEGSPESREM 401
Db      349 DGANMIMHDITLP-----SOLGTVMINADEDEEGTMRKRDETMQPAKPSLEY 398
OY      402 AMMOGEHTVTS 413
Db      399 FEQKEKEMQINS 410

RESULT 5
US-09-111-444-8
: Sequence 8, Application US/09111444
: Patent No. 6045792
: GENERAL INFORMATION:
: APPLICANT: Au-Young, Janice
: APPLICANT: Guegler, Karl J.
: APPLICANT: Hawkins, Phillip R.
: TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
: NUMBER OF SEQUENCES: 9
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Incyte Pharmaceuticals, Inc.
: STREET: 3174 Porter Drive
: CITY: Palo Alto
: STATE: CA
: COUNTRY: U.S.
: ZIP: 94304
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq Version 1.5
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/111,444
: FILING DATE:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/712,709
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Billings, Lucy J
: REGISTRATION NUMBER: 36,749
: REFERENCE/DOCKET NUMBER: PF-0118 US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-855-0555
: TELEFAX: 415-845-4166
: INFORMATION FOR SEQ ID NO: 8:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 487 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:

```

```
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1117791
US-09-111-444-8

Query Match
Best Local Similarity 34.0%; Score 605.5; DB 3; Length 487;
Matches 147; Conservative 70; Mismatches 160; Indels 55; Gaps 9;

10 LKDPVAELFFKDD-----PEKLFSDLRIGHSGAVYFARDVANSVVAIKKMSYSG 63
6 LKNNPRRLKLLDEDSLTKQPEVEFDVLEKLGSGSYKAIHKETGQIVAIKQV-- 63
64 KOSNEKMODIIEVEFLQKLRHPNTIQRGCVLRHTAVLVMYC-LGSASDLEVHKRP 122
123 LOEVEIAAVTHGALOGLAYLHSHNMIRHDYKAGNILLSEPGVLKIDFGSA---SINAP 178
121 LTEDETAATLQSLTKGLELYHFMRKIHRDIKAGNILLNTEGNAKLADFGVAGQLTDTMAK 180
179 ANSFVGTPEYMAPEVILAMDEGOYGVWSLGTICIEIARPKPLFPMNMSALYHIA 238
181 RNTVIGTFPMMAPEVIL--QETGNCVADIMSLGITAIIMAEKRPYADIHPRATFMTIP 237
239 QNESPALQSGH-WSEYFRNFVDSCLQKIPQDRPTSEVLKHFVLRERPPVIMDLQRT 297
238 TNPPTFRKPELMSDNFTFVKQCLVKSPEQRATATQLQHPFVRSKAGVSLRLINRA 297
298 KQAVRELNLQYRKAKKILFQAPNGPCAPAEPEEEEAEPYMHRA----- 342
298 MDVKLRKROESQOREMDQ-----DDEENSEDEMDSGTWRVAVGDMGTVRVASTWT 348
343 -GTLTSLSSHVSVPMSISASSQSSSVNSLADASNEEEEBEEBEEBEEBEGPESRGM 401
349 DGANTMIENDTLP-----SOLGTWVINADEEBEGTKMRDETMOAPAKPSFLEY 398
QY 402 AMOGECHTSTS 413
DB 399 FEQKREKQINS 410

RESULT 6
US-09-541-228-8
Sequence 8, Application US/09541228
Patent No. 6232077
GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Guegler, Karl J.
APPLICANT: Hawkins, Phillip R.
TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSER: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
ZIP: 94304
GENERAL INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTA Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/541.228
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/712,709
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J
```

```
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0118 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 487 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1117791
US-09-541-228-8

Query Match
Best Local Similarity 34.0%; Score 605.5; DB 4; Length 487;
Matches 147; Conservative 70; Mismatches 160; Indels 55; Gaps 9;

10 LKDPVAELFFKDD-----PEKLFSDLRIGHSGAVYFARDVANSVVAIKKMSYSG 63
6 LKNNPRRLKLLDEDSLTKQPEVEFDVLEKLGSGSYKAIHKETGQIVAIKQV-- 63
64 KOSNEKMODIIEVEFLQKLRHPNTIQRGCVLRHTAVLVMYC-LGSASDLEVHKRP 122
123 LOEVEIAAVTHGALOGLAYLHSHNMIRHDYKAGNILLSEPGVLKIDFGSA---SINAP 178
121 LTEDETAATLQSLTKGLELYHFMRKIHRDIKAGNILLNTEGNAKLADFGVAGQLTDTMAK 180
179 ANSFVGTPEYMAPEVILAMDEGOYGVWSLGTICIEIARPKPLFPMNMSALYHIA 238
181 RNTVIGTFPMMAPEVIL--QETGNCVADIMSLGITAIIMAEKRPYADIHPRATFMTIP 237
239 QNESPALQSGH-WSEYFRNFVDSCLQKIPQDRPTSEVLKHFVLRERPPVIMDLQRT 297
238 TNPPTFRKPELMSDNFTFVKQCLVKSPEQRATATQLQHPFVRSKAGVSLRLINRA 297
298 KQAVRELNLQYRKAKKILFQAPNGPCAPAEPEEEEAEPYMHRA----- 342
298 MDVKLRKROESQOREMDQ-----DDEENSEDEMDSGTWRVAVGDMGTVRVASTWT 348
343 -GTLTSLSSHVSVPMSISASSQSSSVNSLADASNEEEEBEEBEEBEEBEGPESRGM 401
349 DGANTMIENDTLP-----SOLGTWVINADEEBEGTKMRDETMOAPAKPSFLEY 398
QY 402 AMOGECHTSTS 413
DB 399 FEQKREKQINS 410

RESULT 7
US-09-393-569-2
Sequence 2, Application US/09393569
Patent No. 6277979
GENERAL INFORMATION:
APPLICANT: BINGHAM, SHARON
APPLICANT: CASE, PATRICK
APPLICANT: LAWSON, SALLY NEALE
APPLICANT: NEWTON, RICHARD ANTHONY
APPLICANT: PIERCE, VALERIE
APPLICANT: RAUSCH, OLIVER LARS
APPLICANT: RAVAL, PRAVIN
APPLICANT: REITH, ALASTAIR DAVID
APPLICANT: SANGER, GARETH JOHN
TITLE OF INVENTION: NEW USE
FILE REFERENCE: P32261
CURRENT APPLICATION NUMBER: US/09/393,569
CURRENT FILING DATE: 1999-09-10
EARLIER APPLICATION NUMBER: GB 9907261.3
```

```
; EARLIER FILING DATE: 1999-03-29
; EARLIER APPLICATION NUMBER: GB 9819779.1
; EARLIER FILING DATE: 1998-09-10
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 1360
; TYPE: PRF
; ORGANISM: HOMO SAPIENS
US-09-393-569-2
```

```
Query Match          28.0%; Score 605; DB 4; Length 1360;
Best Local Similarity 35.0%; Pred. No. 2.4e-42;
Matches 155; Conservative 82; Mismatches 150; Indels 56; Gaps 16;
```

```
QY 1 MPAGGAGSISKDDVALEFQKDPKIFSDLRIGHSFGAVYFARDYNSEVVAIKKMS 60
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 1 MASDSPARSLDEIDLSAL---RDPAGIFELVELVGNQYGVYKGRHVKTGOLAIAIKVMD 57

QY 61 YSGKSNKKMODIIKEVRFLOKL-RHPNTIQYRGCVLREH-----TAWLWMEYC-LGSA 112
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 58 VTGDEEE-----IKQELNMIAKTSIHRNIAITYGAFIKKRPCKMDQMLWMEFCAGSV 113

QY 113 SDLLEVHK-KPLQEVETAAVTHGALQGLAYLHSHNMIRPKAGNILLSEPLVKLGDFG 171
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 114 TDLIKNTKGTMLKEEMIAVTCREILRGSLHGHKVIHRDIKGNVLTTEMAEKKLVDFG 173

QY 172 -SAST---MAPANSFVGTPYMAPEVILAMDE---GOYDGKVDVMSGICITIELAEKRP 224
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 174 VSAQLRTVGRRTTFTIGTPYMAPEVY-ACDENPDATYDCKSLMSIGITAIEMAEAPP 232

QY 225 LFNWNASALYHIAONESPALQSGHSEYFRNFVDSLOKIPQDRPISEVLLKHFVLYRE 284
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 233 LCMHMRALFLPRPAPRLKSKMSKQSTIESCLVNHQRPATELMAHPFI-KD 291

QY 285 RP-----PIYIMDLQRTKDAVRELDNLQYRKMKKTLFOAPNGPGAEAREESEA-EP- 337
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 292 QPNEQVRILQKDHIDRTKKRGEKDETEY-----SGSEEEENDSGEPS 339

QY 338 -YHHRAG-----TITSLESHSVPSMISASSOSSVNSLADASDNEEEEEE 385
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 340 SIINLPGESTLRDFTRLQLANKERSEALRQOLEDOQRENEBKROLLAEROKRIEOK 399

QY 386 EEEEEEEEGPESREMAWMOGE 408
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 400 EQRRRLIEQQRREKELRQOERE 422
```

```
RESULT 8
; Sequence 5, Application US/09211930
; Patent No. 5962265
; GENERAL INFORMATION:
; APPLICANT: Tyrell E. No. 5962265f1s
; APPLICANT: William Craig Moore
; APPLICANT: David Shay Silberstein
; TITLE OF INVENTION: HUMAN SIGNAL TRANSDUCTION
; TITLE OF INVENTION: SERINE/THREONINE KINASE
; FILE REFERENCE: PHM.70296
; CURRENT APPLICATION NUMBER: US/09/211,930
; EARLIER FILING DATE: 1998-12-15
; EARLIER APPLICATION NUMBER: GB 9726851.0
; EARLIER FILING DATE: 1997-12-19
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 431
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-211-930-5
```

```
Query Match          27.5%; Score 594; DB 2; Length 431;
Best Local Similarity 45.8%; Pred. No. 4.3e-42;
```

```
Matches 130; Conservative 48; Mismatches 92; Indels 14; Gaps 7;

QY 21 KDDPEKIFSDLRIGHSFGAVYFARDYNSEVVAIKKMSYSGKSNKKMODIIKEVRL 80
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 17 KADPEELFTLEKRIKGSFGEVFGIDNRQKVAIKIIDL--EEADEDEDIOOEITVL 74

QY 81 OKLRHPNTIQYRGCVLREHAWLWMEYC-LGSASDLEEVHKKPLQEVETAAVTHGALQGL 139
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 75 SQCDSPYVTKYYSYLKDTLMTIMEYLGGSALDLE--PGPLDETQIATILREILKGL 132

QY 140 AYLSHNMIRHDYKAGNILLSEPLVKLGDFGSASIMAPA---NSFVGTPYMAPEVIL 195
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 133 DYLSHSEKKIHRDIKAAVLLSEHGEVYLAQVAGQITDQIKRNTFVGTPYMAPEVIL 191

QY 196 AMDEGQDGVVDVMSGICITIELAEKRPPLFNWNASALYHIAONESPALQSGHSEYFR 255
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 192 --KOSAYDSKADIVMSIGITAIELARGPPEHSELPKMKVFLIIPKNNPPTLE-GNYSKPLK 248

QY 256 NFVDSCLQKIPQDRPTSEVLLKHFVLYREPRPT-VIMDLQRTK 298
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 249 EFVEACLKPEPSRPTAKELKHKFILLRNAAKTSYLTLEIDRYK 292
```

```
RESULT 9
US-09-340-993-5
; Sequence 5, Application US/09340993
; Patent No. 6034228
; GENERAL INFORMATION:
; APPLICANT: Tyrell E. No. 6034228f1s
; APPLICANT: William Craig Moore
; APPLICANT: David Shay Silberstein
; TITLE OF INVENTION: HUMAN SIGNAL TRANSDUCTION SERINE/THREONINE KINASE
; FILE REFERENCE: PHM.70296.N1
; CURRENT APPLICATION NUMBER: US/09/340,993
; EARLIER FILING DATE: 1999-06-25
; EARLIER APPLICATION NUMBER: GB 9726851.0 & US 09/211,930
; EARLIER FILING DATE: 1997-12-19 & 1998-12-15
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 431
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-340-993-5
```

```
Query Match          27.5%; Score 594; DB 3; Length 431;
Best Local Similarity 45.8%; Pred. No. 4.3e-42;
Matches 130; Conservative 48; Mismatches 92; Indels 14; Gaps 7;
```

```
QY 21 KDDPEKIFSDLRIGHSFGAVYFARDYNSEVVAIKKMSYSGKSNKKMODIIKEVRL 80
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 17 KADPEELFTLEKRIKGSFGEVFGIDNRQKVAIKIIDL--EEADEDEDIOOEITVL 74

QY 81 OKLRHPNTIQYRGCVLREHAWLWMEYC-LGSASDLEEVHKKPLQEVETAAVTHGALQGL 139
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 75 SQCDSPYVTKYYSYLKDTLMTIMEYLGGSALDLE--PGPLDETQIATILREILKGL 132

QY 140 AYLSHNMIRHDYKAGNILLSEPLVKLGDFGSASIMAPA---NSFVGTPYMAPEVIL 195
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 133 DYLSHSEKKIHRDIKAAVLLSEHGEVYLAQVAGQITDQIKRNTFVGTPYMAPEVIL 191

QY 196 AMDEGQDGVVDVMSGICITIELAEKRPPLFNWNASALYHIAONESPALQSGHSEYFR 255
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 192 --KOSAYDSKADIVMSIGITAIELARGPPEHSELPKMKVFLIIPKNNPPTLE-GNYSKPLK 248

QY 256 NFVDSCLQKIPQDRPTSEVLLKHFVLYREPRPT-VIMDLQRTK 298
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 249 EFVEACLKPEPSRPTAKELKHKFILLRNAAKTSYLTLEIDRYK 292
```

```
RESULT 10
US-09-152-406-3
; Sequence 3, Application US/09152406
```

Query Match	27.5%;	Score 594;	DB 4;	Length 431;
Best Local Similarity	45.8%;	Pred. NO. 4.3e-42;		
Matches 130;	Conservative 48;	Mismatches 92;	Indels 14;	Gaps 7

RESULT 11  
S-09-468-442-5  
Sequence 5, Application US/09468442

Query Match	27.5%;	Score 594;	DB 4;	Length 431;
Best Local Similarity	45.8%;	Pred. No. 4.3e-42;		

RESULT 12  
US-08-852-743-2

Query Match	27.4%	Score 592;	DB 2;	Length 426;
Best Local Similarity	36.4%	Pred. NO. 6.2e-42;		
Matches 154; Conservative	69;	Mismatches 128;	Indels 72;	Gaps 16;

QY	23	DPEKLEFSLREIGHGSPGAVYFADVBNSEYVAIKKMSYSGKSNEMKODIIEVRERLOK	82
Db	15	DPEELFKLDRIKIGSGFGEYKKGIDNTEKEVYAIKIIDL--EEAEDEDIEDIOEITVLSQ	72
QY	83	LRLHNTIOYRGCVLREHTAMLVMEYC-IGSASDLLEVHKRPLQEVETAAVTHGALQGLAY	141
Db	73	CDSFYITIEFGYSYKSTKRLMTIMEYLELGGGSADLLK--PGLEETVYATILREIKLDY	130
QY	142	LHSHNMTHRDVKAANIILSEEGVTKLDDFGSASIMAA--NSFVOTPRVMAPEVYLLAM	137
Db	131	LHSEKRIHRDIIKAAVNLISEGGVDKCLDFGVAQGLDTQIQRNTEFVATPRWMAPEVY--	187
QY	198	DEGOYDGVNDVMSLGIICIEIAERKEPPLFNWMMASALYHIAONESPLIOGSHSEYRNF	257
Db	188	KQSAVDFKADIMSLGITAIELAKENPNSDIDHRVRVFLPKNSPPLLEQOH-SKPRKEF	246
QY	258	VDLSQKTIPODRPTSEVYLKHFVLR-ERPRVYIMDLIORTKQAVRELMDIYRKMKKIL	316
Db	247	VEACIIMDPRPRPAKELKHKFTTRTKTSFTELIDR-----YKRWMS--	292
QY	317	FOEAPNPGAEAPPEEE---EAE-----PY--MHRAGTSLSSSHS	353
Db	293	-----EGHGSESSSEDDIDGAEADGQGPWTPTTIRSPSKLHKG---TALHSQK	344
QY	354	VPSKISASSOSSVNSLADASDNEEEEBEE--EEDBE-----EEEGPESREM	401
Db	345	-PADAVKROPSPQCLSTLVRPVFCELKEKHQSGSGVGALEBLENMFSLAEESCPIGSDK	403
QY	402	AMM	404
Db	404	LNV	406

```

RESULT 13
US-09-211-930-4
: Sequence 4, Application US/09211930
: Patent No. 5962265
: GENERAL INFORMATION:
: APPLICANT: Tyrell E. No. 5962265r1s
: APPLICANT: William Craig Moore
: APPLICANT: David Shay Silberstein
: TITLE OF INVENTION: HUMAN SIGNAL TRANSDUCTION
: TITLE OF INVENTION: SERINE/THREONINE KINASE
: FILE REFERENCE: PHM 70236
: CURRENT APPLICATION NUMBER: US/09/211,930
: CURRENT FILING DATE: 1998-12-15
: EARLIER APPLICATION NUMBER: GB 9726851.0
: EARLIER FILING DATE: 1997-12-19
: NUMBER OF SEQ ID NOS: 14
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 4
: LENGTH: 426
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-211-930-4

```

Query Match	27.4%;	Score 592;	DB 2;	Length 426;
Best Local Similarity	36.4%;	Pred. No. 6.2e-42;		
Matches 154; Conservative	69;	Mismatches 128;	Indels 72;	Gaps 16

QY 23 DPEKLEFDLLEIGHSGGAVYFAPADVANSVWAKKMSYSGKSNRMDIIEVEFPL 82  
 Db 15 DPELEFKLDRIGKSGSGEVYKGDHNRKRVAAKIILDL-EEADEIEDIQEILVLSQ 72  
 QY 83 LRHNITIOYRGVLTREHTALVMEYC-LGSADLLEVHKRPLOEVELAATGALOGLAY 141  
 Db 73 CDSPYIRYFGSLTKRKLMTIMEYLGSGGADBLK--PEPEETIYATLRLEIRGLGY 130  
 QY 142 LRSHNMTHRDVKAAGNIIISPEGLVLTGDEGSGASIMAPA---NSFVGTRPWNAPEVILAM 197  
 Db 131 LHSERKLRHRIRIKANVLLISQGVYKLADFCVAQQLIDTQIKRNTFEGTGFPMWAEV--- 187

```

QY      198  DEGDYDGVWYMSIGTICIEIAEKRPPLFNNNAMSALYHTAONSSPALOSGHSSEYPRNF 257
           || :||:||||| |||| :|| :|| :|| :|| :|| :|| :|| :||
Db      188  KQSAVDFKADLMISGITAIAELAKEPPNSDLHKRYLFLIPKNSPFLBQOH-SKPPKEF 246
           || :||:||||| |||| :|| :|| :|| :|| :|| :|| :|| :||
QY      258  VDSCLOKIPDQPTSEVLLKHRYFLR-ERPPYVIMDLIOQTKDAVBELMDIQRKMKKL 316
           || :||:||||| |||| :|| :|| :|| :|| :|| :|| :|| :||
Db      247  VEACIKMDPRPRPAKELTKKHKEFTRYTKTSFTELIDR-----YKRMS-- 292
           || :||:||||| |||| :|| :|| :|| :|| :|| :|| :|| :||
QY      317  FQEAHPNGGAPEE-----EAF-----PY--MHRACITLSLESBSHS 353
           || :||:||||| |||| :|| :|| :|| :|| :|| :|| :|| :||
Db      293  -----EGHGEESSSESDIDGEAFADGQGIPTWFFPTIRPSPSHKLHG---TALHSOK 344
           || :||:||||| |||| :|| :|| :|| :|| :|| :|| :|| :||
QY      354  VPSMSISASQSSSSVNSLIADSDNEEBEEBEE------EEEBE-----EEGPEGRM 401
           || :||:||||| |||| :|| :|| :|| :|| :|| :|| :|| :||
Db      345  -PADAVKROPSPQCLSTLVPRVFELKEKHKGSGSVGALJELEENNAFLAEFSCOPGISDK 403
           || :||:||||| |||| :|| :|| :|| :|| :|| :|| :|| :||
QY      402  AMM 404
           || :||:||||| |||| :|| :|| :|| :|| :|| :|| :|| :||
Db      404  LMV 406
           || :||:||||| |||| :|| :|| :|| :|| :|| :|| :|| :||

```

```

RESULT 14
US-09-340-993-4
: Sequence 4, Application US/09340993
: Patent No. 6034228
: GENERAL INFORMATION:
: APPLICANT: Tyrell E. No. 6034228r1s
: APPLICANT: William Craig Moore
: APPLICANT: David Shay Silberstein
: TITLE OF INVENTION: HUMAN SIGNAL TRANSDUCTION SERINE/THREONINE KINASE
: FILE REFERENCE: PHM.70296.N1
: CURRENT APPLICATION NUMBER: US/09/340,993
: CURRENT FILING DATE: 1999-06-25
: EARLIER APPLICATION NUMBER: GB 9726651.0 & US 09/211,930
: EARLIER FILING DATE: 1997-12-19 & 1998-12-15
: NUMBER OF SEQ ID NOS: 14
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 4
: LENGTH: 426
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-09-340-993-4

```

Query Match	27.48;	Score 593;	DB 3;	length 426;
Best local Similarity	36.48;	Pred. No. 6.2e-42;		
Matches 154;	Conservative 69;	Mismatches 128;	Indels 72;	Gaps 16

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QY 23 DPELFSDLEIGHGSGAYVFADVANSFVAVKXKSSYGSKOENKMOOILKEVNFLOK 82
Db 15 DPELFKIDRIGKSGGEYVAKGIDNTEKVAIKIIDL--EAEDEDIEDIOQETIVLSO 72
QY 83 LRHPNTIOYNGCYLREHTAVLWMEYC-LGSASDLEVEYKPKLOEVELAAVTHAGOLGAY 141
Db 73 CDSFYITRYGSGYLSKTKIWMETVYLOGGSALDLD--PEPLEETVYATILRETLGLDY 130
QY 142 LHSNMTHRQVAKGNILLSPGLYKLDPESSATMAPA-----NSPFGTPTVMAAPVYLAM 197
Db 131 LHSERKTHRIKAVNLLSOGDVKLADFGVAQOLDTDTIKRNTFVGTPFWMAPEVI--- 187
QY 198 DEGOYDKVWVMSLIGTICIELAERKPLFPMNMMSALYIAONESPALYSGHSEYFRN 257
Db 188 KQSAVYDKADIMSLGITALELANGEPNSDLHMRVYFLPKNSPTLEQGH-SKEFFKE 246
QY 258 VDSLOKIPDDRPTSEVYLKHFVLR-ERPPVIMDLIOFTKDAVELNDIYRKMKIL 316
Db 247 VEALINMDPFRPRAKLLHKETITRTKTSFTELIDR-----YKRKMS-- 292
QY 317 FOEAPNPGAEAPPEE---EAE-----PY--MHRAGTILSSSHS 353
Db 293 -----EHGGESSSESDIDGELAEDGEOGPIWTFPPPIRPSPSKLHGK---TALSSOK 344
QY 354 VPSMISIASQSSSVNSLADSNEEEEEED---EEEEE-----EEEGPESRGM 401

```

Db 345 -PADAVKRPSCUCLTVRPVFGELKEKHKOGSGSVGALAELENAFSLAESCPGISDK 403  
 QY 402 AMM 404  
 Db 404 LMV 406

RESULT 15  
 US-09-185-370-2  
 ; Sequence 2, Application US/09185370  
 ; Patent No. 6093560  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Force, Thomas  
 ; APPLICANT: Kyriakis, John M.  
 ; APPLICANT: Pombo, Celia M.  
 ; APPLICANT: Bonventure, Joseph  
 ; TITLE OF INVENTION: SOK-1 AND METHODS OF USE  
 ; NUMBER OF SEQUENCES: 10  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Fish & Richardson, P.C.  
 ; STREET: 225 Franklin Street  
 ; CITY: Boston  
 ; STATE: MA  
 ; COUNTRY: US  
 ; ZIP: 02110-2804  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: Windows95  
 ; SOFTWARE: FASTSEQ for Windows Version 2.0  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/185,370  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/852,743  
 ; FILING DATE:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Fraser, Janis K.  
 ; REGISTRATION NUMBER: 34,819  
 ; REFERENCE/DOCKET NUMBER: 00786/327001  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 617/542-5070  
 ; TELEFAX: 617/542-8906  
 ; TELEX: 200154  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 426 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; FRAGMENT TYPE: internal  
 ; US-09-185-370-2

Query Match 27.4%; Score 592; DB 3; Length 426;  
 Best Local Similarity 36.4%; Pred. No. 6.2e-42;  
 Matches 154; Conservative 69; Mismatches 128; Indels 72; Gaps 16;

QY 23 DEKFLSDIREIGHSFGVYFARVNSEVAIAIKKMSYSGKOSNKKMODIIKEVRFLOK 82  
 Db 15 DEELFTKIDRIKSGKSGFGEVYKIDNHTKEVVAIKIIDL-EEADEIEDIOOETIVLSQ 72  
 QY 83 LNHPTIOYRGCYLREHFMALVMEYC-LGSASDLEVHKRPLQEEVIAVTHGALQGLAY 141  
 Db 73 CDSPIYTRFGSYLAKSTKMIIMEXYLGSGSALDLK--PGPLETYIATILREILKGLDY 130  
 QY 142 LHSNMIRHDVAGNILLSEPLVKLGDFGSASIMAPA---NSFVGTPYMAPEVITAM 197  
 Db 131 LHSERKIHDIKAAVNLSEQGDVAKLADGVAGQLTDQIKRNTFVGTFPMAPVYI--- 187  
 QY 198 DEGQDQKVDVMSLGTICELAEKRPPLFNMAASALYHIAQNESPALOSGMSEYFRNF 257  
 Db 188 KQSAVDYKADIVSLGTALEAKGEPNSDLHPMRYLFLIPKNSPTLEGQH-SKPFKEF 246

QY 258 VDSCLOKIPDRPTSEVLKHKREVR-ERRPTVIMDLQRTDAVRELNLQYRKMKIL 316  
 Db 247 VEACLNKDRFPRPTAKELKHKFTYTKTSFLFELDR-----YKRWKS-- 292  
 QY 317 FOEAPNPGAEAPDEE---EAE-----PY--MHRGTLTSLSSHS 353  
 Db 293 -----EGHGESESSSDSDIDGEADEGCPITWFPPTIRPSPHSKLHG--TALHSSOK 344  
 QY 354 VPSMSISASSOSSVNSLADASONEEEEEEEEE-----EEEE-----EEGPEPSEM 401  
 Db 345 -PADAVKRPSCUCLTVRPVFGELKEKHKOGSGSVGALAELENAFSLAESCPGISDK 403  
 QY 402 AMM 404  
 Db 404 LMV 406

Search completed: November 22, 2002, 12:28:06  
 Job time : 11.402 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: November 22, 2002, 12:18:00 ; Search time 25.376 Seconds  
(without alignments)  
2184.436 Million cell updates/sec

Title: US-09-686-346a-4\_COPY\_1\_416

Perfect score: 2161  
Sequence: 1 MPAGRAGSLKDPVALFF.....ESREMMQEGHTVTSHS 416

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: /SID52/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*  
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22: /SID52/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.\*  
23: /SID52/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2161	100.0	993	20	AA49897
2	2133	98.7	1235	21	AA84163
3	2117	98.0	1049	22	AA604366
4	2098	97.1	758	20	AAW97677
5	1728.5	80.0	1001	20	AA49896
6	1726.5	79.9	1001	20	AA55942
7	1726.5	79.9	1001	23	AB97326
8	1670.5	77.3	748	20	AA55938
9	1540.5	71.3	899	21	AA843191
10	1537.5	71.1	898	20	AAW97676

11	1532.5	70.9	898	21	AA44244	Human cell signal1
12	1531.5	70.9	898	20	AA55936	Human SUIU3 protei
13	1320.5	61.1	323	22	AA87114	Novel central nerv
14	1300	60.2	1039	22	AB69116	Drosophila melanog
15	1119	51.8	265	22	AA87435	Novel central nerv
16	1119	51.8	265	22	AAU17256	Novel signal trans
17	1032.5	47.8	982	20	AA55955	Nematode STE20-rel
18	987	45.7	1062	21	AA40294	Human ORFX ORP58 p
19	902.5	41.8	398	22	AA55980	Human protein sequ
20	692.5	32.0	786	20	AA55937	Human SUIU3 protei
21	660	30.5	153	22	AA25383	Human protein sequ
22	614.5	28.4	487	20	AA721674	Human Ste20 homolo
23	606	28.0	1385	22	AA79405	Human protein SEQ
24	605	28.0	1269	22	AA68223	Amino acid sequenc
25	605	28.0	1277	22	AA68220	Amino acid sequenc
26	605	28.0	1298	22	AA68222	Amino acid sequenc
27	605	28.0	1306	22	AA68218	Amino acid sequenc
28	605	28.0	1324	22	AA68221	Amino acid sequenc
29	605	28.0	1332	22	AA68219	Amino acid sequenc
30	605	28.0	1353	22	AA68217	Amino acid sequenc
31	605	28.0	1360	21	AA55263	Human protein kina
32	605	28.0	1360	22	AA50059	Large NIK-related
33	601	27.8	426	18	AA31603	Human protein kina
34	596	27.6	431	22	AA97069	Human polypeptide
35	594	27.5	431	20	AA55950	Human MST3 protein
36	594	27.5	431	20	AA404473	Human Ste20-like s
37	594	27.5	431	21	AA82276	Human Ste20-like k
38	594	27.5	443	23	AA20953	Human N-Kinase pro
39	592	27.4	426	21	AA82275	Human MAPK-pathway
40	591	27.3	413	20	AA421672	Murine C12.2bs pol
41	591	27.3	426	20	AA55949	Human STE20 protei
42	588	27.2	431	21	AA68771	Amino acid sequenc
43	587	27.1	566	22	AB65561	Drosophila melanog
44	585.5	27.1	1339	22	AA78421	Human protein SEQ
45	581	26.9	458	22	AB604990	Novel human diagno

#### ALIGNMENTS

RESULT 1  
AA49897 standard; Protein: 993 AA.  
ID AA49897  
AC AA49897;  
XX  
XX 27-JAN-2000 (first entry)  
XX  
XX  
XX Rat TAO2 kinase.  
DE  
XX  
XX TAO2, TAO2, MEK3; mitogen activated protein kinase; phosphorylation;  
KW p38; protein kinase; cancer; inflammation; autoimmune disease;  
KW degeneration; insulin-resistant diabetes; metabolic disorder;  
KW neurodegeneration; MAP kinase; MAP/ERK kinase.  
XX  
XX Rattus sp.  
OS  
XX  
XX WO9953076-A1.  
XX  
XX 21-OCT-1999.  
XX  
XX 14-APR-1999; 99WO-US08165.  
XX  
XX 14-APR-1998; 98US-0060410.  
XX  
XX (TEXA ) UNIV TEXAS SYSTEM.  
XX  
XX Cobb M, Hutchison M, Chen Z, Berman K;  
PI WPI, 1999-633831/54.  
XX N-PSDB; AA232436.  
XX  
XX New polypeptides that phosphorylate kinase, used to screen for

PT modulators for treating e.g. cancer or inflammation -  
XX  
XX Claim 7; Page 84-87; 95pp; English.  
XX  
CC The present sequence represents rat TAO2 protein kinase, which is capable  
CC of phosphorylating MEK3 (a MAP/ERK kinase). TAO kinases, and related  
CC polypeptides, are used to screen for modulators of stress-responsive  
CC mitogen activated protein (MAP) kinase pathways. These modulators are  
CC potentially useful for treating or preventing: (1) inflammation,  
CC autoimmune disease, cancer and degeneration (inhibitors of  
CC phosphorylation); or (2) insulin-resistant diabetes, metabolic disorders  
CC and neurodegeneration (enhancers of phosphorylation). TAO kinases are  
CC also used to raise specific antibodies, useful therapeutically as  
CC modulators and as immunoassay reagents for detecting TAO kinases.  
CC TAO kinase polynucleotides can be used: (a) for recombinant expression  
CC of TAO kinases; and (b) in the form of fragments, for detecting TAO  
CC kinase polynucleotides in standard hybridisation and amplification  
CC tests. TAO kinases are highly specific for MEK3.  
XX  
SQ Sequence 993 AA:  
  
Query Match 100.0%; Score 2161; DB 20; Length 993;  
Best Local Similarity 100.0%; Pred. No. 4, 1e-175;  
Matches 416; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MPAGGRAGSLKDPDVAELFFKDDPEKLFSDLRIGHSFGAYVFARDVNSEVAIAIKMS 60  
DB 1 MPAGGRAGSLKDPDVAELFFKDDPEKLFSDLRIGHSFGAYVFARDVNSEVAIAIKMS 60  
  
QY 61 YSKQSNENKMODIKRFLQKLRHPNTIYRCGYLRHTAMLVMEYCGSASDLEVHK 120  
DB 61 YSKQSNENKMODIKRFLQKLRHPNTIYRCGYLRHTAMLVMEYCGSASDLEVHK 120  
  
QY 121 KPLQVEIAVTHGALQGLAYLHSHNMIRHDYKAGNILLSEPLVYLGDFGSASIMAPAN 180  
DB 121 KPLQVEIAVTHGALQGLAYLHSHNMIRHDYKAGNILLSEPLVYLGDFGSASIMAPAN 180  
  
QY 181 SFVGTPTWMAPEVILAMDEGOYDGKVDVMSLGTICIELAEKRPPLFNMNMSALYHIAON 240  
DB 181 SFVGTPTWMAPEVILAMDEGOYDGKVDVMSLGTICIELAEKRPPLFNMNMSALYHIAON 240  
  
QY 241 ESPALSGHSEYFRNVDSCLKIPDRPTSEVLKHKRVLREPRPTVIMDLQRIKDA 300  
DB 241 ESPALSGHSEYFRNVDSCLKIPDRPTSEVLKHKRVLREPRPTVIMDLQRIKDA 300  
  
QY 301 VRELIDNLYQKMKKILFQEARPNPGAEPPEEBAEYMRAGTLISLSSHVSPTSIS 360  
DB 301 VRELIDNLYQKMKKILFQEARPNPGAEPPEEBAEYMRAGTLISLSSHVSPTSIS 360  
  
QY 361 ASSOSSVNSLADASDNEEEEEEEEEEEEGPESREMANMQEGEHTVTSHS 416  
DB 361 ASSOSSVNSLADASDNEEEEEEEEEEEEGPESREMANMQEGEHTVTSHS 416  
  
RESULT 2  
AAB41663  
ID AAB41663 standard; Protein: 1235 AA.  
AC AAB41663;  
XX  
DT 08-FEB-2001 (first entry)  
XX  
DE Human ORFX ORF1427 polypeptide sequence SEQ ID NO:2854.  
XX  
KW Human: open reading frame; ORFX: detection; cytostatic; hepatotropic;  
KW vulnerrary; antiproliferative; antiparkinsonian; nootropic; neuroprotective;  
KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiac;  
KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;  
KW hypotensive; dermatological; immunosuppressive; antiinflammatory;  
KW antiviral; antibacterial; antifungal; antifungal; antihemorrhagic;  
KW antianemic; gene therapy; cancer; proliferative disorder; hypertension;  
KW neurodegenerative disorder; osteoarthritis; graft vs host disease;  
KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;

KW cholesterol ester storage; systemic lupus erythematosus; infection;  
KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;  
KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;  
KW bone damage; cartilage damage; antiinflammatory disease; coagulation;  
KW thrombosis; contraceptive.  
XX  
OS Homo sapiens.  
XX  
PN WO200058473-A2.  
XX  
PD 05-OCT-2000.  
XX  
XX 31-MAR-2000; 2000MO-US08621.  
PF  
XX 31-MAR-1999; 99US-0127607.  
PR 02-APR-1999; 99US-0127636.  
PR 05-APR-1999; 99US-0127728.  
PR 30-MAR-2000; 2000US-0540763.  
XX  
XX (CURA-) CURAGEN CORP.  
PA  
XX  
XX Shinkets RA, Leach M;  
PI  
XX WPI; 2000-602362/57.  
DR  
XX N-PSDB; AAC75872.  
XX  
XX Novel nucleic acids and peptides derived from open reading frame X,  
PT useful for treating e.g. cancers, proliferative disorders,  
XX neurodegenerative disorders and cardiovascular disease -  
XX  
XX Claim 11; Page 2092-2095; 5507pp; English.  
XX  
CC AACT7446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,  
CC which represent the human ORFX open reading frames 1 to 3161. The ORFX  
CC sequences have activities such as: cytostatic; hepatotropic; vulnerrary;  
CC antiproliferative; antiparkinsonian; nootropic; neuroprotective;  
CC osteopathic; anticonvulsant; antiarthritic; immunosuppressant;  
CC immunostimulant; cardiac; thrombolytic; coagulant; vasotropic;  
CC antidiabetic; hypotensive; dermatological; immunosuppressive;  
CC antiinflammatory; antibacterial; antiviral; antifungal; antihemorrhagic;  
CC antihypertensive; and antianemic. The sequences can be used for determining  
CC the presence of or predisposition to, or preventing or treating  
CC pathological conditions associated with an ORFX-associated disorder. The  
CC nucleic acids can be used to express ORFX proteins in gene therapy  
CC vectors. The proteins and nucleic acids may be used to treat cancers,  
CC proliferative disorders, neurodegenerative disorders, osteoarthritis,  
CC graft vs host disease, cardiovascular disease, diabetes mellitus,  
CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus  
CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,  
CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,  
CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,  
CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance  
CC coagulation; to inhibit thrombosis; and as a contraceptive.  
XX  
SQ Sequence 1235 AA:  
  
Query Match 98.7%; Score 2133; DB 21; Length 1235;  
Best Local Similarity 99.0%; Pred. No. 1, 4e-172;  
Matches 412; Conservative 1; Mismatches 1; Indels 2; Gaps 1;  
  
QY 1 MPAGGRAGSLKDPDVAELFFKDDPEKLFSDLRIGHSFGAYVFARDVNSEVAIAIKMS 60  
DB 1 MPAGGRAGSLKDPDVAELFFKDDPEKLFSDLRIGHSFGAYVFARDVNSEVAIAIKMS 60  
  
QY 61 YSKQSNENKMODIKRFLQKLRHPNTIYRCGYLRHTAMLVMEYCGSASDLEVHK 120  
DB 61 YSKQSNENKMODIKRFLQKLRHPNTIYRCGYLRHTAMLVMEYCGSASDLEVHK 120  
  
QY 121 KPLQVEIAVTHGALQGLAYLHSHNMIRHDYKAGNILLSEPLVYLGDFGSASIMAPAN 180  
DB 121 KPLQVEIAVTHGALQGLAYLHSHNMIRHDYKAGNILLSEPLVYLGDFGSASIMAPAN 180  
  
QY 181 SFVGTPTWMAPEVILAMDEGOYDGKVDVMSLGTICIELAEKRPPLFNMNMSALYHIAON 240  
DB 181 SFVGTPTWMAPEVILAMDEGOYDGKVDVMSLGTICIELAEKRPPLFNMNMSALYHIAON 240

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Db      181 SFVGTPTWMAPEVILAMDEQYDGKDVWSLGTICIEIARKKPPLFNNMNSALYHTAQN 240
QY      241 ESPALSGHMSSEFRNFVDSCLQIKIPDRPTSEVLKHKRVLERRPTVTMDLIQRTKDA 300
Db      241 ESPVLOSGHMSSEFRNFVDSCLQIKIPDRPTSEVLKHKRVLERRPTVTMDLIQRTKDA 300
QY      301 VRELDNLQYRKMKKILFQEAPNGPGAEPPEEAEPEYMHRACTLTSLSSHVSPTSMSIS 360
Db      301 VRELDNLQYRKMKKILFQEAPNGPGAEPPEEAEPEYMHRACTLTSLSSHVSPTSMSIS 360
QY      361 ASSQSSSVNSLADSDNNEEEEEEEEGPSPSRMAMQGEHTVTSHSS 416
Db      361 ASSQSSSVNSLADSDN--EEEEEEEEEEEGGPEAREMAMQGEHTVTSHSS 414

RESULT 3
AAE04366
ID      AAE04366 standard; Protein; 1049 AA.
XX
AC      AAE04366;
XX
DT      04-SEP-2001 (first entry)
XX
DE      Human kinase (PKIN)-7.
XX
KW      Human kinase; PKIN-7; therapy; immune disorder; Addison's disease; AIDS;
KW      acquired immune deficiency syndrome; growth and developmental disorder;
KW      arteriosclerosis; mixed connective tissue disease; MCTD; adenocarcinoma;
KW      leukaemia; cardiovascular disease; myocardial infarction; hypertension;
KW      lipid disorder; cancer; fatty liver; cholestasis; transgenic animal;
KW      gene therapy; antiallergic; antiasthmatic; antihypertensive; dermatological;
KW      antidiabetic; nephrotoxic; antitumor; antidiabetic; antirheumatic;
KW      antipsychotic; neuroprotective; cytostatic; hepatotropic; osteopathic;
KW      vasotropic; antidiabetic; anorectic.
XX
OS      Homo sapiens.
XX
FH      Location/Qualifiers
FT      Domain
FT      28..281
FT      /note="Eukaryotic protein kinase domain"
FT      Domain
FT      30..269
FT      /note="Protein kinase domain"
FT      Region
FT      147..158
FT      /note="Protein kinase ST"
FT      Region
FT      618..777
FT      /note="Serine/threonine protein kinase TAO1"
XX
PN      WO200146397-A2.
XX
PD      28-JUN-2001..
XX
PF      20-DEC-2000; 2000WO-US35304.
XX
PR      23-DEC-1999; 99US-0172066.
PR      14-JAN-2000; 2000US-0176107.
PR      21-JAN-2000; 2000US-0177731.
PR      28-JAN-2000; 2000US-0178573.
XX
PA      (INCYTE GENOMICS INC.
PI      Yang J, Baughn MR, Buford N, Au-Young J, Lu DM, Reddy R, Yue H;
PI      Yao MG, Lal P, Khan FA;
XX
DR      MPI: 2001-418059/44.
DR      N-PSDB; AAD08640.
XX
XX      Novel human kinase proteins (PKIN) useful for diagnosing, treating,
XX      preventing immune disorders, cardiovascular diseases and disorders
XX      affecting growth and development associated with abnormal expression of
XX      PKIN
XX
PS      Claim 1; Page 111-113; 128pp; English.

```

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XX      The invention relates to novel human kinase proteins (PKIN) and
CC      nucleic acid molecules encoding them. PKIN is useful for identifying
CC      compounds that modulates its activity. PKIN cDNA is useful for
CC      assessing toxicity of a test compound. PKIN and its cDNA are useful
CC      for diagnosis, prevention and treatment of immune disorders such as
CC      acquired immune deficiency syndrome (AIDS), Addison's disease, anaemia,
CC      adult respiratory distress syndrome, allergies, amyloidosis, psoriasis,
CC      autoimmune haemolytic anaemia, autoimmune thyroiditis, multiple
CC      sclerosis, asthma, osteoarthritis, osteoporosis, rheumatoid arthritis,
CC      ulcerative colitis and diabetes mellitus; growth and developmental
CC      disorders such as actinic keratosis, arteriosclerosis, atherosclerosis,
CC      bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD),
CC      and myelofibrosis; cancers such as adenocarcinoma and leukaemia,
CC      cardiovascular diseases such as myocardial infarction and hypertension;
CC      and lipid disorders such as fatty liver and cholestasis. PKIN cDNA is
CC      useful to detect upstream sequences such as promoters and regulatory
CC      elements, for creating knock in or knock out in humanised animals or
CC      transgenic animals to model human disease and for somatic or germ-line
CC      gene therapy for treating the above mentioned disorders. The present
CC      sequence is human kinase (PKIN)-7.
XX
SQ      Sequence      1049 AA:
XX
Query Match      98.0%; Score 2117; DB 22; Length 1049;
Best Local Similarity 98.3%; Pred. No. 2,5e-171;
Matches 409; Conservative 2; Mismatches 3; Indels 2; Gaps 1;
QY      1 MPAGRGASLKDPDVAELFFKDDPEKLFSDLRIGHSFGAYVFARDVNSEVAIAIKMS 60
Db      1 MPAGRGASLKDPDVAELFFKDDPEKLFSDLRIGHSFGAYVFARDVNSEVAIAIKMS 60
QY      61 YSKQSNSEKMODIIKEVRFQKLHPTIOYRGCVLREHNAIMVEYCGSASDILEVHK 120
Db      61 YSKQSNSEKMODIIKEVRFQKLHPTIOYRGCVLREHNAIMVEYCGSASDILEVHK 120
QY      121 KPLOEVEIAAVTGAAGLAVLHSHNMHRDVKAGNLTISEPGLVKGDFGSASIMAPAN 180
Db      121 KPLOEVEIAAVTGAAGLAVLHSHNMHRDVKAGNLTISEPGLVKGDFGSASIMAPAN 180
QY      181 SFVGTPTWMAPEVILAMDEQYDGKDVWSLGTICIEIARKKPPLFNNMNSALYHTAQN 240
Db      181 SFVGTPTWMAPEVILAMDEQYDGKDVWSLGTICIEIARKKPPLFNNMNSALYHTAQN 240
QY      241 ESPALSGHMSSEFRNFVDSCLQIKIPDRPTSEVLKHKRVLERRPTVTMDLIQRTKDA 300
Db      241 ESPVLOSGHMSSEFRNFVDSCLQIKIPDRPTSEVLKHKRVLERRPTVTMDLIQRTKDA 300
QY      301 VRELDNLQYRKMKKILFQEAPNGPGAEPPEEAEPEYMHRACTLTSLSSHVSPTSMSIS 360
Db      301 VRELDNLQYRKMKKILFQEAPNGPGAEPPEEAEPEYMHRACTLTSLSSHVSPTSMSIS 360
QY      361 ASSQSSSVNSLADSDNNEEEEEEEEGPSPSRMAMQGEHTVTSHSS 416
Db      361 ASSQSSSVNSLADSDN--EEEEEEEEEEEGGPEAREMAMQGEHTVTSHSS 414

RESULT 4
AAW97677
ID      AAW97677 standard; Protein; 758 AA.
XX
AC      AAW97677;
XX
DT      10-MAY-1999 (first entry)
XX
DE      Human KDS2 protein kinase.
XX
KW      KDS2; kinase domain related to Ste20; human; serine kinase;
KW      threonine kinase; protein kinase; signal transduction.
XX
OS      Homo sapiens.
XX
PN      WO9902699-A1.

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XX 21-JAN-1999.  
 PD 07-JUL-1998; 98WO-US14231.  
 PF 08-JUL-1997; 97US-0889518.  
 PR (CADU-) CADUS PHARM CORP.  
 PA Johnson GL, Fleiman CM;  
 PI WPI: 1999-120900/10.  
 PS N-PSDB: AAX07075.  
 XX New isolated vertebrate kinase - used to develop products for the  
 PT diagnosis and treatment of disorders involving cellular processes  
 PT such as signal transduction processes  
 PS Claim 31: Page 85-88; 100pp: English.  
 XX This polypeptide comprises human protein kinase KDS2, a novel  
 CC protein associated with signal transduction. KDS2 has a  
 CC kinase domain related to that of Ste20 (KDS1 = Kinase Domain  
 CC related to Ste20). KDS2 cDNA (see AAX07075) was isolated from a  
 CC human bone marrow cDNA library. A clone (see AAX07074) encoding the  
 CC highly homologous KDS1 (see AAW97676) was also obtained. Both KDS1  
 CC and KDS2 have Glu/Gln-rich regions at their C-terminus (see also  
 CC AAW97678-79) suggesting an alpha-helical structure that may play a  
 CC role in covalently localising these proteins to a specific site  
 CC within the cells, which may be necessary for function. A method  
 CC for producing KDS polypeptides in host cells is provided. Since  
 CC KDS molecules have kinase activity, they are useful as modulating  
 CC agents in regulating a variety of cellular processes such as signal  
 CC transduction pathways. These pathways may regulate cytoskeleton,  
 CC secretion, growth, apoptosis, superoxide generation, and specific  
 CC gene transcription. KDS polypeptides and polynucleotides can be  
 CC used for treating disorders involving aberrant expression of  
 CC mammalian KDS genes. They can also be used for detection,  
 CC diagnosis and drug screening.  
 XX Sequence 758 AA:  
 SQ Query Match 97.1%; Score 2098; DB 20; Length 758;  
 Best Local Similarity 97.6%; Pred. No. 6,6e-170;  
 Matches 406; Conservative 3; Mismatches 5; Indels 2; Gaps 1;  
 QY 1 MAGGAGAGSLKDPDAELFFKDDPEKLFSDLRREIGHSGGAYFPADVNSEVVAIKKMS 60  
 DB 1 MPAGGAGAGSLKDPDAELFFKDDPEKLFSDLRREIGHSGGAYFPADVNSEVVAIKKMS 60  
 QY 61 YSGKSNEMKMODIIKEVRFLQKLRHPTIOYRGCYLRHTAMLVMEYCGSASDLEEVHK 120  
 DB 61 YSGKSNEMKMODIIKEVRFLQKLRHPTIOYRGCYLRHTAMLVMEYCGSASDLEEVHK 120  
 QY 121 KPLQVEYIAAVTHGALQGLAYLHSHNMIRHDYKAGNILLSEPLVKLGDFGSASIMAPAN 180  
 DB 121 KPLQVEYIAAVTHGALQGLAYLHSHNMIRHDYKAGNILLSEPLVKLGDFGSASIMAPAN 180  
 QY 181 SFGVGPYMAAPVILLAMDGOYDKVDVWSLGTCTELAEKRPPLFNMMASALYHIAON 240  
 DB 181 SFGVGPYMAAPVILLAMDGOYDKVDVWSLGTCTELAEKRPPLFNMMASALYHIAON 240  
 QY 241 ESPALQSGHMSSEYFRNFVSCLOKIPDRPTSSEVLKHKRFVLRERPTVIMDLQRTKA 300  
 DB 241 ESPALQSGHMSSEYFRNFVSCLOKIPDRPTSSEVLKHKRFVLRERPTVIMDLQRTKA 300  
 QY 301 VEELNLQYRKMKKILFQAPNGPGAELPEEPEEAPYMHRAATLTSLSHVSPTS 360  
 DB 301 VEELNLQYRKMKKILFQAPNGPGAELPEEPEEAPYMHRAATLTSLSHVSPTS 360  
 QY 361 ASSOSSVNSLADASDNEEEEEEEEEEEBEGPESREMAAMQGEHTVTSHS 416  
 DB 361 ASSOSSVNSLADASDNEEEEEEEEEEEBEGPESREMAAMQGEHTVTSHS 416

RESULT 5  
 AAY49896  
 ID AAY49896 standard; Protein; 1001 AA.  
 XX AAY49896;  
 AC AAY49896;  
 XX 27-JAN-2000 (first entry)  
 DT Rat TAO1 kinase.  
 DE TAO1; TAO2; MEK3; mitogen activated protein kinase; phosphorylation;  
 XX p38; protein kinase; cancer; inflammation; autoimmune disease;  
 KW degeneration; insulin-resistant diabetes; metabolic disorder;  
 KW neurodegeneration; MAP kinase; MAP/ERK kinase.  
 XX Rattus sp.  
 OS WO9953076-A1.  
 XX 21-OCT-1999.  
 XX 14-APR-1999; 99WO-US08165.  
 XX 14-APR-1998; 98US-0060410.  
 PR (TEXA) UNTV TEXAS SYSTEM.  
 XX Cobb M, Hutchison M, Chen Z, Berman K;  
 PI WPI: 1999-633831/54.  
 DR N-PSDB: AA32435.  
 XX New polypeptides that phosphorylate kinase, used to screen for  
 PT modulators for treating e.g. cancer or inflammation  
 PT Claim 1; Fig 1; 95pp: English.  
 PS The present sequence represents rat TAO1 protein kinase, which is capable  
 CC of phosphorylating MEK3 (a MAP/ERK kinase). TAO kinases, and related  
 CC polypeptides, are used to screen for modulators of stress-responsive  
 CC mitogen activated protein (MAP) kinase pathways. These modulators are  
 CC potentially useful for treating or preventing: (1) inflammation,  
 CC autoimmune disease, cancer and degeneration (inhibitors of  
 CC phosphorylation); or (2) insulin-resistant diabetes, metabolic disorders  
 CC and neurodegeneration (enhancers of phosphorylation). TAO kinases are  
 CC also used to raise specific antibodies, useful therapeutically as  
 CC modulators and as immunoassay reagents for detecting TAO kinases.  
 CC TAO kinase polynucleotides can be used: (a) for recombinant expression  
 CC of TAO kinases; and (b) in the form of fragments, for detecting TAO  
 CC kinase polynucleotides in standard hybridisation and amplification  
 CC tests. TAO kinases are highly specific for MEK3.  
 XX Sequence 1001 AA:  
 SQ Query Match 80.0%; Score 1728.5; DB 20; Length 1001;  
 Best Local Similarity 79.6%; Pred. No. 2.9e-138;  
 Matches 331; Conservative 32; Mismatches 32; Indels 21; Gaps 1;  
 QY 1 MPAGGAGAGSLKDPDAELFFKDDPEKLFSDLRREIGHSGGAYFPADVNSEVVAIKKMS 60  
 DB 1 MSTRNAGAGSLKDPDAELFFKDDPEKLFSDLRREIGHSGGAYFPADVNSEVVAIKKMS 60  
 QY 61 YSGKSNEMKMODIIKEVRFLQKLRHPTIOYRGCYLRHTAMLVMEYCGSASDLEEVHK 120  
 DB 61 YSGKSNEMKMODIIKEVRFLQKLRHPTIOYRGCYLRHTAMLVMEYCGSASDLEEVHK 120  
 QY 121 KPLQVEYIAAVTHGALQGLAYLHSHNMIRHDYKAGNILLSEPLVKLGDFGSASIMAPAN 180  
 DB 121 KPLQVEYIAAVTHGALQGLAYLHSHNMIRHDYKAGNILLSEPLVKLGDFGSASIMAPAN 180  
 QY 181 SFGVGPYMAAPVILLAMDGOYDKVDVWSLGTCTELAEKRPPLFNMMASALYHIAON 240



PI Tang YF, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;  
PI Xue AJ, Yang Y, Weinman T, Drmanac RT;  
XX  
XX WPI: 2002-292408/33.  
DR N-PSDB: ABN32512.  
XX  
PT An isolated polynucleotide for treating diseases associated with its  
PT encoded polypeptide such as cancer and multiple sclerosis -  
XX  
XX Example 2; SEQ ID NO 594; 509pp; English.  
XX  
XX The present invention provides the protein and coding sequences of 444  
CC novel human proteins. These were isolated from expressed sequences tags  
CC (ESTs). They can be used to stimulate cell growth, to regulate  
CC haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth  
CC e.g. in burn treatment, to regulate the immune system e.g. to treat  
CC multiple sclerosis, to regulate activin or inhibin e.g. to treat  
CC infertility, to regulate haemostasis or thrombolysis e.g. to treat  
CC stroke and cancer, to screen for drugs, to treat inflammatory conditions  
CC e.g. rheumatoid arthritis, and to treat nervous system disorders e.g.  
CC Parkinson's disease. The present sequence is a protein of the invention.  
XX  
XX  
SQ Sequence 1001 AA;

Query Match 79.9%; Score 1726.5; DB 23; Length 1001;  
Best Local Similarity 79.3%; Pred. No. 4.3e-138;  
Matches 330; Conservative 33; Mismatches 32; Indels 21; Gaps 1;

OY 1 MPAGRAGSLKDPDVAELFFKDDPEKLFSDREIGHSGFAYFARDVNSEVAIKKMS 60  
DB 1 MSTNRAGSLKDPDVAELFFKDDPEKLFSDREIGHSGFAYFARDVNSEVAIKKMS 60  
OY 61 YSGKSNKEMKQDIIKEVRFLOKLRHPTIQRGCVLRHTAWLWMEYCLGSASDLELVH 120  
DB 61 YSGKSTKEMKQDIIKEVRFLOKLRHPTIQRGCVLRHTAWLWMEYCLGSASDLELVH 120  
OY 121 KPLQVEIAIAVTHGALQGLAYLHSHNMIRDVAKNIIISFGLVAKLDFGASAMAPAN 180  
DB 121 KPLQVEIAIAVTHGALQGLAYLHSHNMIRDVAKNIIISFGLVAKLDFGASAMAPAN 180  
OY 181 SFVGTPIYMAPEVILAMDEGOYDGKVDVMSLGTICIELAERKPLFNNMAMSLYHIAON 240  
DB 181 SFVGTPIYMAPEVILAMDEGOYDGKVDVMSLGTICIELAERKPLFNNMAMSLYHIAON 240  
OY 241 ESPALOSGHWSEYFRNFVDSCLQITQDRPTSVLLKHPVLRPPYIMDIQRTKDA 300  
DB 241 ESPALOSGHWSEYFRNFVDSCLQITQDRPTSVLLKHPVLRPPYIMDIQRTKDA 300  
OY 301 VRELDMLOTRKMKKILFOEAPNGCAEAPDEEAPRYNHRAGTGLSLSSSHSVPMST 360  
DB 301 VRELDMLOTRKMKKILFOEAPNGCAEAPDEEAPRYNHRAGTGLSLSSSHSVPMST 360  
OY 361 ASSQSSSVNSLADASNEEEEEEDEEEDEEGEPESREMMAMQGEHTVTHSS 416  
DB 361 ASSQSSSVNSLADASNEEEEEEDEEEDEEGEPESREMMAMQGEHTVTHSS 416

AAV55938  
ID AAV55938 standard; Protein; 748 AA.  
XX  
XX  
AC AAV55938;  
XX  
XX  
DT 18-FEB-2000 (first entry)  
XX  
XX  
DE Murine SULU3 protein.  
XX  
XX

Antirheumatic; antiarthritic; antiinflammatory; antiallergic; osteopathic;  
neutropenic; antiarteriosclerotic; antiasthmatic; immunosuppressive;  
cardioprotective; cardiatic; cerebroprotective; cytostatic; antidiabetic;  
vulnary; STE20; protein kinase; STRK3; STRK4; STRK5; STRK6; STRK7;  
ZC1; ZC2; ZC3; ZC4; KHS2; SULU3; GSK3; PAK4; PAK5; antagonist;  
antibody; gene therapy; rheumatoid arthritis; artherosclerosis; asthma;

KW inflammatory bowel disease; Crohn's disease; osteoarthritis; psoriasis;  
KW rhinitis; autoimmunity; organ transplantation; multiple sclerosis;  
KW myocardial infarction; cardiovascular disease; stroke; renal failure;  
KW oxidative stress-related neurodegenerative disorder; Parkinson's disease;  
KW amyotrophic lateral sclerosis; Leigh syndrome; cancer; cardiomyopathy;  
KW ischemic disorder; inflammation; diabetes mellitus; fibrosis; mitosis;  
KW mesangial disorder; growth regulation; wound healing; T cell activation;  
KW immunosuppressant.  
XX  
XX Mus sp.  
XX  
XX WO9953036-A2.  
XX  
XX 21-OCT-1999.  
XX  
XX 13-APR-1999; 99WO-US08150.  
XX  
XX 14-APR-1998; 98US-0081784.  
XX  
XX (SUGEN) SUGEN INC.  
XX  
XX PLOWMAN G, Martinez R, Whyte D;  
PI  
XX  
XX WPI: 1999-611301/52.  
DR N-PSDB: AA240490.  
XX  
XX Novel kinase-related polypeptides used for the diagnosis and treatment  
XX of kinase-related diseases and disorders -  
XX  
XX Claim 11; Page 299-301; 387pp; English.

This sequence represents a novel STE20-related protein kinase. The  
invention relates to nucleic acid molecule encoding a kinase polypeptide  
selected from STRK2, STRK3, STRK4, STRK5, STRK6, STRK7, ZC1, ZC2, ZC3,  
ZC4, KHS2, SULU3, GSK3, PAK4 and PAK5. The proteins are used to  
identify agonists and antagonists, and to raise antibodies. The  
polynucleotides are useful in gene therapy protocols. The polynucleotides,  
polypeptides, antibodies, antagonists and agonists may be used to treat  
diseases such as immune-related disorders and diseases (e.g. rheumatoid  
arthritis, atherosclerosis, chronic inflammatory bowel disease (e.g.  
Crohn's disease), asthma, osteoarthritis, psoriasis, atherosclerosis,  
rhinitis, autoimmunity, and organ transplantation, chronic inflammatory  
disease, multiple sclerosis, organ transplantation, myocardial  
infarction, cardiovascular disease, stroke, renal failure, oxidative  
stress-related neurodegenerative disorders (e.g. amyotrophic lateral  
sclerosis, Parkinson's disease and Leigh syndrome), cancer,  
cardiomyopathies, ischemic disorders, inflammatory disorders, diabetes  
mellitus, fibrotic and mesangial disorders. The proteins may also be  
useful for cell growth regulation (e.g. in wound healing), T cell  
activation, mitosis control, and as immunosuppressants.

Sequence 748 AA;  
Query Match 77.3%; Score 1670.5; DB 20; Length 748;  
Best Local Similarity 77.9%; Pred. No. 1.7e-133;  
Matches 324; Conservative 32; Mismatches 31; Indels 29; Gaps 2;

OY 1 MPAGRAGSLKDPDVAELFFKDDPEKLFSDREIGHSGFAYFARDVNSEVAIKKMS 60  
DB 1 MSTNRAGSLKDPDVAELFFKDDPEKLFSDREIGHSGFAYFARDVNSEVAIKKMS 60  
OY 61 YSGKSNKEMKQDIIKEVRFLOKLRHPTIQRGCVLRHTAWLWMEYCLGSASDLELVH 120  
DB 61 YSGKSTKEMKQDIIKEVRFLOKLRHPTIQRGCVLRHTAWLWMEYCLGSASDLELVH 120  
OY 121 KPLQVEIAIAVTHGALQGLAYLHSHNMIRDVAKNIIISFGLVAKLDFGASAMAPAN 180  
DB 121 KPLQVEIAIAVTHGALQGLAYLHSHNMIRDVAKNIIISFGLVAKLDFGASAMAPAN 180  
OY 181 SFVGTPIYMAPEVILAMDEGOYDGKVDVMSLGTICIELAERKPLFNNMAMSLYHIAON 240  
DB 181 SFVGTPIYMAPEVILAMDEGOYDGKVDVMSLGTICIELAERKPLFNNMAMSLYHIAON 240

QY	261	ESALASOSHMSEYFNFDLSOLQKIPQDRPSSEVLKHKRFLRLRRRPPTVYIMDLQIRKDA	300
Db	241	ESPTLQS-----NMDSLOLQKIPQDRPSSEILKMFVLRRLRRPPTVLLQIRKDA	292
QY	301	VRELDNLQYRKMKKILFQEAENGCAEAPDEEPEEAAPMHAGTUTLSHSSVSPMSIS	360
Db	293	VRELDNLQYRKMKKILFQEAHNGRAVEAQDEEEDDHGVGTGVNSVGSQSPMSIS	352
QY	361	ASSGSSVSNLSADASDNEEEEEEEEEEEBEGPESREMANAQEGHTVTSHS	416
Db	353	ASSGSSVSNLSPDASDDKSELD-----MMEDHTVMSNSS	387
RESULT 9			
ID	AAB43191	AAB43191 standard; Protein: 899 AA.	
AC	AAB43191;		
DT	08-FEB-2001	(first entry)	
DE	Human ORFX ORF2955	polypeptide sequence SEQ ID NO:5910.	
KM	Human; open reading frame; ORFX; detection: cytostatic; hepatotropic; vulnerrary; antiparasitic; antiparkinsonian; nootropic; neuroprotective; anticovulsant; osteopathic; antihistritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antinflammatory; antiviral; antibacterial; antifungal; antirheumatic; antihypoid; antinaeamic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; severe combined immunodeficiency; malaria; autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound; bone damage; cartilage damage; antinflammatory disease; coagulation; thrombosis; contraceptive.		
OS	Homo sapiens.		
PN	WO200058473-A2.		
PD	05-OCT-2000.		
PF	31-MAR-2000; 2000WO-US08621.		
PR	31-MAR-1999; 99US-0127607.		
PR	02-APR-1999; 99US-0127636.		
PR	05-APR-1999; 99US-0127728.		
PR	30-MAR-2000; 2000US-0540763.		
PA	(CURA-) CURAGEN CORP.		
PI	Shimkels RA, Leach M;		
DR	WPI: 2000-602362/57.		
DR	N-PSDB: AAC77400.		
PT	Novel nucleic acids and peptides derived from open reading frame X, neurodegenerative disorders and cardiovascular disease -		
PS	Claim 11; Page 5088-5090; 5507pp; English.		
CC	AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerrary; antiparasitic; antiparkinsonian; nootropic; neuroprotective; osteopathic; anticovulsant; antihistritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antinflammatory; antibacterial; antiviral; antifungal; antirheumatic; antihypoid; and antinaeamic. The sequences can be used for determining		

CC	the presence of or predisposition to, or preventing or treating
CC	pathological conditions associated with an ORFX-associated disorder. The
CC	nucleic acids can be used to express ORFX proteins in gene therapy
CC	vectors. The proteins and nucleic acids may be used to treat cancers,
CC	proliferative disorders, neurodegenerative disorders, osteoarthritis,
CC	graft vs host disease, cardiovascular disease, diabetes mellitus,
CC	hypernatension, hypothyroidism, cholesterol ester storage, systemic lupus
CC	erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
CC	bacterial or fungal infection, malaria, autoimmune disorders, asthma,
CC	allergies, aplastic anemia, burns, wounds, bone and cartilage damage,
CC	nocturnal haemoglobinuria, antiinflammatory disease; to enhance
CC	coagulation; to inhibit thrombosis; and as a contraceptive.
CC	
XX	
SQ	Sequence 899 AA;
Query Match	71.3%; Score 1540.5; DB 21; Length 899;
Best Local Similarity	71.3%; Pred. No. 2.ee-122;
Matches 293:	Conservative 44; Mismatches 55; Indels 19; Gaps 1;
QY	6 RAGSLKDDPVALFPRKDDPEKLFSDLREIGHSGSFAYVFARVRNSEVVAIKMSYSKGQ 65           : : : : :           : : : : :           : : : : :           : : : : : DB 2 RKGVAKDEPIDALFYKKDDEELFIGLHGHGSPFAVVFATNAHTSEVVAIKMYSYGQ 61
QY	66 SNEKKODIKEYRFLQOKLRHPNTIOYRCGYLREHTPAVLVMEXCIGSASDLLVEHKRPLOE 125 : : : : :   : : : : :   : : : : :   : : : : :   : : : : :   : : : : :   : : : : : DB 62 THEKKMODLIKEYKFLROLKHPTITIEYKCICYLKEHTPAVLMEYCIGSASADLLVEHKRPLOE 121
QY	126 VRIAAVTGALOGILYLSSHNMHHVDVKAAGNLTISEPLVKLGDCGSASIMAPAFVGT 185           : : : : :   : : : : :   : : : : :   : : : : :   : : : : :   : : : : : DB 122 VELAITTGHALGLLYLSHALIHRODKRAGNLTLEPGQVKLADGSAMASPASFVGT 181
QY	186 PYWMAPEVILANDEGOYGYKVDSGLGITCIETLARCKPPLFNMMNASLYHAQNESPAL 245           : : : : :   : : : : :   : : : : :   : : : : :   : : : : :   : : : : : DB 182 PYWMAPEVILANDEGOYGYKVDSGLGITCIETLARCKPPLFNMMNASLYHAQNDSFTL 241
QY	246 OSGHWSEYFRNFVDSCLQIPDRPTSEVLLKNRFVLRERPPFVIIMDIQRTKDAVREL 305     : : :         : : :     : : :     : : :     : : :     : : :     : : : DB 242 OSNEWTFDFRRFDYCLQIKIPQERTSALLRHDFVRDRPLRVILDIQRTKDAVREL 301
QY	306 NIQYRKMKILFOENPNNGGAEPREEEAEMYMRAGTLTSLSHSVPSMTSASSQS 365           : : : : :   : : : : :   : : : : :   : : : : :   : : : : :   : : : : : DB 302 NIQYRKMKILFOETRNGLNSQDEEDSEHGTSLNREMDSLGNHSIPSMVSFTGSQS 361
QY	366 SSVNSLADASDNEEEEEEEEEESGPFSSREMANMOEGEHVTSHSS 416       : :   : : : :   : : : :   : : : :   : : : :   : : : :   : : : : DB 362 SSVNSMQEVMD-----SSSLVMMHDESTINSSS 393
RESULT 10	
ID AAM97676	AAM97676 standard; Protein: 898 AA.
XX AAM97676;	
AC AAM97676;	
XX	
XX	10-MAY-1999 (first entry)
DT	
XX	
DE	Human KDSL serine/threonine kinase.
XX	
KM	KDSL: kinase domain related to Ste20, human; serine kinase;
XX	threonine kinase; protein kinase; signal transduction.
XX	
OS	Homo sapiens.
XX	
PN	WO9902699-A1.
XX	
PD	21-JAN-1999.
XX	
XX	07-JUL-1998; 98WO-US14231.
PF	
XX	
PR	08-JUL-1997; 97US-0889518.
XX	
XX	(CADU-) CADUS PHARM CORP.
XX	

PI Johnson GL, Plesman CM;  
XX  
XX WPI: 1999-120900/10.  
DR N-PSDB; AAX07074.  
XX  
PT New isolated vertebrate kinase - used to develop products for the  
PT diagnosis and treatment of disorders involving cellular processes  
PT such as signal transduction processes  
XX  
XX  
PS Claim 30; Page 78-81; 100pp; English.  
XX  
XX This polypeptide comprises human serine/threonine kinase KDS1, a  
CC novel protein associated with signal transduction. KDS1 has a  
CC kinase domain related to that of Ste20 (KDS1 = Kinase Domain  
CC related to Ste20). KDS1 cDNA (see AAX07074) was isolated from a  
CC human bone marrow cDNA library. A clone (see AAX07075) encoding the  
CC highly homologous KDS2 (see AAW97677) was also obtained. Both KDS1  
CC and KDS2 have Glu/Gln-rich regions at their C-terminus (see also  
CC AAW97678-79) suggesting an alpha-helical structure that may play a  
CC role in covalently localising these proteins to a specific site  
CC within the cells, which may be necessary for function. A method  
CC for producing KDS polypeptides in host cells is provided. Since  
CC KDS molecules have kinase activity, they are useful as modulating  
CC agents in regulating a variety of cellular processes such as signal  
CC transduction pathways. These pathways may regulate cytoskeleton,  
CC secretion, growth, apoptosis, superoxide generation, and specific  
CC gene transcription. KDS polypeptides and polynucleotides can be  
CC used for treating disorders involving aberrant expression of  
CC mammalian KDS genes. They can also be used for detection,  
CC diagnosis and drug screening.  
XX  
XX Sequence 898 AA;

Query Match 71.1%; Score 1537.5; DB 20; Length 898;  
Best local Similarity 71.0%; Pred. No. 4.6e-122;  
Matches 292; Conservative 45; Mismatches 55; Indels 19; Gaps 1;

QY 6 RAGSLKDPVAELFFKDDPEKFLSDREIGHSGFAGVYFARDNSEVVAIKRMYSQKQ 65  
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :  
DB 2 RKGVLDPETIADLFYKDDPEELFGLHEIGHSGFAGVYFATNMHTNEVVAIKRMYSQKQ 61  
QY 66 SNEKMODIKREVFLOKLRPNTIOYRGCVLREHTAMLVMEYCLGASDLEVHKRPLOE 125  
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QY 186 PYWMAPEVILIADDEGOYDGKVDVWSUGITCIELAEKRPPLFNMMAMSALYHIAQNESPAL 245  
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AC AAV44244;  
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DT 28-FEB-2000 (first entry)

XX  
DE Human cell signalling protein-7.  
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XX Cell signalling protein-7; CSIG-7; cell proliferation; arteriosclerosis;  
KW inflammatory disorder; cirrhosis; cancer; hepatitis; AIDS;  
KW Addison's disease; multiple sclerosis.  
XX  
OS Homo sapiens.  
XX  
FH Key  
FT Modified-site  
FT /note= "Potential phosphorylation site"  
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FT /note= "Potential phosphorylation site"  
FT 502  
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FT /note= "Potential phosphorylation site"  
FT 503  
FT Modified-site







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PR 05-DEC-2000; 2000US-0256719.  
PR 06-DEC-2000; 2000US-0251479.  
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PR 08-DEC-2000; 2000US-0251869.  
PR 08-DEC-2000; 2000US-0251899.  
PR 08-DEC-2000; 2000US-0251990.  
PR 11-DEC-2000; 2000US-0254097.  
PR 05-JAN-2001; 2001US-0259678.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Rosen CA, Barash SC, Ruben SM;  
XX  
XX WPI; 2001-581633/65.  
XX  
XX N-PSDB; ABR43444.  
XX  
XX New isolated nucleic acid encoding a protein for diagnosing,  
PT preventing, treating or ameliorating medical conditions and used as  
PT food additives or preservatives -  
XX  
XX  
PS Claim 9; SEQ ID No 632; 837pp; English.  
XX  
XX  
XX The invention describes an isolated nucleic acid molecule (I) encoding a  
CC novel central nervous system protein. (I) and polypeptides (II) encoded  
CC by (I), are used to treat a medical conditions and in diagnosis of a  
CC pathological condition. Disorders which are diagnosed or treated include  
CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative  
CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders  
CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,  
CC angiogenesis, nervous system disorders e.g. Alzheimer's disease and  
CC amyotrophic lateral sclerosis, infections caused by bacteria, viruses

CC e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders  
CC e.g. corneal infection, gastrointestinal disorders e.g. dysphagia,  
CC adenocarcinomas and irritable bowel syndrome, reproductive system  
CC disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes  
CC and pituitary dwarfism, cancers and disorders at the cellular level e.g.  
CC leukaemia, disorders involving neovascularisation e.g. malignancies,  
CC respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g.  
CC acute kidney failure and blood related disorders e.g. myocardial  
CC infarction. The polypeptides can also be used to aid wound healing and  
CC epithelial cell proliferation, to prevent skin aging due to sunburn, to  
CC maintain organs before transplantation, for supporting cell culture of  
CC primary tissues, to regenerate tissues and in chemotaxis. The  
CC polypeptides can also be used as a food additive or preservative to  
CC increase or decrease storage capabilities, fat content, lipid, protein,  
Query Match 61.1%; Score 1320.5; DB 22; Length 323;  
Best Local Similarity 75.7%; Pred. No. 3.5e-104;  
Matches 256; Conservative 24; Mismatches 37; Indels 21; Gaps 1;  
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QY 139 LAYLHSHNMIRHDYKAGNILLSEPGLVKLGDFGSASIMAPANSFVGTYPMAPEVILAMD 198  
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QY 199 EGYDYGKVDVWSIGTCTIEAERKRPPLFNMMAMSALYHIAONESPALQSGHMEYFNFV 258  
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QY 259 DSCLOKIPDPRPSEVLKREPRPVIMDLIORTDAVELDNLQYRKXKLLFQ 318  
Db 181 DSCLOKIPDPRPSEVLKREPRPVIMDLIORTDAVELDNLQYRKXKLLFQ 240  
QY 319 EAPNGPAEAPEEEEAEPYHNRAGTLTSSSHSVSMSTASQSSSVNLADASDNE 378  
Db 241 EAHNGPAVEAOEEEDDHGXTGTVNSGNSISXMSXSASQSSSVNLPDVSDDK 300  
QY 379 EEEEEEDEEEDEDEBPESREMANMOEGHTVTSHS 416  
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XX 26-MAR-2002 (first entry)  
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XX Drosophila melanogaster polypeptide SEQ ID NO 34140.  
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XX Drosophila; developmental biology; cell signalling; insecticide;  
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XX pharmaceutical.  
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XX Drosophila melanogaster.  
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XX WO200171042-A2.  
XX  
XX 27-SEP-2001.  
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XX 23-MAR-2001; 2001WO-US09231.  
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XX 23-MAR-2000; 2000US-191637P.  
XX  
XX 11-JUL-2000; 2000US-0614150.  
XX  
XX (PEKE ) PE CORP NY.  
XX  
XX Venter JC, Adams M, Li PWD, Myers EW;  
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XX WPI; 2001-656860/75.

DR N-PSDB; ABL13219.  
XX  
PT New isolated nucleic acid detection reagent for detecting 1000 or more  
PT genes from Drosophila and for elucidating cell signalling and cell-cell  
PT interactions -  
XX  
PS Disclosure; SEQ ID NO 34140; 21bp + Sequence Listing; English.  
XX  
CC The invention relates to an isolated nucleic acid detection reagent  
CC capable of detecting 1000 or more genes from Drosophila. The invention is  
CC useful in developmental biology and in elucidating cell signalling and  
CC cell-cell interactions in higher eukaryotes for the development of  
CC insecticides, therapeutics and pharmaceutical drugs. The invention  
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
CC sequences (ABL1640-ABL16175) and the encoded proteins  
CC (AB57737-AB572072).  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pcl\_sequences.  
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SQ Sequence 1039 AA;  
  
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AC AAU87435;  
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DT 05-JUN-2002 (first entry)  
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DE Novel central nervous system protein #345.  
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KW Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;  
KW hyperproliferative disorder; neoplasm; cardiovascular disorder;  
KW cardiac arrest; cerebrovascular disorder; leukaemia; angiodysplasia;  
KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;  
KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;  
KW adenocarcinoma; reproductive system disorder; testicular feminisation;  
KW endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;  
KW respiratory disorder; renal disorder; kidney failure; blood disorder;  
KW

KW myocardial infarction; wound healing; cell proliferation; skin aging;  
KW food additive; food preservative; gene therapy.  
XX Homo sapiens.  
XX WO200155318-A2.  
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PR 31-JAN-2000; 2000US-0179065.  
PR 04-FEB-2000; 2000US-0180628.  
PR 24-FEB-2000; 2000US-0184664.  
PR 02-MAR-2000; 2000US-0186350.  
PR 16-MAR-2000; 2000US-0189874.  
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PR 18-APR-2000; 2000US-0198123.  
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PR 21-SEP-2000; 2000US-0234274.

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PR 20-OCT-2000; 2000US-0241785.  
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PR 08-NOV-2000; 2000US-0246477.  
PR 08-NOV-2000; 2000US-0246478.  
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PR 17-NOV-2000; 2000US-0249244.  
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PR 01-DEC-2000; 2000US-0250160.  
PR 01-DEC-2000; 2000US-0250391.  
PR 05-DEC-2000; 2000US-0251030.  
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PR 08-DEC-2000; 2000US-0251989.  
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PR 11-DEC-2000; 2000US-0254097.

PR 05-JAN-2001; 2001US-0259678.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Rosen CA, Barash SC, Ruben SM;  
XX  
DR WPI; 2001-581633/65.  
XX  
N-PSDB; ABR43765.  
PT New isolated nucleic acid encoding a protein for diagnosing,  
PT preventing, treating or ameliorating medical conditions and used as  
PT food additives or preservatives -  
XX  
PS Claim 9; SEQ ID No 953; 837pp; English.  
XX  
CC The invention describes an isolated nucleic acid molecule (I) encoding a  
CC novel central nervous system protein. (I) and polypeptides (II) encoded  
CC by (I), are used to treat a medical conditions and in diagnosis of a  
CC pathological condition. Disorders which are diagnosed or treated include  
CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative  
CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders  
CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischemia,  
CC angiogenesis, nervous system disorders e.g. Alzheimer's disease and  
CC amyotrophic lateral sclerosis, infections caused by bacteria, viruses  
CC e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders  
CC e.g. corneal infection, gastrointestinal disorders e.g. dysphagia,  
CC adenocarcinomas and irritable bowel syndrome, reproductive system  
CC disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes  
CC and pituitary dwarfism, cancers and disorders at the cellular level e.g.  
CC leukaemia, disorders involving neovascularisation e.g. malignancies,  
CC respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g.  
CC acute kidney failure and blood related disorders e.g. myocardial  
CC infarction. The polypeptides can also be used to aid wound healing and  
CC epithelial cell proliferation, to prevent skin aging due to sunburn, to  
CC maintain organs before transplantation, for supporting cell culture of  
CC primary tissues, to regenerate tissues and in chemotaxis. The  
CC polypeptides can also be used as a food additive or preservative to  
CC increase or decrease storage capabilities, fat content, lipid, protein,  
Query Match 51.88; Score 119; DB 22; Length 265;  
Best Local Similarity 87.5%; Pred. No. 3.9e-87;  
Matches 210; Conservative 11; Mismatches 19; Indels 0; Caps 0;  
QY 91 YRGCTLRHETAWLMEVCLGASDLEVHKRPDLQEVETAAVTHGALGCLATLHSHNMTHR 150  
Db 1 YKGCXLRHETXWLMVETCLGASDLEVHKRPDLQEVETAAVTHGALGCLATLHSHNMTHR 60  
QY 151 DVKAGNILLSEPLVKLGDFGSASIMAPANSFVGTPTPMAPAVILAMDEGQYDKVDVWS 210  
Db 61 DIKAGNILLTEPGVYKLADFGSASMAPANSFVGTPTPMAPAVILAMDEGQYDKVDVWS 120  
QY 211 LGITCIELAEKRPPLFNMMNASALYHIAONESPLQSGHMSYRNFEVDSCLQKIPODRP 270  
Db 121 LGITCIELAEKRPPLFNMMNASALYHIAONESPLQSGHMSYRNFEVDSCLQKIPODRP 180  
QY 271 TSEVLKRRFVLRBRPPVIMDLQRTKDAVRELDNIOYRKMKILIQEANGGAEPK 330  
Db 181 TSEVLKRRFVLRBRPPVIMDLQRTKDAVRELDNIOYRKMKILFRHRTNGPAVEAK 240

Search completed: November 22, 2002, 12:23:42  
job time : 30.376 secs

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: November 22, 2002, 12:20:50 ; Search time 17.76 Seconds  
(without alignments)  
3712.561 Million cell updates/sec

Title: US-09-686-346a-4\_COPY\_1\_320

Perfect score: 1678

Sequence: 1 MPAGGRAGSLKDPDVAELFF.....VRELNDLQYRKMKILFQEA 320

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPREMBL\_21:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_unclassified:\*  
14: sp\_vertebrate:\*  
15: sp\_virus:\*  
16: sp\_bacteriophage:\*  
17: sp\_archaeal:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1678	100.0	1235	11	Q9JLS3
2	1674	99.8	1049	4	Q94957
3	1674	99.8	1235	4	Q9JLS3
4	1529	91.1	1001	11	Q9JLS3
5	1527	91.0	1005	4	Q9P216
6	1519	90.5	1001	4	Q9P216
7	1384	83.1	898	13	Q919E0
8	1382	83.0	898	4	Q9H7S5
9	1382	83.0	898	4	Q9H7S5
10	1389	82.8	898	4	Q9H7S5
11	1383	82.4	898	4	Q9H7S5
12	1239.5	73.9	1039	5	Q9VW88
13	703	41.9	398	4	Q9H7S5
14	640	38.1	842	10	Q9FNU3
15	631.5	37.6	836	10	Q9FNU3
16	631.5	37.6	1120	10	Q9LQAI

17	618.5	36.9	825	10	Q9ARL7
18	616.5	36.7	825	10	Q9ARL7
19	611	36.4	809	10	Q9VYCI
20	596	35.5	431	11	Q99KH8
21	593	34.7	461	5	Q91125
22	576	34.3	426	4	Q96BA2
23	575	34.3	487	11	Q9J111
24	574.5	34.2	596	5	Q9VW84
25	574.5	34.2	669	5	Q9VW84
26	573.5	34.2	478	5	Q9VW84
27	570	34.0	445	11	Q9VW84
28	570	34.0	497	11	Q9J110
29	567	33.8	416	4	Q9P289
30	567	33.8	416	11	Q9J110
31	567	33.8	491	4	Q9VW84
32	567	33.8	491	11	Q9VW84
33	565	33.7	651	5	Q952N6
34	565	33.7	653	5	Q952N6
35	565	33.7	1268	4	Q9UKD8
36	565	33.7	1276	4	Q9UKD8
37	565	33.7	1297	4	Q9UKD9
38	565	33.7	1305	4	Q9UKD9
39	565	33.7	1323	4	Q9UKD9
40	565	33.7	1331	4	Q9UKD9
41	565	33.7	1352	4	Q9UKD9
42	565	33.7	1360	4	Q9UKD9
43	557.5	33.2	642	5	Q9VW84
44	555.5	33.1	421	5	Q952M5
45	555.5	33.1	497	5	Q9VW84

#### ALIGNMENTS

RESULT 1  
ID Q9JLS3 PRELIMINARY; PRT; 1235 AA.  
AC Q9JLS3  
DT 01-OCT-2000 (TEMBLrel. 15, Created)  
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)  
DT 01-MAR-2002 (TEMBLrel. 20, Last annotation update)  
DE Serine/threonine protein kinase TAO2.  
GN TAO2.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP MEDLINE=99428563; PubMed=10497253;  
RA Chen Z., Hutchison M., Cobb M.H.;  
RT "Isolation of the protein kinase TAO2 and identification of its  
RT mitogen-activated protein kinase/extracellular signal-regulated kinase  
RT kinase binding domain."  
RL J. Biol. Chem. 274:28803-28807(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Chen Z., Hutchison M., Cobb M.H.;  
RA Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
DR EMBL: AF140556; AAD39480.2; -  
DR HSP: P24941; 1B38.  
DR InterPro: IPR000719; Euk\_pkinase.  
DR InterPro: IPR001899; Gram\_pos\_anchor.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR002290; Ser\_thr\_pkinase.  
DR InterPro: IPR001245; Tyr\_pkinase.  
DR Pfam: PF00069; pkinase; 1.  
DR PRINTS: PR00109; TYRKINASE.  
DR ProDom: PD000001; Euk\_pkinase; 1.  
DR SMART: SM00220; S\_TKc; 1.  
DR PROSITE: PS00343; GRAM\_POS\_ANCHORING; UNKNOWN\_1.  
DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_1.

DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
 SQ SEQUENCE 1235 AA; 138750 MW; 426960D0812518AD CRC64;

Query Match 100.0%; Score 1678; DB 11; Length 1235;  
 Best Local Similarity 100.0%; Pred. No. 3.4e-140;  
 Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAGGAGSLKPDVALEFFKDDPEKLFSDLRIGSGFGAYFADVANSSEVVAIKKMS 60  
 DB 1 MPAGGAGSLKPDVALEFFKDDPEKLFSDLRIGSGFGAYFADVANSSEVVAIKKMS 60  
 QY 61 YSGKOSNEKMODIIKEVRFLQKLHNPNTIYRGCYLREHTAWLWMEYCLGSASDLEVHK 120  
 DB 61 YSGKOSNEKMODIIKEVRFLQKLHNPNTIYRGCYLREHTAWLWMEYCLGSASDLEVHK 120  
 QY 121 KPLQVEIETAAVTHGALQGLAYLHSHNMIRHDYKAGNILLSEPGVLKLGDFGSASIMAPAN 180  
 DB 121 KPLQVEIETAAVTHGALQGLAYLHSHNMIRHDYKAGNILLSEPGVLKLGDFGSASIMAPAN 180  
 QY 181 SFVGTPTYYMAPEVITLAMDGOYDKVDVWSLGTCTELAEKRPPLFNMMASALYHIAON 240  
 DB 181 SFVGTPTYYMAPEVITLAMDGOYDKVDVWSLGTCTELAEKRPPLFNMMASALYHIAON 240  
 QY 241 ESPALOSGHMSEYFRNFVDSCLQKIPQDRPTSEVLLKHFVLRERPPYIMDLIQRTKDA 300  
 DB 241 ESPALOSGHMSEYFRNFVDSCLQKIPQDRPTSEVLLKHFVLRERPPYIMDLIQRTKDA 300  
 QY 301 VRELDNLQYRKMKKILFOEA 320  
 DB 301 VRELDNLQYRKMKKILFOEA 320

## RESULT 2

Q94957 PRELIMINARY; PRT; 1049 AA.

AC 094957;  
 DT 01-MAY-1999 (TREMblrel. 10, Created)  
 DT 01-MAY-1999 (TREMblrel. 10, last sequence update)  
 DT 01-MAR-2002 (TREMblrel. 20, last annotation update)  
 DE KIA00881 protein (STE20-like kinase).  
 GN KIA00881.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-BRAIN;  
 RA MEDLINE=99156230; PubMed=10048485;  
 RA Nagase T., Ishikawa K., Suyama M., Kikuno R., Hirose M.,  
 RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.,  
 RA "Prediction of the coding sequences of unidentified human genes. XII.  
 RA The complete sequences of 100 new cDNA clones from brain which code  
 RA for large proteins in vitro."  
 RL DNA Res. 5:355-364(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Yustein J.T., Rodinson D., Templeton D.J., Kung H.-J.,  
 RA "Characterization of a Subfamily of Human STE20-like kinases that  
 RA Selectively Activate p38 Through MK3 and are Regulated via a PP2A-  
 RA dependent Mechanism."  
 RL Submitted (MAY-2000) to the EMBL/Genbank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 DR EMBL; AB020688; BAA74904.1; -;  
 DR EMBL; AF263313; AAC38503.1; -;  
 DR HSSP; P24941; 1838.  
 DR InterPro; IPR000719; Euk\_pkinase.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR Pfam; PF00069; pkinase; 1.

DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD000001; Euk\_pkinase; 1.  
 DR SMART; SM00220; S\_TKC; 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE: PS00109; PROTEIN\_KINASE\_ST; 1.  
 DR ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
 SQ SEQUENCE 1049 AA; 119280 MW; D6C5062P47794030 CRC64;

Query Match 99.8%; Score 1674; DB 4; Length 1049;  
 Best Local Similarity 99.7%; Pred. No. 6.1e-140;  
 Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPAGGAGSLKPDVALEFFKDDPEKLFSDLRIGSGFGAYFADVANSSEVVAIKKMS 60  
 DB 1 MPAGGAGSLKPDVALEFFKDDPEKLFSDLRIGSGFGAYFADVANSSEVVAIKKMS 60  
 QY 61 YSGKOSNEKMODIIKEVRFLQKLHNPNTIYRGCYLREHTAWLWMEYCLGSASDLEVHK 120  
 DB 61 YSGKOSNEKMODIIKEVRFLQKLHNPNTIYRGCYLREHTAWLWMEYCLGSASDLEVHK 120  
 QY 121 KPLQVEIETAAVTHGALQGLAYLHSHNMIRHDYKAGNILLSEPGVLKLGDFGSASIMAPAN 180  
 DB 121 KPLQVEIETAAVTHGALQGLAYLHSHNMIRHDYKAGNILLSEPGVLKLGDFGSASIMAPAN 180  
 QY 181 SFVGTPTYYMAPEVITLAMDGOYDKVDVWSLGTCTELAEKRPPLFNMMASALYHIAON 240  
 DB 181 SFVGTPTYYMAPEVITLAMDGOYDKVDVWSLGTCTELAEKRPPLFNMMASALYHIAON 240  
 QY 241 ESPALOSGHMSEYFRNFVDSCLQKIPQDRPTSEVLLKHFVLRERPPYIMDLIQRTKDA 300  
 DB 241 ESPALOSGHMSEYFRNFVDSCLQKIPQDRPTSEVLLKHFVLRERPPYIMDLIQRTKDA 300  
 QY 301 VRELDNLQYRKMKKILFOEA 320  
 DB 301 VRELDNLQYRKMKKILFOEA 320

## RESULT 3

Q90U54 PRELIMINARY; PRT; 1235 AA.

AC 090U54;  
 DT 01-MAY-2000 (TREMblrel. 13, Created)  
 DT 01-MAY-2000 (TREMblrel. 13, last sequence update)  
 DT 01-MAR-2002 (TREMblrel. 20, last annotation update)  
 DE Prostate derived STE20-like kinase PSK.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-BREAST CARCINOMA.  
 RA MEDLINE=20127920; PubMed=10660600;  
 RA Moore T.M., Garg R., Johnson C., Copcoat M.J., Ridley A.J.,  
 RA Morris J.D.H.,  
 RA "PSK, a novel STE20-like kinase derived from prostatic carcinoma that  
 RA activates the JNK MAPK pathway and regulates actin cytoskeletal  
 RA organization."  
 RL J. Biol. Chem. 275:4311-4322(2000).  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 DR EMBL; AF061943; AAD45616.1; -;  
 DR HSSP; P24941; 1838.  
 DR InterPro; IPR000719; Euk\_pkinase.  
 DR InterPro; IPR002290; Ser\_thr\_pkinase.  
 DR InterPro; IPR001245; Tyr\_pkinase.  
 DR Pfam; PF00069; pkinase; 1.  
 DR PRINTS; PR00109; TYRKINASE.  
 DR ProDom; PD000001; Euk\_pkinase; 1.  
 DR SMART; SM00220; S\_TKC; 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE: PS00109; PROTEIN\_KINASE\_ST; 1.



KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 1235 AA; 138232 MW; 3AB9BE8E90934307 CRC64;

Query Match 99.8%; Score 1674; DB 4; Length 1235;  
Best Local Similarity 99.7%; Pred. No. 7.6e-140;  
Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPAGGAGSLKPDVAELFFKDDPEKLFSDLRIGSGFGAVYFARDVNSEVVAIKKMS 60  
DB 1 MAGGAGSLKPDVAELFFKDDPEKLFSDLRIGSGFGAVYFARDVNSEVVAIKKMS 60  
QY 61 YSGKSNEMKMODIIEKVEFLQKLRHPNTIQYRGCYLREHTAMLVMEYCLGSASDILLEVHK 120  
DB 61 YSGKSNEMKMODIIEKVEFLQKLRHPNTIQYRGCYLREHTAMLVMEYCLGSASDILLEVHK 120  
QY 121 KPLQVEIATAVTHGALQGLAYLHSHNMTRDVKAGNIIISLSEGLVKLGPGSGASIMAPAN 180  
DB 121 KPLQVEIATAVTHGALQGLAYLHSHNMTRDVKAGNIIISLSEGLVKLGPGSGASIMAPAN 180  
QY 181 SFVGFPPYMAPEVYILAMDGOYDGKDVMSLGTICIELAEKRPPLFNMMASALYHIAON 240  
DB 181 SFVGFPPYMAPEVYILAMDGOYDGKDVMSLGTICIELAEKRPPLFNMMASALYHIAON 240  
QY 241 ESPALQSGHMSSEYFRNFVDSCLQKIPQDRPTSEVLLKHFVLRERPPYIMDLIQRTKDA 300  
DB 241 ESPALQSGHMSSEYFRNFVDSCLQKIPQDRPTSEVLLKHFVLRERPPYIMDLIQRTKDA 300  
QY 301 VRELDNLQYRKMKKILFOEA 320  
DB 301 VRELDNLQYRKMKKILFOEA 320

## RESULT 4

QY 088664 PRELIMINARY; PRT; 1001 AA.  
AC 088664;  
DT 01-NOV-1998 (TREMBLrel. 08, Created)  
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)  
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
DE Serine/threonine protein kinase TAO1.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID-10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-9003202; PubMed-9786855;  
RA Hutchison M., Berman K.S., Cobb M.H.;  
RT "Isolation of TAO1, a protein kinase that activates MEKs in stress-  
RT activated protein kinase cascades.";  
RL J. Biol. Chem. 273:28625-28632(1998).  
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
DR EMBL: AF084205; AAC71014.1; -;  
DR HSSP: P24941; 1B38.  
DR InterPro: IPR000719; Euk\_pkinase.  
DR InterPro: IPR002290; Ser\_thr\_pkinase.  
DR Pfam: PF000069; pkinase.1.  
DR ProDom: PD000001; Euk\_pkinase.1.  
DR SMART: SM00220; S\_TKc.1.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP.1.  
DR PROSITE: PS0011; PROTEIN\_KINASE\_DOM.1.  
DR PROSITE: PS00108; PROTEIN\_KINASE\_SF.1.  
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 1001 AA; 115952 MW; 85511B62DBD62FCC CRC64;

Query Match 91.1%; Score 1529; DB 11; Length 1001;

Best Local Similarity 88.8%; Pred. No. 4.5e-127;  
Matches 284; Conservative 22; Mismatches 14; Indels 0; Gaps 0;

QY 1 MPAGGAGSLKPDVAELFFKDDPEKLFSDLRIGSGFGAVYFARDVNSEVVAIKKMS 60  
DB 1 MPSTNRAGSLKPDVAELFFKDDPEKLFSDLRIGSGFGAVYFARDVNSEVVAIKKMS 60

QY 61 YSGKSNEMKMODIIEKVEFLQKLRHPNTIQYRGCYLREHTAMLVMEYCLGSASDILLEVHK 120  
DB 61 YSGKSNEMKMODIIEKVEFLQKLRHPNTIQYRGCYLREHTAMLVMEYCLGSASDILLEVHK 120  
QY 121 KPLQVEIATAVTHGALQGLAYLHSHNMTRDVKAGNIIISLSEGLVKLGPGSGASIMAPAN 180  
DB 121 KPLQVEIATAVTHGALQGLAYLHSHNMTRDVKAGNIIISLSEGLVKLGPGSGASIMAPAN 180  
QY 181 SFVGFPPYMAPEVYILAMDGOYDGKDVMSLGTICIELAEKRPPLFNMMASALYHIAON 240  
DB 181 SFVGFPPYMAPEVYILAMDGOYDGKDVMSLGTICIELAEKRPPLFNMMASALYHIAON 240  
QY 241 ESPALQSGHMSSEYFRNFVDSCLQKIPQDRPTSEVLLKHFVLRERPPYIMDLIQRTKDA 300  
DB 241 ESPALQSGHMSSEYFRNFVDSCLQKIPQDRPTSEVLLKHFVLRERPPYIMDLIQRTKDA 300  
QY 301 VRELDNLQYRKMKKILFOEA 320  
DB 301 VRELDNLQYRKMKKILFOEA 320

## RESULT 5

QY 09P216 PRELIMINARY; PRT; 1005 AA.  
AC 09P216; Q96L75;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE KIAA1361 protein (Serine/threonine kinase TAO1) (Fragment).  
GN KIAA1361.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID-9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-BRAIN;  
RX MEDLINE-20181126; PubMed-10718198;  
RA Nagase T., Kikuno R., Ishikawa K., Hirose M., Ohara O.;  
RT "Prediction of the coding sequences of unidentified human genes. XVI.  
RT The complete sequences of 150 new cDNA clones from brain which code  
RT for large proteins in vitro.";  
RL DNA Res. 7:65-73(2000).  
RN [2]  
RP SEQUENCE OF 5-1005 FROM N.A.  
RA Jenkins S.G., D'Andrea R.J., Gamble J.R., Vadas M.A.;  
RT "Characterization of human TAO1.";  
RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
DR EMBL: AB037782; BAA92599.1; -;  
DR EMBL: AY049015; AAL12217.1; -;  
DR HSSP: P24941; 1B38.  
DR InterPro: IPR000719; Euk\_pkinase.  
DR InterPro: IPR002290; Ser\_thr\_pkinase.  
DR InterPro: IPR001245; Tyr\_pkinase.  
DR Pfam: PF000069; pkinase.1.  
DR PRINTS: PR00109; TYRKINASE.  
DR ProDom: PD000001; Euk\_pkinase.1.  
DR SMART: SM00220; S\_TKc.1.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP.1.  
DR PROSITE: PS0011; PROTEIN\_KINASE\_DOM.1.  
DR PROSITE: PS00108; PROTEIN\_KINASE\_SF.1.  
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
FT NON\_TER  
SQ SEQUENCE 1005 AA; 116540 MW; A83BD4E53569BCB5 CRC64;

Query Match 91.0%; Score 1527; DB 4; Length 1005;

Best Local Similarity 88.8%; Pred. No. 6.8e-127;  
Matches 284; Conservative 22; Mismatches 14; Indels 0; Gaps 0;

QY 1 MPAGGAGSLKPDVAELFFKDDPEKLFSDLRIGSGFGAVYFARDVNSEVVAIKKMS 60  
DB 5 MPSTNRAGSLKPDVAELFFKDDPEKLFSDLRIGSGFGAVYFARDVNSEVVAIKKMS 64

Oy	61	YSGKOSNKKMODIIKEVFELOKHNPNTIOYRGXYLREHNAWLMMEXCISASDLEVHK	120
Db	65	YSGKOSTKKMODIIKEVFELOKHNPMSIEFKGCLREHNAMWLMMEXCISASDLEVHK	124
Oy	121	KPLEVEIAAVTNGALOGIAYLASHSHNMITHRVKAGNILLSEBPGUYVKDGFGSASIMAPAN	180
Db	125	KPLGEVEIAALTGHGALOGLAYLASHHTMIMHRDKANGNILLTEBPQVUKLADFGSASMSPAN	184
Oy	181	SFVGPRYMAAEVILLANDEGOYDKRVYWVSIGTICIELAEKKRPLEFMNAMSALYHTAON	240
Db	185	SFVGPRYMAAEVILLANDEGOYDKRVYWVSIGTICIELAEKKRPLEFMNAMSALYHTAON	244
Oy	241	ESPALOSGHMSEYFRNFEDSCLOKIPDDRPTSEVYLKHRFYLRERPTVYMDILORTKDA	300
Db	245	ESPFLQSHEMSDYFRNFVDSLOKTIPODRPTSBEELLHFIVLYKRERPTVYIDLQRTKDA	304
Oy	301	VREDLNLOYRKMKKILFOEA	320
Db	305	VREDLNLOYRKMKKILFOEA	324

RESULT	6
Q9H2K7	PRELIMINARY; PRT; 1001 AA.
ID	Q9H2K7
AC	Q9H2K7;
DT	01-MAR-2001 (TrEMBLrel. 16, Created)
DT	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT	01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE	STE20-like kinase (Fragment).
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RA	Yustein J.T., Robinson D., Kung H.-J.;
RT	"Characterization of a Subfamily of Human STE20-like Kinases that Selectively Activate p38 Through MKK3 and are Regulated via a PP2A dependent Mechanism.";
RL	Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR	EMBL: AF263312; AAC38502.1; -.
DR	HSSP: P24941; 1B38
DR	InterPro: IPR000719; Euk_p_kinase.
DR	InterPro: IPR002290; Ser_thr_pkinase.
DR	Pfam: PF00069; pkinase; 1.
DR	ProDom: PD000001; Euk_pkinase; 1.
DR	SMART: SM00220; S_TKc; 1.
DR	SMART: SM00219; TYKc; 1.
DR	PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR	PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR	PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR	kinase.
FT	NON_TER 1001 1001
QC	SEQUENCE 1001 AA; 115957 MW; 7F0E534D3E7E159E CRC64;

	Query Match	Best Local Similarity	90.5%	Score 1519;	DB 4;	Length 1001;
	Matches 283;	Conservative 22;	Mismatches 15;	Indels 0;	Gaps 0;	
QY	1	MPAGRAGSLDPDPAVELFPPKDDPEKLFSDIREIHGSGFAYFARDVNSEVAIAIKMS	60			
Db	1	MPSTNNRAGSLKDPDELAELEFFKEDPEKLTLDREIHGSGFAYFARDVKTNEVAIAIKMS	60			
QY	61	YSGKQSNKKWODIIEVARELFQKLRHPNTIQYRGCYLRHTAMLVMEYCLGASADLLEVHK	120			
Db	61	YSGKQSTKKWODIIEVARELFQKLRHPNHSIEYKGYCLREHTAMLVMEYCLGASADLLEVHK	120			
QY	121	KPIQEVETAAVTHALQGLAYLHSHNMTHRVYKAGNIIILSEGLVYKLDGFGASITMAAPN	180			
Db	121	KPIQEVETAAVTHALQGLAYLHSHNMTHRIKAGNIIILTEGQVYKLDGFGASVNASAPN	180			

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0Y 181 SFVGVPRYMAAEVILLAMDEGQYDKRVWVSGTICIELAEKKRPLFNMNMSALYHNAON 240
Db 181 SFVGVPRYMAAEVILLAMDEGQYDKRVWVSGTICIELAEKKRPLFNMNMSALYHNAON 240
0Y 241 ESPALQSGHSESEYFNFVDSCLKIPDRPISEVLLKHFRLRERPRPTVIMDLIQRTKA 300
Db 241 ESPALQSGHSESEYFNFVDSCLKIPDRPISEVLLKHFRLRERPRPTVIMDLIQRTKA 300
0Y 301 VRELDNLTQYRKMKKILFOEA 320
Db 301 VRELDNLTQYRKMKKILFOEA 320

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RESULT 7		
ID	0919E0	PRELIMINARY;
AC	0919E0	PRT;
DT	0919E0	898 AA.
01-Oct-2000	(TREMBlrel. 15, Created)	
01-Oct-2000	(TREMBlrel. 15, Last sequence update)	
01-MAR-2002	(TREMBlrel. 20, Last annotation update)	
KFC (Fragment) .		
Gallus gallus (Chicken) .		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
Archosauia; Aves; Neognathae; Galliformes; Psittacidae; Psittacinae;		
Gallus.		
NCBI_TaxID=9031;		
[1]		
SEQUENCE FROM N.A.		
MEDLINE=20162342; Pubmed=10698516;		
Yustein J.T., Li D., Robinson D., Kung H.J.;		
"KFC, a Ste20-like kinase with mitogenic potential and capability to		
activate the SAPK/JNK pathway.";		
Oncogene 19:710-718(2000).		
EMBL; AF263314; AAF73045.1; .		
HSSP; P24941; 1B38.		
InterPro; IPR000719; Euk_Pkinase.		
InterPro; IPR002290; Ser_Thr_Pkinase.		
InterPro; IPR000130; Zn_MTPetdse.		
Pfam; PF00069; pkinase; 1.		
ProDom; PD000001; Euk_pkinase; 1.		
SMART; SM00220; S_TKc; 1.		
PROSITE; PS00107; PROTEIN_KINASE_APF; 1.		
PROSITE; PSS0011; PROTEIN_KINASE_DOM; 1.		
PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.		
NON_TER		
898 898		
SEQUENCE 898 AA; 105289 MW; 46265937E218AA8 CRC64;		

Query Match	83.1%	Score 1394	DB 13	Length 898
Best Local Similarity	82.2%	Pred. No. 3.9e-115		
Matches 258	Conservative	30	Mismatches 26	Indels 0
				Gaps 0
QY	6	RAGSLKDPDVLELFKDDPEKLFDSLRREIGSGFCFAYVFARVRNSEVVAIKKMSYSKQ	65	
		:           :           :           :		
Db	2	RKGVYPKDEPDLIDLYFKDDPEELFVGLHEIGHGSGFCFAYFATNSHTNEVAVKMSYSKQ	61	
QY	66	SNEKMODIKKFEVRELOKLRHPNTIOYRCZYRREHTAMLYMEYCLASASADLLEVHKPPQE	125	
		:           :           :           :           :		
Db	62	TNEKMODIKKFEVRELOKLRHPNTIEYKCCYKERTAMLYMEYCLASASADLLEVHKPPQE	121	
QY	126	VEIAAVTHGALOGGLAYLHSHMMIHRDVAAGNILLSEPLVKIDFGSGASIMAPANSFVGT	185	
		:           :           :           :		
Db	122	VEIAAITHGALOGGLAYLHSHCKIHRDIKAGNILLTEPQVYVLADFGSASIVSPANSFVGT	181	
QY	186	PYMAAPEVILLAMDEGOYDGVAVVSLGTTCTETELERKPEPLENNAMASALYHIAQNESPAL	245	
		:           :           :           :		
Db	182	PYMAAPEVILLAMDEGOYDGVAVVSLGTTCTETELAORPPPLENNAMASALYHIAQNDSEPL	241	
QY	246	QSGHWESEYFRNFVDSLOKTIPODRPTSEVLLKHFVLERRPPVYIMDLIQRTKDAVRELD	305	
		:           :           :           :		
Db	242	QSNEMSDSFRGFEVYCIQKTIPOERKPSADLLRHDFVRRDRPPVILIDLIQRTKDAVRELD	301	
QY	306	NLOYRKKKKKILIFOE	319	
		:           :           :           :		

Db	302	NLOYRKKMKKILFQ	315
RESULT	8		
ID	Q9UHG7	PRELIMINARY;	PRT; 898 AA.
AC	Q9UHG7		
DT	01-MAY-2000 (TREMblrel. 13, Created)		
DT	01-MAY-2000 (TREMblrel. 13, Last sequence update)		
DT	01-MAY-2002 (TREMblrel. 20, Last annotation update)		
DE	STE20-like kinase.		
DE	JTK.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniota; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=20026851; Pubmed=10559204;		
RA	Tassi E., Blesova Z., Di Fiore P.P., Gutkind J.S., Wong W.T.;		
RT	"Human Jtk, a novel member of the STE20 kinase family that inhibits		
RT	JNK and is negatively regulated by epidermal growth factor";		
RL	J. Biol. Chem. 274.33287-33295(1999).		
CC	-I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.		
DR	EMBL; AF179867; AAF14559.1; -.		
DR	HSSP; P24941; 1B38.		
DR	InterPro; IPR000719; Euk_Pkinase.		
DR	InterPro; IPR002290; Ser_thr_kinase.		
DR	InterPro; IPR001245; Tyr_kinase.		
DR	InterPro; IPR000130; Zn_MTPeptide.		
DR	Pfam; PF00069; Pkinase.1.		
DR	PRINTS; PR00109; TYRKINASE.		
DR	ProDom; PD000001; Euk_pkinase.1.		
DR	SMART; SM00220; S_TKc.1.		
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP.1.		
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM.1.		
DR	PROSITE; PS00108; PROTEIN_KINASE_ST.1.		
DR	PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN.1.		
KW	ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.		
SQ	SEQUENCE 898 AA; 105657 MW; 61F04628713E6025 CRC64;		
Query Match	83.0%;	Score 1392;	DB 4; Length 898;
Best Local Similarity	81.8%;	Pred. NO. 5.9e-115;	
Matches 257;	Conservative 31;	Mismatches 26;	Indels 0; Gaps 0;
QY	6	RAGSLKDPVLELFKDPDEKLFSDRLREIGHGSGFAYVFARYNRSEVVAITKKMSYSGKQ	65.
Db	2	RKGVYLKDEIDLFKYKDDPEELFICLHEIGHGSGFAVVFATNAHTSEVVAITKKMSYSGKQ	61
QY	66	SNEKMODLIEKVEFLQKLRLHPNTIOYRCGYLREHFAWLVMEYCLGASDLEVRHKPLQ	125
Db	62	THEKMODLIEKVEFLQKLRLHPNTIEYKCYLKEHFAWLVMEYCLGASDLEVRHKPLQ	121
QY	126	VEIAVTAHTGALQGLAYLHSHNMIRHDVAAGNILLSEPLGVKIGDGSASIMAPANSFVGT	185
Db	122	VEIAITITGALHGLAYLHSHLIRHSDIKAGNILLTEPQGVKLADGSGASMAPANSFVGT	181
QY	186	PYMAAPEVILAMDQGVYGVKVDVMSLGTCTELARKRPPLPFMMNMSALYHIAONDSPTL	245
Db	182	PYMAAPEVILAMDQGVYGVKVDVMSLGTCTELARKRPPLPFMMNMSALYHIAONDSPTL	241
QY	246	QSGHSEYFRNFVDSCLQIKPODRTSEVYLKHLRFVLEBERPPTVIMDLIQRTKDAVRELD	305
Db	242	QSNEMTIDSRFRVDCYCLQIKPOERTSALLRLHDPVVRDRPLRVLIDLIQRTKDAVRELD	301
QY	306	NLOYRKKMKKILFQ	319
Db	302	NLOYRKKMKKILFQ	315
RESULT	9		
ID	Q9HC79	PRELIMINARY;	PRT; 898 AA.

ID	Q9NZM9	PRELIMINARY:	PRT:	898 AA.
AC	Q9NZM9			
DT	01-MAR-2001			
DT	01-MAR-2001			
DT	01-JUN-2002			
DE	Serine kinase (STRE20-like kinase).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_Taxid=9606;			
RP	SEQUENCE FROM N.A.			
RP	Medline=20384190; PubMed=10924369;			
RA	Zhang W., Chen T., Wan T., He L., Li N., Yan Z., Cao X.;			
RT	"Cloning of PKP, a novel dendritic cell-derived protein kinase			
RT	activating the ERK1/ERK2 and JNK/SAPK pathways.";			
RL	Biochem. Biophys. Res. Commun. 274:872-879(2000).			
RN	[2]			
RE	SEQUENCE FROM N.A.			
RC	Tissue=PLACENTA;			
RA	Strausberg R.;			
RL	Submitted (Feb-2001) to the EMBL/Genbank/DBJ databases.			
DR	EMBL: AF135158; AAC09131.1; -			
DR	EMBL: BC002756; AA02756.1; -			
DR	HSSP: P24941; 1B38.			
DR	InterPro: IPR000719; Euk_kinase.			
DR	InterPro: IPR002290; Ser_thr_kinase.			
DR	InterPro: IPR001245; Tyr_kinase.			
DR	InterPro: IPR000130; Zn_MTPeptide.			
DR	Pfam: PF00069; kinase_1.			
DR	PRINTS: PR00109; TYRKINASE.			
DR	ProDom: PD000001; Euk_kinase; 1.			
DR	SMART: SM00220; S_TKc; 1.			
DR	SMART: SM00219; Tyrc; 1.			
DR	PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.			
DR	PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.			
DR	PROSITE: PS00108; PROTEIN_KINASE_ST; 1.			
DR	PROSITE: PS00142; ZINC_PROTEASE; UNKNOWN_1.			
DR	ATP-binding; Kinase; Transferase.			
SO	SEQUENCE 898 AA; 105405 MW; AE7E30745B09763C CRC64;			
Query Match	83.0%; Score 1392; DB 4; Length 898;			
Best Local Similarity	81.8%; Pred. No. 5.9e-115;			
Matches 257; Conservative	31; Mismatches 26; Indels 0; Gaps 0;			
QY	6 RAGSLKDPVAFELFKDPEKLFSDLRREIGHGSGFAGVYFAPRVNRSSEVYAIKKMSYSGKQ 65			
DB	2 RKGVLKDPFIADLFKDPDEELFTGLHEIGHGSGFAGVYFATNAHSEVYAIKKMSYSGKQ 61			
QY	66 SNEKMODITKEVRFLOKLRHPTIYRGCYLREHTAMLVMEYCLGSASDLEVHKRPLOE 125			
DB	62 THEKMODILKEVKFLRQKHPNTIEYKGCYLEKHTAMLVMEYCLGSASDLEVHKRPLOE 121			
QY	126 VELAIVTHALOGGLAYLHSHNMTHRDYKAGNILLSEPGLYKIGDYGSAITAPANSFVGT 185			
DB	122 VELAIITHGALGLAYLHSHALIHRIKAGNILLTEPGVGLADGSGASMAPANSFVGT 181			
QY	186 PFWMAPEVILADEGOYDCKVDVWSIGTICTELAERKPPLEFMNMAISALYHTAONDSPAL 245			
DB	182 PFWMAPEVILADEGOYDCKVDVWSIGTICTELAERKPPLEFMNMAISALYHTAONDSPAL 241			
QY	246 QSGHSEVFRNFVDSCLQKIPDRPTSEVILKHFVLRERPTVIMDLTIQRTKDAVRELD 305			
DB	242 QSGNEMTDSFRRRVDCLOKIPDRPTSAELLHDFVRDRPLRVYLDLQRTKDAVRELD 301			
QY	306 NLYRKMKKILFOE 319			
DB	302 NLYRKMKKILFOE 315			
RESULT	10			
ID	Q9NZM9			
AC	Q9NZM9;			

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DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, last annotation update)
DE Serine/threonine kinase.
GN KDS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
CX NCBL_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Carter T.G., Benton B., Fruhling D., Monks C.R.F., Windmiller D.,
RA Kupfer A., Manfredi J., Johnson G.L., Pleiman C.M.;
RT "KDS and TAO1, two related proteins with kinase domain homology to
RT STE20, differentially relocate in mitogen stimulated T lymphocytes.";
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AF181985; AAF25817.1; -.
DR HSSP: P24941; 1B38.
DR InterPro: IPR000719; Euk_Pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR InterPro: IPR000130; Zn_MTpeptidse.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD000001; Euk_pkinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW ATP-binding; kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 898 AA; 105432 MW; 9738B5D5CFA12AC9 CRC64;

Query Match 82.8%; Score 1389; DB 4; Length 898;
Best Local Similarity 81.5%; Pred. No. 1,1e-114;
Matches 256; Conservative 32; Mismatches 26; Indels 0; Gaps 0;

QY 6 RAGSLKDPVALEFFKDDPEKLFSDLRIGHSFGAYFARDVNSSEVVAIKKMSYSGQ 65
DB 2 RKGVLKPEIDLYKKDDPELFGLHEIGHSGFAYFAFNATNEVVAIKKMSYSGQ 61
QY 66 SNEKWODIKVEFLQKLRHNTIYRGCYLREHTAMLVMEYCGSASDLEVAKKPLQE 125
DB 62 THEKWODLKEVKFLROLKHPNTEYKGYLKEHTAMLVMEYCGSASDLEVAKKPLQE 121
QY 126 VEIAAVTHGALOGIAYLHSHNMIRVDKAGNIIISSEGLVKLGDFGSASIMAPNSVGT 185
DB 122 VEIAAITHGALHGLAYLHSHNLHRODKAGNIIITTEPGQVKLADFGSASMAPNSVGT 181
QY 186 PYWMAPEVILIAMDGOYDGVKDVWSLGTCTELAEKRPPLFNMMAMSAHYHIAONESPAL 245
DB 182 PYWMAPEVILIAMDGOYDGVKDVWSLGTCTELAEKRPPLFNMMAMSAHYHIAONESPAL 241
QY 246 QSGHWSSEYFNFVDSCLQKIPDRPTSEVLKHFVLRERPPVIMDLIQRTKDAVRELD 305
DB 242 QSNEMWDSFRFVYDCLQKIPQERPTSABELLRHDFVRDRPLRLIDLIOQTKDAVRELD 301
QY 306 NLOYRKKMKILFQE 319
DB 302 NLOYRKKMKILFQE 315

RESULT 11
Q9H2K8 PRELIMINARY; PRT; 898 AA.
AC Q9H2K8;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
DE STE20-like kinase (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
CX NCBL_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Yustein J.T., Robinson D., Kung H.-J.;
RT "Characterization of a Subfamily of Human STE20-like kinases that
RT selectively activate p38 Through MKK3 and are Regulated via a PP2A-
RT dependent Mechanism.";
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF263311; AAG38501.1; -.
DR HSSP: P24941; 1B38.
DR InterPro: IPR000719; Euk_Pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR InterPro: IPR000130; Zn_MTpeptidse.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD000001; Euk_pkinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR SMART: SM00219; TYRK; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW Kinase.
FT NON_TER
SQ SEQUENCE 898 AA; 105501 MW; E52C5BFEDD67264E CRC64;

Query Match 82.4%; Score 1383; DB 4; Length 898;
Best Local Similarity 81.2%; Pred. No. 3.7e-114;
Matches 255; Conservative 31; Mismatches 28; Indels 0; Gaps 0;

QY 6 RAGSLKDPVALEFFKDDPEKLFSDLRIGHSFGAYFARDVNSSEVVAIKKMSYSGQ 65
DB 2 RKGVLKPEIDLYKKDDPELFGLHEIGHSGFAYFAFNATNEVVAIKKMSYSGQ 61
QY 66 SNEKWODIKVEFLQKLRHNTIYRGCYLREHTAMLVMEYCGSASDLEVAKKPLQE 125
DB 62 THEKWODLKEVKFLROLKHPNTEYKGYLKEHTAMLVMEYCGSASDLEVAKKPLQE 121
QY 126 VEIAAVTHGALOGIAYLHSHNMIRVDKAGNIIISSEGLVKLGDFGSASIMAPNSVGT 185
DB 122 VEIAAITHGALHGLAYLHSHNLHRODKAGNIIITTEPGQVKLADFGSASMAPNSVGT 181
QY 186 PYWMAPEVILIAMDGOYDGVKDVWSLGTCTELAEKRPPLFNMMAMSAHYHIAONESPAL 245
DB 182 PYWMAPEVILIAMDGOYDGVKDVWSLGTCTELAEKRPPLFNMMAMSAHYHIAONESPAL 241
QY 246 QSGHWSSEYFNFVDSCLQKIPDRPTSEVLKHFVLRERPPVIMDLIQRTKDAVRELD 305
DB 242 QSNEMWDSFRFVYDCLQKIPQERPTSABELLRHDFVRDRPLRLIDLIOQTKDAVRELD 301
QY 306 NLOYRKKMKILFQE 319
DB 302 NLOYRKKMKILFQE 315

RESULT 12
Q9VWG8 PRELIMINARY; PRT; 1039 AA.
AC Q9VWG8;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, last annotation update)
DE CG14217 protein.
GN CG14217.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephyroidae; Drosophilidae; Drosophila.
CX NCBL_TaxID=7227;
RN [1]
SQ SEQUENCE FROM N.A.

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RC STRAIN=BERKELEY;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Gelniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blaise R.G., Champe M., Pfeiffer B.D.,  
 RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Milos G.L.G.,  
 RA Abri J.F., Abhayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu U., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Boriova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,  
 RA Burris K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Deyes A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,  
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Mei M.-H., Ibegwam C.,  
 RA Jalili M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Mervinov G., Mlshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclab J.M.,  
 RA Palczolo M., Pittman G.S., Pan S., Pollard J., Pui Y., Reese M.G.,  
 RA Reilert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Spier E., Spredling A.C., Stapleton M., Strong R., Sun E.,  
 RA Svitskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,  
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of *Drosophila melanogaster*.";  
 RL Science 287:2185-2195(2000).  
 DR EMBL: AE003512; AAF48973.1; -.  
 DR HSSP: P24941; 1B38.  
 DR FLYbase: FBgn0031030; CGI4217.  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR002290; Ser\_thr\_pkinase.  
 DR Pfam: PF00069; pkinase; 1.  
 DR ProDom: PD000001; Euk\_pkinase; 1.  
 DR SMART: SM00220; S\_TKC; 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 KW ATP-binding; Transferase.  
 SO SEQUENCE 1039 AA; 118298 MW; 391D15216D295F3A CRC64;

Query Match 73.9%; Score 1239.5; DB 5; Length 1039;  
 Best Local Similarity 73.7%; Pred. No. 2.7e-101;  
 Matches 233; Conservative 35; Mismatches 47; Indels 1; Gaps 1;

QY 1 MPAGGAGAGSLKDPDVADLPFKDPEKLFSDLREIGHGSEAFVAFARDYRSEVVAIAKKMS 60  
 DB 1 MPAS-ARPGSLKDPDLADLPFKHDPKIFEDLRIGHGSEAFVAVYARCNTLRIVAIKKMS 59

QY 61 YSGKOSNEKMODITKEVRFLOKLRHPNTIQRCGLREHFAWLVMEICGASADLLEVHK 120  
 DB 60 YTKOSQDEKMODITKEVRFLOKLRHPNTIEYKGCYLRERSTAMVMEYCVASADLLEVHK 119

QY 121 KPLQVEYIAAVTGAAGLALYLSHNMIRHDVAKAGNILLSEPLVLKLGDSASIMAPAN 180  
 DB 120 KPLHEDEIAIACGLVLSGLYLSLGRIRHDIKAGNILLDNCVVKLADGSAIAIKCPAN 179

QY 181 SFVGTPTWMAPEVYILAMDEGQYDGKVDVWSLGTICIEFLAERKPPLENNMAMSALYHIAON 240  
 DB 180 SFVGTPTWMAPEVYILAMDEGQYDGKVDVWSLGTICIEFLAERKPPLENNMAMSALYHIAON 239

QY 241 ESPALOSGHWSEYFRNFVDSCLQIKIPQDRPTSEVLKHKRFVLRERPPYIMDLIORTKDA 300  
 DB 240 ESPTLEPKNMDSAFCSFVELCLKKMAERPSAKLLTHAVYVRPSDYVLLELIARTKSA 299

QY 301 VRELDNLQYRKMKIL 316  
 DB 300 VRELDNLNRYRKMKIL 315

RESULT 13  
 Q9H7S5 PRELIMINARY; PRT; 398 AA.

AC Q9H7S5;  
 DT 01-MAR-2001 (TREMblrel. 16, Created)  
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)  
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)  
 DE CDNA FL14314 f1s, clone PLACE3000350, weakly similar to  
 DE serine/chreonine-protein kinase SUVU (EC 2.7.1.-).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=PLACENTA;  
 RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,  
 RA Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,  
 RA Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,  
 RA Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,  
 RA Wakamatsu A., Nakamura Y., Nagahari K., Masuno Y., Oshima A.;  
 RT "NEO human cDNA sequencing project."  
 RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AK024376; BAB14901.1; -.  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR002290; Ser\_thr\_pkinase.  
 DR Pfam: PF00069; pkinase; 1.  
 DR ProDom: PD000001; Euk\_pkinase; 1.  
 DR SMART: SM00220; S\_TKC; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 KW ATP-binding; Transferase.  
 SO SEQUENCE 398 AA; 46177 MW; BLADDIDA45D46FA4 CRC64;

Query Match 91.9%; Score 703; DB 4; Length 398;  
 Best Local Similarity 91.7%; Pred. No. 3.7e-54;  
 Matches 132; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 177 APANSEFVGPYMAPEVYILAMDEGQYDGKVDVWSLGTICIEFLAERKPPLENNMAMSALYH 236  
 DB 3 SPANSEFVGPYMAPEVYILAMDEGQYDGKVDVWSLGTICIEFLAERKPPLENNMAMSALYH 62

QY 237 IANESPALOSGHWSEYFRNFVDSCLQIKIPQDRPTSEVLKHKRFVLRERPPYIMDLIOR 296  
 DB 63 IANESPTLOSNEWTDFRNHFVDSCLQIKIPQDRPTSEELKHILFVLRERETVLIDLIOR 122

QY 297 TKDAVRELDNLQYRKMKILFOEA 320  
 DB 123 TKDAVRELDNLQYRKMKILFOEA 146

RESULT 14  
 Q9FNJ3 PRELIMINARY; PRT; 842 AA.

AC Q9FNJ3;  
 DT 01-MAR-2001 (TREMblrel. 16, Created)  
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)  
 DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)  
 DE 3615.3.  
 OS Oryza sativa (Rice).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 OC Ehrhartoideae; Oryzae; Oryza.  
 OX NCBI\_TaxID=4530;  
 RN [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN=CV. NIPPONBARE; TRANSPOSON-GAIGAN;  
 RX MEDLINE=21140318; PubMed=11244114;  
 RA Dubcovsky J., Ramakrishna W., SanMiguel P.J., Busso C.S., Yan L.,  
 RA Shiloff B.A., Bennetzen J.L.,  
 RT "Comparative sequence analysis of colinear barley and rice bacterial  
 RT artificial chromosomes."  
 RL Plant Physiol. 125:1342-1353(2001).  
 DR EMBL; AY013245; AAG45491.1; -.  
 DR HSSP; O63450; 1A06.  
 DR Interpro: IPR000719; Euk\_pkinase.  
 DR Interpro: IPR002290; Ser\_thr\_pkinase.  
 DR Interpro: IPR001245; Tyr\_pkinase.  
 DR Pfam; PF00069; pkinase; 1.  
 DR ProDom; PD000001; Euk\_pkinase; 1.  
 DR SMART; SM00220; S\_TKC; 1.  
 DR SMART; SM00219; TYRC; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR ATP-binding; Transferase.  
 KW SEQUENCE 842 AA; 91646 MW; EBE222157E40558C CRC64;

Query Match 38.1%; Score 640; DB 10; Length 842;  
 Best Local Similarity 42.6%; Pred. No. 4,3e-48;  
 Matches 133; Conservative 56; Mismatches 91; Indels 32; Gaps 6;

QY 2 PAGGRAGSLKDP-----DVALEFFKDDPEKLFSDIREIGHGSGF 40  
 DB 214 PAVGGSEELRQPALVQQHQHQOQNSRRKPSVSVESYREDPSRKYELHLGSGSG 273  
 QY 41 AYYFADVNSEVVAIKKSYSGKSNKMODIKKEVRLQKIRHNTIQRGCTREHT 100  
 DB 274 AYYKADLTQELVAILKIIISLT--EGEEGYEDIRGEIEMLOQCSHPNVVRYFGSYGEEY 331  
 QY 101 AMLVMEYC-LGSASDLLEVHKRPLOEVEIAATVHGALOGIAYHSHNMTHROKKAENILL 159  
 DB 332 LMIWMEYCGGSAVDLIGITEERLDSQIAYIREALKGLATIHSTFFKVRDKGNNILL 391  
 QY 160 SEPGVLKIDFGSAS---IMAPANSFVGTPLYWMAPEVILAMDEGOYDGKVDWVSLGITC 215  
 DB 392 TEGGEVKLIDFGVAALQUTRTMSKRNTFICTPHMAPEVI---QESYDGKVDWVWALGVSA 448  
 QY 216 IELAERKPLPLFMNMANMSALYHIAONSPLALQSH-WSEYFRNVDSCLQIPODRPTSEV 274  
 DB 449 IEMAEQMPRSTYVHPRVIFMISSEPAFMLEDKEKWSLTFHFIAKCLTRKDLRPAASE 508  
 QY 275 LKHKRFVLRER 286  
 DB 509 MLKKFTIEKCNP 520

RESULT 15  
 024527 PRELIMINARY: PRT; 836 AA.  
 AC 024527;  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE Serine/threonine kinase.  
 GN SIK1 OR F23010.20.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=CV. COLUMBIA; TISSUE=HYPOCOTYL;  
 RA Winge P., Brembu T., Bones A.M.;  
 RL Submitted (Apr-1997) to the EMBL/Genbank/DBJ databases.  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=CV. COLUMBIA;

RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Wu D.,  
 RA Maiti R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R.,  
 RA Barstead M.E., Bowman C.L., White O., Nierman W.C., Fraser C.M.;  
 RT "Arabidopsis thaliana chromosome I BAC F23010 genomic sequence."  
 RL Submitted (JAN-2001) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; U96613; AAB68776.1; -.  
 DR EMBL; AC018364; AAG52499.1; -.  
 DR HSSP; Q00534; 1B18.  
 DR Interpro: IPR000719; Euk\_pkinase.  
 DR Interpro: IPR002290; Ser\_thr\_pkinase.  
 DR Pfam; PF00069; pkinase; 1.  
 DR ProDom; PD000001; Euk\_pkinase; 1.  
 DR SMART; SM00220; S\_TKC; 1.  
 DR PROSITE; PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE; PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR ATP-binding; Kinase; Transferase.  
 KW SEQUENCE 836 AA; 92721 MW; 805F18DF4A30762 CRC64;

Query Match 37.6%; Score 631.5; DB 10; Length 836;  
 Best Local Similarity 47.2%; Pred. No. 2.4e-47;  
 Matches 127; Conservative 54; Mismatches 77; Indels 11; Gaps 5;

QY 21 KDDPEKLFSDIREIGHGSGAYFADVNRSEVVAIKKSYSGKSNKMODIKKEVRL 80  
 DB 242 REDPTTKYEFELMLGKSGSYGKARDLKTSEIYAVKVISLT--EGEEGYEELRGEIEM 299  
 QY 81 OKLRHNTIQRGCTREHTAMLVMEYC-LGSASDLLEVHKRPLOEVEIAATVHGALOGI 139  
 DB 300 QQCNNHNVVRYLGSYGCEIYLMVMEYCGGSAVDLMNTEERLEFYQIAYIREALKGL 359  
 QY 140 AYLSHNMTHIRDYKKAENILLSEPGVLKIDFGSAS---IMAPANSFVGTPLYWMAPEVIL 195  
 DB 360 AYLSHYKVRHDKGNNILLTEGGEVKLIDFGVAALQUTRTMSKRNTFICTPHMAPEVI- 418  
 QY 196 ANDEGOYDGKVDWVSLGITCIELAEKRPPLFMNMANMSALYHIAONSPLALQSH-WSEYF 254  
 DB 419 --QENRYDGKVDWVWALGVSAIEMAEGLPPRSVHPRVIFMISSEPAFMLEDKEKWSLVF 476  
 QY 255 RNFVDSCLQIPDRPTSEVLLKHFVLR 283  
 DB 477 HDFVAKCLTRKRLRPTAEMLKHKRVER 505

Search completed: November 22, 2002, 12:26:13  
 Job time : 23.76 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: November 22, 2002, 12:18:20 ; Search time 4.96 Seconds  
(without alignments)  
2675.892 Million cell updates/sec

Title: US-09-686-346a-4\_COPY\_1\_320  
Perfect score: 1678  
Sequence: 1 MPAGSRAGSLKDPVAFELFF.....VRELDNLQYRKMKILFQEA 320

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	ID	Description
1	1008	60.1	982	1	SUUU_CAEEL
2	594	33.4	443	1	ST24_HUMAN
3	580	34.6	426	1	ST25_MOUSE
4	576	34.3	426	1	ST25_HUMAN
5	574	34.2	487	1	STK4_HUMAN
6	567	33.8	491	1	STK3_HUMAN
7	510	30.4	544	1	PAK1_RAT
8	508	30.3	545	1	PAK1_HUMAN
9	508	30.3	545	1	PAK1_MOUSE
10	505	30.1	544	1	PAK3_RAT
11	504	30.0	544	1	PAK3_HUMAN
12	500	29.8	544	1	ST10_MOUSE
13	498.5	29.7	966	1	SPK1_MOUSE
14	495.5	29.5	490	1	SPK1_YEAST
15	495.5	29.5	968	1	PAK2_HUMAN
16	491	29.3	524	1	PAK2_HUMAN
17	491	29.3	524	1	PAK2_RABIT
18	489	29.1	524	1	PAK2_RAT
19	461	27.5	1080	1	NRK1_YEAST
20	450.5	26.8	1230	1	ST20_CANAL
21	449	26.8	658	1	PAK1_SCHPO
22	441	26.3	1062	1	CC7_SCHPO
23	440	26.2	939	1	ST20_YEAST
24	438.5	26.1	591	1	PAK4_HUMAN
25	436	26.0	589	1	SHK2_SCHPO
26	432.5	25.8	1080	1	ML15_CAEEL
27	431	25.7	719	1	PAK7_HUMAN
28	430	25.6	719	1	PAK7_HUMAN
29	423	25.2	547	1	SPAK_HUMAN
30	423	25.2	553	1	SPAK_MOUSE
31	423	25.2	556	1	SPAK_MOUSE
32	418	24.9	655	1	SKM1_YEAST
33	415	24.7	842	1	CLA4_YEAST

34	403.5	24.0	1401	1	WIS4_SCHPO
35	400	23.8	974	1	CC15_YEAST
36	394.5	23.5	626	1	M3K3_HUMAN
37	388.5	23.2	626	1	M3K3_MOUSE
38	383.5	22.9	1501	1	NINC_DROME
39	382	22.8	1478	1	BCK1_YEAST
40	373.5	22.3	618	1	M3K2_HUMAN
41	372.5	22.2	619	1	M3K2_MOUSE
42	347	20.7	1493	1	M3K1_RAT
43	347	20.7	1493	1	M3K1_HUMAN
44	346	20.6	1493	1	M3K1_MOUSE
45	345.5	20.6	506	1	NEK3_HUMAN

## ALIGNMENTS

RESULT 1  
SUUU\_CAEEL STANDARD: PRT; 982 AA.  
AC P46549;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Serine/threonine-protein kinase SUUU (EC 2.7.1.1-).  
GN KIN-18 OR SUUU OR T17E9.1.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;  
OC Rhabditidae; Pelodermidae; Caenorhabditis.  
OX NCBI\_TaxId=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-Bristol N2.  
RA Du Z.;  
RL Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-Bristol N2;  
RA Cope M.J.T.V., Kendrick-Jones A.;  
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
-----  
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CC EMBL: U11280; AAA19437.1; -  
CC EMBL: U32275; AAA15370.1; -  
CC Wormpep; T17E9.1; CE01405.  
CC InterPro: IPR000719; Euk\_pkinase.  
CC InterPro: IPR002290; Ser\_thr\_pkinase.  
CC Pfam: PR00069; pkinase.1.  
CC ProbDom: PD000001; Euk\_pkinase.1.  
CC SMART; SM00220; S\_TKc.1.  
CC PROSITE; PS00107; PROTEIN\_KINASE\_ATP.1.  
CC PROSITE; PS0011; PROTEIN\_KINASE\_DOM.1.  
CC DR PROSITE; PS00108; PROTEIN\_KINASE\_ST; FALSE\_NEG.  
CC KW Transferase; Serine/threonine-protein kinase; ATP-binding.  
CC FT DOMAIN 30 289  
CC FT NP\_BIND 36 44  
CC FT BINDING 59 59  
CC FT ACT\_SITE 153 153  
CC FT BY SIMILARITY.  
CC FT BY SIMILARITY.  
CC FT BY SIMILARITY.  
SQ SEQUENCE 982 AA; 112870 MW; 745CEIE2890977D CRC64;  
Query Match 60.1%; Score 1008; DB 1; Length 982;  
Best Local Similarity 57.9%; Pred. No. 3.4e-68;  
Matches 184; Conservative 57; Mismatches 71; Indels 6; Gaps 1;  
QY 6 RAGSLKDPVAFELFFKDDPEKLFSDRLREIGHSGFGAVYFARDVRNSEVAIAIKMSYSGNQ 65

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Db      8 KGVGIDPISIALFNKDEQRYODIREIGHSGFVYFAYDKKQDYAIKRMNSGQ 67
Oy      66 SNEKKDITKEVRLPOTLHPTIOYRGCYLREHPAMLVMECLGASDLLEVHKHKL 125
Db      68 AVEKNDILKEVSLFTVYVHPHIVDKACFLDTTCMLVMEICISGAIVDVKRGM 127
Oy      126 VEIAAVTHGALOGVAVLHSHNMIRHVKNAGNILLSEPLVKGDEGSASIMAPNSVGT 185
Db      128 VEIAAICSGTLDALRYLHSLKRIHRDKAGNILLSDHAIVKLADPGSASLVDPAGTIGT 187
Oy      166 PYWMAPEVILADEGOYDKVYVMSLGTICIELAEKRPPLFNMNMSALYHIAQNESPL 245
Db      188 PEYMAPEVILADEGHYDADRWISLGTICIELAEKRPPLFNMNMSALYHIAQNDPPTL 247
Oy      246 -----OSGHMSEYRNFVDSCTKIPDRPTSEVILKHFVLRFPVIMDLIORTKD 299
Db      248 SPIDTSEQPEMSLEFVQFIDKCLRKPAERMSAECECFHPTQSRPSDTIOELIORTKN 307
Oy      300 AVRELDNTQYRRKKKILF 317
Db      308 MVLIEDNFQYKKMKRLMY 325

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RESULT 2
ST24_HUMAN STANDARD: PRT; 443 AA.
ID ST24_HUMAN
AC 09Y6E0: 014840;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Serine/threonine protein kinase 24 (EC 2.7.1.37) (STE20-like kinase
MS3) (MST-3) (Mammalian STE20-like protein kinase 3).
GN STR24 OR MST3 OR STRK3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN 11
RP SEQUENCE FROM N.A. (ISOFORM A).
RX MEDLINE=98019249; PubMed=9353338;
RA Schinkmann K., Bennis J.;
RT "Cloning and characterization of a human STE20-like protein kinase
RT with unusual cofactor requirements.";
RL J. Biol. Chem. 272:28695-28703(1997).
[2]
RP SEQUENCE FROM N.A. (ISOFORM B), AND MUTAGENESIS OF THR-18.
RC TISU-BRAIN;
RX MEDLINE=20112812; PubMed=10644707;
RA Zhou T.-H., Ling K., Guo J., Zhou H., Wu Y.-L., Jing Q., Ma L.,
RA Pei G.;
RT "Identification of a human brain-specific isoform of mammalian
RT STE20-like kinase 3 that is regulated by cAMP-dependent protein
RT kinase.";
RL J. Biol. Chem. 275:2513-2519(2000).
CC -1- FUNCTION: PROTEIN KINASE THAT ACT ON BOTH SERINE AND THREONINE
CC RESIDUES.
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- COFACTOR: ISOFORM A REQUIRES MANGANESE FOR ITS ACTIVITY.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A AND B (SHOWN HERE); ARE
CC PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: ISOFORM A IS UBQUITOUS. ISOFORM B IS
CC EXPRESSED IN BRAIN WITH HIGH EXPRESSION IN HIPPOCAMPUS AND
CC CEREBRAL CORTEX.
CC -1- PM: AUTOPHOSPHORYLATED. ISOFORM B IS ACTIVATED BY PHOSPHORYLATION
CC BY PKA.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC STE20 SUBFAMILY.
CC -----
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CC EMBL: AF024636; AAB82560.1; -.
CC EMBL: AF083420; AAD42039.1; -.
CC HSSP: P24941; ICRP.
CC Genew: HGNC:11403; STRK24.
CC MIM: 604984; -.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD000001; Euk_pkinase; 1.
DR SMART: SMO0220; S-TKC; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; FALSE_NEG.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR Transfase: Serine/threonine-protein kinase; ATP-binding;
KW Phosphorylation; Alternative splicing.
FT DOMAIN 36 286 PROTEIN KINASE.
FT NP_BIND 42 50 ATP (BY SIMILARITY).
FT BINDING 65 65 ATP (BY SIMILARITY).
FT ACT_SITE 156 156 BY SIMILARITY.
FT MOD_RES 18 18 PHOSPHORYLATION (BY PKA).
FT VARSPPLIC 1 26 MDSRAQGLINKRAATLPHRGSGT -> MAHSPVQGLP
FT MUTAGEN 18 18 T->A; LOSS OF PHOSPHORYLATION BY PKA.
FT CONFLICT 414 414 A -> V (IN REF. 2).
SQ SEQUENCE 443 AA; 49307 MW; 4A9FF1F6B6A8A97 CRC64;

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Query Match 35.4%; Score 594; DB 1; Length 443;  
 Best Local Similarity 45.8%; Pred. No. 1.6e-37;  
 Matches 130; Conservative 48; Mismatches 92; Indels 14; Gaps 7;

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Oy      21 KDDPEKLSFSDLREIGHSGFVYFADYVNSEVVAIKKMSYSGKOSNEKMODIIEVRL 80
Db      29 KADPELEFTLKEIKIGKSGEYFKGIDNRTQYVAIKIIDL--EAADEIEDIOQEIYVL 86
Oy      81 OKLRHPTIOYRGCYLREHTAVLMEYC-LGSASDLLEVHKHKLDEVEIAVTHGALOG 139
Db      87 SCODSPYVYKYYGYSLKPKTKIWEIYLGSGSALDLE--PGPLDEFOIATILREILKGL 144
Oy      140 AYLHSHNMIRHVKNAGNILLSEPLVKGDEGSASIMAP-----NSFQTPYWMAPEVIL 195
Db      145 DYLHSEKKIHRDKANAVLSEHGEVKLADPGVAGQLDTQIKRNTVGTGTPWMAPEVIL- 203
Oy      196 AMDEGOYDKVYVMSLGTICIELAEKRPPLFNMNMSALYHIAQNESPALSGHNSFYR 255
Db      204 --KQSAVYSKADWISLGTIAIELARGEPHSELHMKVFLPLKNNPYLE-GNYSKPLK 260
Oy      256 NFVDSCLQIKIPDRPTSEVILKHFVLRFPVIMDLIORTK 298
Db      261 EFVEACLNKPEPSFRTAKELLKHFILRNKAKTSYLTETLIDRYK 304

```

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RESULT 3
ST25_MOUSE STANDARD: PRT; 426 AA.
ID ST25_MOUSE
AC 09Z2W1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Serine/threonine protein kinase 25 (EC 2.7.1.37) (Sterile 20/oxidant
DE stress-response kinase 1) (Ste20/oxidant stress response kinase-1)
DE (SOK-1) (Ste20-like kinase).
GN STR25 OR SOK1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

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RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Melnick M.B.;
RT "Genetic mapping of human and mouse pak genes.";
RL Submitted (May-1997) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: OXIDANT STRESS-ACTIVATED SERINE/THREONINE KINASE THAT
CC MAY PLAY A ROLE IN THE RESPONSE TO ENVIRONMENTAL STRESS (BY
CC SIMILARITY).
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- ENZYME REGULATION: ACTIVATED BY PHOSPHORYLATION, PROBABLY
CC AUTOPHOSPHORYLATION. THE C-TERMINAL NON-CATALYTIC REGION INHIBITS
CC THE KINASE ACTIVITY (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC STE20 SUBFAMILY.
-----
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CC or send an email to license@isb-sib.ch).
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CC EMBL: AF004934; AAD01208.1; -.
CC MGD: MGI:1891699; STK25.
CC InterPro: IPR000719; Euk_pkinase.
CC InterPro: IPR002290; Ser_thr_pkinase.
CC InterPro: IPR001245; Tyr_pkinase.
CC Pfam: PF00069; pkinase; 1.
CC PRINTS: PR00109; TYRKINASE.
CC ProDom: PD000001; Euk_pkinase; 1.
CC SMART: SM00220; S_TKc; 1.
CC PROSITE: PS00108; PROTEIN_KINASE_ST; FALSE_NEG.
CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
CC Trasnferase: Serine/threonine-protein kinase; ATP-binding;
CC phosphorylation.
CC KW DOMAIN 20 270 PROTEIN KINASE.
CC NP_BIND 26 34 ATP (BY SIMILARITY).
CC BINDING 49 49 ATP (BY SIMILARITY).
CC ACT_SITE 140 140 BY SIMILARITY.
CC FT ACT_SITE 140 140
CC SEQUENCE 426 AA; 48175 MW; 6A01916034E26362 CRC64;

Query Match 34.6%; Score 580; DB 1; Length 426;
Best Local Similarity 45.4%; Pred. No. 1.8e-36;
Matches 128; Conservative 49; Mismatches 91; Indels 14; Gaps 7;

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AC 000506; Q15522;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DT Serine/threonine protein kinase 25 (Ec 2.7.1.37) (Sterile 20/oxidant
DE stress-response kinase 1) (Ste20/oxidant stress response kinase-1)
DE (SOK-1) (Ste20-like kinase).
DE STK25 OR SOK1 OR YSK1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-97042345; PubMed-8887545;
RA Pombo C.M., Bonventre J.V., Molnar A., Kyriakis J., Force T.,
RT "Activation of a human Ste20-like kinase by oxidant stress defines a
RL novel stress response pathway."
RL EMBO J. 15:4537-4546(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-97304522; PubMed-9160885;
RA Osada S.-I., Izawa M., Saito R., Mizuno K., Suzuki A., Hirai S.-I.,
RA Ohno S.;
RT "YSK1, a novel mammalian protein kinase structurally related to Ste20
RT and sps1, but is not involved in the known MAPK pathways."
RL Oncogene 14:2047-2057(1997).
CC -1- FUNCTION: OXIDANT STRESS-ACTIVATED SERINE/THREONINE KINASE THAT
CC MAY PLAY A ROLE IN THE RESPONSE TO ENVIRONMENTAL STRESS.
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -1- ENZYME REGULATION: ACTIVATED BY PHOSPHORYLATION, PROBABLY
CC AUTOPHOSPHORYLATION. THE C-TERMINAL NON-CATALYTIC REGION INHIBITS
CC THE KINASE ACTIVITY.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- TISSUE SPECIFICITY: UBQUITOUSLY EXPRESSED. HIGHEST LEVELS ARE
CC FOUND IN TESTIS, LARGE INTESTINE, BRAIN AND STOMACH FOLLOWED BY
CC HEART AND LUNG.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC STE20 SUBFAMILY.
-----
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CC or send an email to license@isb-sib.ch).
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CC EMBL: X99325; CAA67700.1; -.
CC EMBL: D63780; BAA20420.1; -.
CC HSSP: P12931; IPRK.
CC DR Genew; HGNC:11404; STK25.
CC MIM: 602255; -.
CC InterPro: IPR000719; Euk_pkinase.
CC InterPro: IPR002290; Ser_thr_pkinase.
CC Pfam: PF00069; pkinase; 1.
CC ProDom: PD000001; Euk_pkinase; 1.
CC SMART: SM00220; S_TKc; 1.
CC PROSITE: PS00108; PROTEIN_KINASE_ST; FALSE_NEG.
CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
CC Trasnferase: Serine/threonine-protein kinase; ATP-binding;
CC phosphorylation.
CC KW DOMAIN 20 270 PROTEIN KINASE.
CC NP_BIND 26 34 ATP (BY SIMILARITY).
CC BINDING 49 49 ATP (BY SIMILARITY).
CC ACT_SITE 140 140 BY SIMILARITY.
CC FT ACT_SITE 140 140
CC CONFLICT 347 348 EP -> DA (IN REF. 1).
CC SEQUENCE 426 AA; 48111 MW; 183CE5700FCEA716 CRC64;

Query Match 34.3%; Score 576; DB 1; Length 426;
Best Local Similarity 45.4%; Pred. No. 3.5e-36;
Matches 128; Conservative 48; Mismatches 92; Indels 14; Gaps 7;

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RT Cloning and characterization of a member of the MST subfamily of  
 RT Ste20-like kinases." ;  
 RL Gene 167:303-306(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96413604; PubMed=8816758;  
 RA Taylor L.K., Wang H.C., Erikson R.L.;  
 RT "Newly identified stress-responsive protein kinases, Krs-1 and Krs-  
 2." ;  
 RL Proc. Natl. Acad. Sci. U.S.A. 93:10099-10104(1996).  
 RN [3]  
 RP SEQUENCE OF 96-203 FROM N.A.  
 RX MEDLINE=94100173; PubMed=8274451;  
 RA Schultz S.J., Nigg E.A.;  
 RT "Identification of 21 novel human protein kinases, including 3 members  
 of a family related to the cell cycle regulator nimA of *Aspergillus*  
*nidulans*." ;  
 RL Cell Growth Differ. 4:821-830(1993).  
 CC -1- FUNCTION: OXIDANT STRESS-ACTIVATED SERINE/THREONINE KINASE THAT  
 MAY PLAY A ROLE IN THE RESPONSE TO ENVIRONMENTAL STRESS (BY  
 SIMILARITY).  
 CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
 CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN ADULT KIDNEY,  
 SKELETAL AND PLACENTA TISSUES AND AT VERY LOW LEVELS IN ADULT  
 HEART, LUNG AND BRAIN TISSUES.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC STE20 SUBFAMILY.  
 CC -----  
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 CC -----  
 CC EMBL: U26424; AAC50386.1; -  
 DR EMBL: U60206; AAB17261.1; -  
 DR EMBL: P25422; CAB0909.1; -  
 DR HSSP: P24941; 1HCL.  
 DR GeneW: HGNC:11406; STRK3.  
 DR MIM: 605030; -  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR002290; Ser\_thr\_pkinase.  
 DR Pfam: PF000069; kinase, 1.  
 DR ProDom: PD000001; Euk\_pkinase, 1.  
 DR SMART: SM00220; S\_TKC; 1.  
 DR PROSITE: PS00107; PROTEIN KINASE ATP; 1.  
 DR PROSITE: PS00108; PROTEIN KINASE ST; FALSE\_NEG.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR Transfaser: Serine/threonine-protein kinase; ATP-binding.  
 KW DOMAIN 27  
 FT NP\_BIND 33 41  
 FT BINDING 56 56  
 FT ACT\_SITE 146 146  
 FT DOMAIN 308 314  
 FT DOMAIN 370 375  
 FT CONFLICT 96 98  
 FT CONFLICT 121 121  
 FT CONFLICT 203 203  
 FT CONFLICT 303 303  
 FT CONFLICT 332 334  
 FT SEQUENCE 491 AA; 56261 MW; 9CA3B0644F3C14A9 CRC64;  
 SQ  
 Query Match 33.8%; Score 567; DB 1; Length 491;  
 Best local Similarity 40.4%; Pred. No. 2e-35;  
 Matches 120; Conservative 55; Mismatches 108; Indels 14; Gaps 5;  
 QY 24 PEKLFSDLRIGSGFGAYFADVRNNEVAIAIKMSYSGKQSNEMKWDIIKEVRLQKL 83  
 DB 23 PEEVFLVLEKIGSGYGVFAIKHESGQVAIAIKQV-----ESDLOETIKELISIMQC 77

QY 84 RHPNTIQRGCLYREHTAWLVMYC-LGSASDLLVHKRPLOVEIAAATNGALQGLAVL 142  
 DB 78 DSPYVVKYGYFKKNDIMVMEYCGAGSYDILRLRNKTLIEDLATILKSLKGLLEYL 137  
 QY 143 HSHNMTHRDYKAGNILLSEGLVKGDFGSA----SIMAPNSFVGTPTWMADEVILAMD 198  
 DB 138 HFMRKIHRIKAGNILLNTEGHAKLADFGVAGOLTPTMAKRNIVIGTFPMMAPEVI--Q 194  
 QY 199 EGOYDGRVDYWSIGTICIELAEKRPPLFNMMASALYHIAQNSPALQSH-MSEYFRNF 257  
 DB 195 EIGYCNVADYWSIGTISIEAEKRPYADIHPRALFMTPTNPPFRKPELWSDPTDF 254  
 QY 258 VDSCLQKIPDRPTSEVLLKHPFLRERPTVIMDLIORTKDAVREIDNLYRKMK 314  
 DB 255 VKKCIYKNPGRATFQQLQHPFIKNAKRPYIIRDLITEMEIKARHNDQGNLEEE 311  
 RESULT 7  
 ID PAK1\_RAT STANDARD; PRT; 544 AA.  
 AC P35465; O62934.  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Serine/threonine-protein kinase PAK 1 (EC 2.7.1.-) (p21-activated  
 kinase 1) (PAK-1) (p68-PAK) (Alpha-PAK) (Protein kinase MKK2).  
 GN PAK1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OC NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RP TISSUE-Brain;  
 RX MEDLINE=94150588; PubMed=8107774;  
 RA Manser E., Leung T., Sallhuddin H., Zhao Z.-S., Lim L.;  
 RT "A brain serine/threonine protein kinase activated by Cdc42 and  
 Rac1." ;  
 RL Nature 367:40-46(1994).  
 RN [2]  
 RP REVISIONS.  
 RA Zhao Z.-S.;  
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Osada S.-I., Izawa M., Saito R., Mizuno K., Suzuki A., Hirai S.-I.,  
 RA Ohno S.;  
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP TISSUE SPECIFICITY.  
 RX MEDLINE=96027610; PubMed=7559638;  
 RA Manser E., Chong C., Zhao Z.-S., Leung T., Michael G., Hall C.,  
 RA Lim L.;  
 RT "Molecular cloning of a new member of the p21-Cdc42/Rac-activated  
 kinase (PAK) family." ;  
 RL J. Biol. Chem. 270:25070-25078(1995).  
 CC -1- FUNCTION: THE ACTIVATED KINASE ACTS ON A VARIETY OF TARGETS.  
 LIKELY TO BE THE GTPASE EFFECTOR THAT LINKS THE RHO-RELATED  
 GTPASES TO THE JNK MAP KINASE PATHWAY.  
 CC -1- SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND  
 CDC42/P21 AND RAC1 (BY SIMILARITY).  
 CC -1- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN THE BRAIN, WITH  
 HIGHER EXPRESSION IN NEURONAL GROUPS ASSOCIATED WITH MOTOR  
 FUNCTION, AND AT LOWER LEVELS IN THE SPLEEN.  
 CC -1- DEVELOPMENTAL STAGE: FOUND IN THE EMBRYONIC CNS WITH LITTLE  
 EXPRESSION ELSEWHERE.  
 CC -1- PTM: AUTOPHOSPHORYLATED WHEN ACTIVATED BY CDC42/P21.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC -1- SIMILARITY: CONTAINS 1 CRIB DOMAIN.  
 CC STE20 SUBFAMILY.  
 CC -----  
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DR EMBL: U23443; AAB95646.1; -  
 DR EMBL: U49953; AAB61533.1; -  
 DR PIR: S40482; S40482.  
 DR HSSP: P24941; ICKP.  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR000095; Pakbox/Rhobndng.  
 DR InterPro: IPR002290; Ser\_thr\_pkinase.  
 DR Pfam: PF00069; pkinase; 1.  
 DR Pfam: PF00786; PBD; 1.  
 DR ProDom: PD000001; Euk\_pkinase; 1.  
 DR SMART: SM00285; PBD; 1.  
 DR SMART: SM00220; S\_TKC; 1.  
 DR PROSITE: PS00108; CRIB; 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR Transferrase; Serine/threonine-protein kinase; ATP-binding;  
 KW phosphorylation.  
 FT DOMAIN 75 88 CRIB.  
 FT DOMAIN 134 268 LINKER.  
 FT NP\_BIND 269 520 PROTEIN\_KINASE.  
 FT NP\_BIND 275 283 ATP (BY SIMILARITY).  
 FT BINDING 298 298 ATP (BY SIMILARITY).  
 FT ACT\_SITE 388 388 BY SIMILARITY.  
 SQ SEQUENCE 544 AA: 60577 MW: 938E3D8222F5B7B CRC64;

Query Match 30.4%; Score 510; DB 1; Length 544;  
 Best Local Similarity 40.9%; Pred. No. 4.2e-31;  
 Matches 117; Conservative 52; Mismatches 103; Indels 14; Gaps 6;

QY 23 DPEKLFSDLRREIGHGSGFAVYFARVNSEVAIAIKMSYSGQSNKKMODIKEYFLQK 82  
 DB 264 DPKKTYTREKRGQSGAGVYAMVATGQEAIAIKQMN--QOQPKKLLINELVARE 320  
 QY 83 LHPNTIOYRGCYLREHRTAMLVMEYCL-GSASDLEVHKRPLOEVEIAVTHGALOGLAY 141  
 DB 321 KKNPNIVNLDYSIVGDELWVMEYIAGGSLTDV--VTETCDEGIIAIVCEGLOALEF 378  
 QY 142 LHSNNHIDVKAAGNILLSEPLVLKIDFGSASIVAPANS---FVGYPMAPVEYIILAM 197  
 DB 379 LHSNOVIHNDISDNLILGMDGSVKLTDFGCAQITPEQSKRSTWGTGYMAPAEVY--- 435  
 QY 198 DEGOYDGKVDVSLGTCTELAEKRPPLFNMMASALYIIAQNESPALQSGH-WSEYFRN 256  
 DB 436 TRKAYGPKVDISLGLMATEMTEGEPYINENPLRLALYLITANGPELONPEKLSAIFRD 495  
 QY 237 FVDSCLQKIPQDPTSEVLLKHFVLRERPPYIMDLQIFRDAVR 302  
 DB 496 FLNRCLMDVEKRGSAKELLQHFLLKIKAPLSSILPPLIAAANEAKR 541

RESULT 8  
 PAK1\_HUMAN STANDARD; PRT; 545 AA.  
 ID 013153; 013567;  
 AC 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Serine/threonine-protein kinase PAK 1 (EC 2.7.1.1-) (p21-activated  
 DE kinase 1) (PAK-1) (p65-PAK) (Alpha-PAK).  
 GN PAK1.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCB1\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RX MEDLINE-97199447; PubMed-9395435;  
 RA Sells M.A., Knaus U.G., Bagrodia S., Ambrose D.M., Bokoch G.M.,  
 RA Chernoff J.;  
 RT "Human p21-activated kinase (Pak1) regulates actin organization in  
 RT mammalian cells";  
 RL Curr. Biol. 7:202-210(1997).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=placenta;  
 RX MEDLINE-96398842; PubMed=8805275;  
 RA Brown J.L., Stowers L., Baer M., Trejo J., Coughlin S., Chant J.;  
 RT "Human Ste20 homologue hPAK1 links GTPases to the JNK MAP kinase  
 RT pathway";  
 RL Curr. Biol. 6:598-605(1996).  
 CC -I- FUNCTION: THE ACTIVATED KINASE ACTS ON A VARIETY OF TARGETS.  
 CC LIKELY TO BE THE GTPASE EFFECTOR THAT LINKS THE RHO-RELATED  
 CC GTPASES TO THE JNK MAP KINASE PATHWAY.  
 CC -I- SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND  
 CC CDC42/P21 AND RAC1.  
 CC -I- PTM: AUTOPHOSPHORYLATED WHEN ACTIVATED BY CDC42/P21.  
 CC -I- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC -I- SIMILARITY: CONTAINS 1 CRIB DOMAIN.

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DR EMBL: U24152; AAA5441.1; -  
 DR EMBL: U51120; AAC50590.1; -  
 DR HSSP: P24941; ICKP.  
 DR GeneW: HGNC:8590; PAK1.  
 DR MIM: 602390; -  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR000095; Pakbox/Rhobndng.  
 DR InterPro: IPR002290; Ser\_thr\_pkinase.  
 DR Pfam: PF00069; pkinase; 1.  
 DR Pfam: PF00786; PBD; 1.  
 DR ProDom: PD000001; Euk\_pkinase; 1.  
 DR SMART: SM00285; PBD; 1.  
 DR SMART: SM00220; S\_TKC; 1.  
 DR PROSITE: PS00108; CRIB; 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
 DR Transferrase; Serine/threonine-protein kinase; ATP-binding;  
 KW phosphorylation.  
 FT DOMAIN 75 88 CRIB.  
 FT DOMAIN 134 269 LINKER.  
 FT NP\_BIND 276 521 PROTEIN\_KINASE.  
 FT NP\_BIND 299 298 ATP (BY SIMILARITY).  
 FT ACT\_SITE 389 389 ATP (BY SIMILARITY).  
 FT MUTAGEN 107 107 L->F: CONSTITUTIVELY ACTIVE.  
 FT CONFLICT 26 26 R -> A (IN REF. 2).  
 FT CONFLICT 237 237 F -> S (IN REF. 2).  
 FT CONFLICT 379 379 D -> E (IN REF. 2).  
 FT CONFLICT 503 503  
 SQ SEQUENCE 545 AA: 60661 MW: 14A1E70E6480CD7E CRC64;

Query Match 30.3%; Score 508; DB 1; Length 545;  
 Best Local Similarity 40.9%; Pred. No. 5.9e-31;  
 Matches 117; Conservative 51; Mismatches 104; Indels 14; Gaps 6;

QY 23 DPEKLFSDLRREIGHGSGFAVYFARVNSEVAIAIKMSYSGQSNKKMODIKEYFLQK 82  
 DB 265 DPKKTYTREKRGQSGAGVYAMVATGQEAIAIKQMN--QOQPKKLLINELVARE 320  
 QY 83 LHPNTIOYRGCYLREHRTAMLVMEYCL-GSASDLEVHKRPLOEVEIAVTHGALOGLAY 141

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Db      322 NKNPNINVLDSYLVGDELMWVMEYLAGGSLTDV--VTEFCMDGQIAAVCRECLQALEF 379
      142 LHSNMHTRDYKAGNILLSEPGIVKLDGFGSASIMAPANS---FVGTPTYMADEVILAM 197
      380 LHSNQVTHRDIKSDNILLGMDGSYKLDGFCQAITEPQSKRSTWGTPTPYMADEVY--- 436
Qy      198 DEGOYDKVDVWSLGTICIELAEKRPPLFNMMASALYHIAQNSPALQSGH-WSEYFRN 256
      437 TRRAYGKRVIVWSLGTIAEMIEEGEPYLNENPLRALYLTATNGTPELQNEKLSAIFRD 496
Qy      257 FVDSCLQIKIPQDRPTSEVLKHFVLRERPPVTIMDLIORTKDAVR 302
      497 FLNCLMDVYKRSKAKELLQHOFLKIAKPLSLTPLMAKKEATK 542

RESULT 9
PAK1_MOUSE
ID      PAK1_MOUSE      STANDARD;      PRT;      545 AA.
AC      088643;
DT      15-DEC-1998 (Rel. 37, Created)
DT      15-DEC-1998 (Rel. 37, Last sequence update)
DT      15-JUN-2002 (Rel. 41, Last annotation update)
DE      Serine/threonine-protein kinase PAK 1 (EC 2.7.1.-) (p21-activated
DE      kinase 1) (PAK-1) (P65-PAK) (Alpha-PAK) (CDC42/RAC effector kinase
DE      PAK-1).
GN      PAK1 OR PAKA.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_Taxid=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      MEDLINE=99282526; PubMed=10352232;
RA      Burdello P.D., Kozak C.A., Finegold A.A., Hall A., Pirone D.M.;
RT      "Cloning, central nervous system expression and chromosomal mapping of
RT      the mouse PAK-1 and PAK-3 genes.";
RL      Gene 232:209-215(1999).
CC      -1- FUNCTION: THE ACTIVATED KINASE ACTS ON A VARIETY OF TARGETS.
CC      LIKELY TO BE THE GTPASE EFFECTOR THAT LINKS THE RHO-RELATED
CC      GTPASES TO THE JNK MAP KINASE PATHWAY (BY SIMILARITY).
CC      -1- SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND
CC      CDC42/P21 AND RAC1 (BY SIMILARITY).
CC      -1- PTM: AUTOPHOSPHORYLATED WHEN ACTIVATED BY CDC42/P21 (BY
CC      SIMILARITY).
CC      -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC      STE20 SUBFAMILY.
CC      -1- SIMILARITY: CONTAINS 1 CRIB DOMAIN.
CC      -----
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CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
CC      EMBL: AF082077; AAC32375.1; -.
CC      HSSP: P24941; ICKP.
CC      MGD: MG1:133975; PAK1.
CC      InterPro: IPR000719; Euk_pkinase.
CC      InterPro: IPR000095; PAKbox/Rhopndng.
CC      InterPro: IPR002290; Ser_thr_pkinase.
CC      Pfam: PF00069; pkinase; 1.
CC      Pfam: PF00786; Pbd; 1.
CC      ProDom: PD000001; Euk_pkinase; 1.
CC      SMART: SM00285; PBD; 1.
CC      SMART: SM00220; S_TKc; 1.
CC      PROSITE: PS50107; CRIB; 1.
CC      PROSITE: PS50108; PROTEIN_KINASE_ATP; 1.
CC      PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
CC      PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW      transferase; Serine/threonine-protein kinase; ATP-binding;

```

```

KW      phosphorylation.
FT      DOMAIN      75      88      CRIB.
FT      DOMAIN      134      267      LINKER.
FT      DOMAIN      270      521      PROTEIN KINASE.
FT      NP_BIND      276      284      ATP (BY SIMILARITY).
FT      BINDING      296      299      ATP (BY SIMILARITY).
FT      ACT_SITE      389      389      BY SIMILARITY.
SQ      SEQUENCE      545 AA; 60737 MW; A4861289534C3819 CRC64;

Query Match      30.38; Score 508; DB 1; Length 545;
Best Local Similarity 40.6%; Pred. No. 5,9e-31;
Matches 116; Conservative 52; Mismatches 104; Indels 14; Gaps 6;

Qy      23 DPEKFSDLREIGHGSGFAYFARDVARNSEVVAATKMSYSKQENKEMQDIIKEVRLQK 82
      265 DPKKRYTPFERKIGGAGGYTTADVAATGQVATKQMLN---QOQPKRELINILVLR 321
Qy      83 LRHNTIQRCYGLREHTAMLVMECL-GSASDLEVHKRPLQVEIAVTHGALQIAY 141
      322 NKNPNINVLDSYLVGDELMWVMEYLAGGSLTDV--VTEFCMDGQIAAVCRECLQALEF 379
Qy      142 LHSNMHTRDYKAGNILLSEPGIVKLDGFGSASIMAPANS---FVGTPTYMADEVILAM 197
      380 LHSNQVTHRDIKSDNILLGMDGSYKLDGFCQAITEPQSKRSTWGTPTPYMADEVY--- 436
Qy      198 DEGOYDKVDVWSLGTICIELAEKRPPLFNMMASALYHIAQNSPALQSGH-WSEYFRN 256
      437 TRRAYGKRVIVWSLGTIAEMIEEGEPYLNENPLRALYLTATNGTPELQNEKLSAIFRD 496
Qy      257 FVDSCLQIKIPQDRPTSEVLKHFVLRERPPVTIMDLIORTKDAVR 302
      497 FLOCCLEMDVYKRSKAKELLQHOFLKIAKPLSLTPLMAKKEATK 542

RESULT 10
PAK3_MOUSE
ID      PAK3_MOUSE      STANDARD;      PRT;      544 AA.
AC      062829;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      15-JUN-2002 (Rel. 41, Last annotation update)
DE      Serine/threonine-protein kinase PAK 3 (EC 2.7.1.-) (p21-activated
DE      kinase 3) (PAK-3) (Beta-PAK) (P65-PAK).
GN      PAK3.
OS      Rattus norvegicus (Rat).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX      NCBI_Taxid=10116;
RN      [1]
RP      SEQUENCE FROM N.A. AND PARTIAL SEQUENCE OF 37-56.
RA      TISSUE=Brain;
RA      MEDLINE=96027610; PubMed=7559638;
RA      Manser E., Chong C., Zhao Z.-S., Leung T., Michael G., Hall C.,
RA      Lim L.;
RT      "Molecular cloning of a new member of the p21-Cdc42/Rac-activated
RT      kinase (PAK) family.";
RL      J. Biol. Chem. 270:25070-25078(1995).
CC      -1- FUNCTION: THE ACTIVATED KINASE ACTS ON A VARIETY OF TARGETS.
CC      -1- SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND
CC      CDC42/P21 AND RAC1. SHOWS HIGHLY SPECIFIC BINDING TO THE SH3
CC      DOMAINS OF PHOSPHOLIPASE C-GAMMA AND OF ADAPTER PROTEIN NCK (BY
CC      SIMILARITY).
CC      -1- TISSUE SPECIFICITY: DETECTED AT HIGH LEVELS IN THE BRAIN AND AT
CC      LOW LEVELS IN THE TESTIS.
CC      -1- DEVELOPMENTAL STAGE: FOUND IN THE EMBRYONIC CNS WITH LITTLE
CC      EXPRESSION ELSEWHERE.
CC      -1- PTM: AUTOPHOSPHORYLATED WHEN ACTIVATED BY CDC42/P21.
CC      -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC      STE20 SUBFAMILY.
CC      -1- SIMILARITY: CONTAINS 1 CRIB DOMAIN.
CC      -----
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL: U33314; AAC52268.1; -  
CC HSSP: P24941; ICKP.  
DR InterPro: IPR000719; Euk\_pkinase.  
DR InterPro: IPR000095; PAKbox/Rhodoping.  
DR InterPro: IPR002290; Ser\_thr\_pkinase.  
DR Pfam: PF00069; pkinase; 1.  
DR Pfam: PF00786; PBD; 1.  
DR ProDom: PD000001; Euk\_pkinase; 1.  
DR SMART: SM00285; PBD; 1.  
DR SMART: SM00220; S\_TKC; 1.  
DR PROSITE: PS50108; CRIB; 1.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE: PS00101; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
KW Transferase; Serine/threonine-protein kinase; ATP-binding;  
KW Phosphorylation.  
FT DOMAIN 70 83 CRIB.  
FT DOMAIN 129 267 LINKER.  
FT DOMAIN 268 519 PROTEIN\_KINASE.  
FT NP\_BIND 274 282 ATP (BY SIMILARITY).  
FT BINDING 297 297 ATP (BY SIMILARITY).  
FT ACT\_SITE 387 387 BY SIMILARITY.  
SQ SEQUENCE 544 AA; 60710 MW; 7B940FC204A2B48B CRC64;

Query Match 30.1%; Score 505; DB 1; Length 544;  
Best Local Similarity 40.6%; Pred. No. 9.9e-31;  
Matches 116; Conservative 52; Mismatches 104; Indels 14; Gaps 6;

QY 23 DPEKLFSDLEIGHGSEFAGVYFARDVNSSEVAIKKMSYSGKSNKMODIKEVFLQK 82  
DB 263 DPKKKTTRFKKIGGASGVYTTALDITATGGEVALIKQNL---QQQPKKELINELLVRE 319  
QY 83 LRHPNTIYRGCTLRHTAMLVMEYCL-GSASDLEVHKRPLOEVEIAVTHGALOGLAY 141  
DB 320 NKPNTIVNYLDSYLVDELVMVMEYLAGSLTDV--VTECMDEGOIAAVCRCLQALDF 377  
QY 142 LHSNMIHNDVKAGNILLSPGLVKLDGSGASIMAPANS----FVGTPWMAPEVILAM 197  
DB 378 LHSNMIHNDVKAGNILLSPGLVKLDGSGASIMAPANS----FVGTPWMAPEVILAM 434  
QY 198 DEQYDGKVDVMSLITCTELAEKRPPLFNMMASALYHIAQNESPALOS-GHMSEYFRN 256  
DB 435 TRKAYGPKVDVMSLITCTELAEKRPPLFNMMASALYHIAQNESPALOS-GHMSEYFRN 494  
QY 257 FVDSCLQKIPQDRPTSEVLKRRFVLRERPPVYIMDLQRTKDAVR 302  
DB 495 FLNRCLEMDVDRGSAKELLQHPFLKLAFLPLSLTPLLIAAKAIVK 540

RESULT 11  
PAK3\_HUMAN STANDARD; PRT; 544 AA.  
AC 075914;  
DT 15-DEC-1998 (Rel. 37, Created)  
DT 15-DEC-1998 (Rel. 37, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Serine/threonine-protein kinase PAK 3 (EC 2.7.1.-) (p21-activated  
DE kinase 3) (PAK-3) (Beta-PAK) (Oligophrenin-3).  
GN PAK3 OR OPN3.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98400251; PubMed=9731525;  
RA Allen K.M., Gleeson J.G., Bagrodia S., Partington M.W.,

RA Macmillan J.C., Cerione R.A., Mullley J.C., Walsh C.A.;  
RT "PAK3 mutation in nonsyndromic X-linked mental retardation.";  
RL Nat. Genet. 20:25-30(1998).  
CC -1- FUNCTION: THE ACTIVATED KINASE ACTS ON A VARIETY OF TARGETS.  
CC -1- SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND  
CC CDCA2/P21 AND RAC1. SHOWS HIGHLY SPECIFIC BINDING TO THE SH3  
CC DOMAINS OF PHOSPHOLIPASE C-GAMMA AND OF ADAPTER PROTEIN NCK.  
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN POSTMITOTIC NEURONS OF THE  
CC DEVELOPING AND POSTNATAL CEREBRAL CORTEX AND HIPPOCAMPUS.  
CC -1- PTM: AUTOPHOSPHORYLATED WHEN ACTIVATED BY CDCA2/P21.  
CC -1- DISEASE: DEFECTS IN PAK3 ARE A CAUSE OF AN X-LINKED FORM OF  
CC NONSYNDROMIC MENTAL RETARDATION (MRX30).  
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
CC STE20 SUBFAMILY.  
CC -1- SIMILARITY: CONTAINS 1 CRIB DOMAIN.

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL: AF068864; AAC36097.1; -  
CC HSSP: P24941; ICKP.  
DR Genew: HGNC:8592; PAK3.  
DR MIM: 300142; -  
DR InterPro: IPR000719; Euk\_pkinase.  
DR InterPro: IPR000095; PAKbox/Rhodoping.  
DR InterPro: IPR002290; Ser\_thr\_pkinase.  
DR Pfam: PF00069; pkinase; 1.  
DR Pfam: PF00786; PBD; 1.  
DR ProDom: PD000001; Euk\_pkinase; 1.  
DR SMART: SM00285; PBD; 1.  
DR SMART: SM00220; S\_TKC; 1.  
DR PROSITE: PS50108; CRIB; 1.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE: PS00101; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
KW Transferase; Serine/threonine-protein kinase; ATP-binding;  
KW SH3-binding; Phosphorylation.  
FT DOMAIN 70 83 CRIB.  
FT DOMAIN 129 267 LINKER.  
FT DOMAIN 268 519 PROTEIN\_KINASE.  
FT NP\_BIND 274 282 ATP (BY SIMILARITY).  
FT BINDING 297 297 ATP (BY SIMILARITY).  
FT ACT\_SITE 387 387 BY SIMILARITY.  
SQ SEQUENCE 544 AA; 60692 MW; 230AF6952CB049E2 CRC64;

Query Match 30.0%; Score 504; DB 1; Length 544;  
Best Local Similarity 40.6%; Pred. No. 1.2e-30;  
Matches 116; Conservative 52; Mismatches 104; Indels 14; Gaps 6;

QY 23 DPEKLFSDLEIGHGSEFAGVYFARDVNSSEVAIKKMSYSGKSNKMODIKEVFLQK 82  
DB 263 DPKKKTTRFKKIGGASGVYTTALDITATGGEVALIKQNL---QQQPKKELINELLVRE 319  
QY 83 LRHPNTIYRGCTLRHTAMLVMEYCL-GSASDLEVHKRPLOEVEIAVTHGALOGLAY 141  
DB 320 NKPNTIVNYLDSYLVDELVMVMEYLAGSLTDV--VTECMDEGOIAAVCRCLQALDF 377  
QY 142 LHSNMIHNDVKAGNILLSPGLVKLDGSGASIMAPANS----FVGTPWMAPEVILAM 197  
DB 378 LHSNMIHNDVKAGNILLSPGLVKLDGSGASIMAPANS----FVGTPWMAPEVILAM 434  
QY 198 DEQYDGKVDVMSLITCTELAEKRPPLFNMMASALYHIAQNESPALOS-GHMSEYFRN 256  
DB 435 TRKAYGPKVDVMSLITCTELAEKRPPLFNMMASALYHIAQNESPALOS-GHMSEYFRN 494  
QY 257 FVDSCLQKIPQDRPTSEVLKRRFVLRERPPVYIMDLQRTKDAVR 302  
DB 495 FLNRCLEMDVDRGSAKELLQHPFLKLAFLPLSLTPLLIAAKAIVK 540



DR	EMBL, D849728; BAA24073.1. -	
DR	HSSP, P24941; ICRP.	
DR	MGD; MG1:1099439; Stk10.	
DR	InterPro: IPR000719; Euk_Pkinase.	
DR	InterPro: IPR002290; Ser_Thr_pkinase.	
DR	Pfam, PF00069; Pkinase_1.	
DR	ProDom, PD000001; Euk_pkinase; 1.	
DR	SMART, SM00220; S_TKc1.1.	
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.	
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.	
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.	
KW	Transferase; Serine/threonine-protein kinase; ATP-binding; Phosphorylation; coiled coil.	
FT	DOMAIN	36 .. 294
FT	DOMAIN	588 .. 936
FT	DOMAIN	749 .. 883
FT	GN BIND	42 .. 50
FT	BINDING	65 .. 65
FT	ACT_SITE	157 .. 157
FT	SEQUENCE	966 AA; 11992 MW; 7115EAC01032BF94 CRC64;



ST10_HUMAN	STANDARD:	PR:	968 AA.
ID	ST10_HUMAN		
AC	094804; Q9UW4;		
DT	16-OCT-2001 (Rel. 40, Created)		
DT	16-OCT-2001 (Rel. 40, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Serine/threonine-protein kinase 10 (EC 2.7.1.37) (Lymphocyte-oriented kinase).		
GN	STK10 OR LOK.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.		
OX	NCBI_TaxId=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=99215434; PubMed=10199912;		
RA	Kuramochi S., Matsuda Y., Okamoto M., Kitamura F., Yonekawa H.,		
RA	Karasuyama H.;		
RT	"Molecular cloning of the human gene STK10 encoding lymphocyte-		
RT	oriented kinase, and comparative chromosomal mapping of the human,		
RL	mouse, and rat homologues.";		
RN	Immunogenetics 49:369-375(1999).		
RP	[2]		
RC	SEQUENCE OF 814-968 FROM N.A.		
RC	TISSUE=Testis;		
RA	Bloecher H., Boeher M., Brandt P., Mewes H.-W., Gassenhuber J.,		
RA	Wieman S.;		
RL	Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.		
CC	- FUNCTION: CAN ACT ON SUBSTRATES SUCH AS MYELIN BASIC PROTEIN AND		
CC	HISTONE IIA ON SERINE AND THREONINE RESIDUES (BY SIMILARITY).		
CC	- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphorylated		
CC	- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN LYMPHOID ORGANS.		
CC	- PM: AUTOPHOSPHORYLATED (BY SIMILARITY).		
CC	- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.		
CC	STK20 SUBFAMILY.		
CC	-----		
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CC	modified and this statement is not removed. Usage by and for commercial		
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CC	or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).		
CC	-----		
DR	EMBL; AB015718; BAA35073.1; -		
DR	EMBL; AL133081; CAB61400.1; -		
DR	HSSP; P24941; 1HCL.		
DR	GeneW; HGNC:11388; STK10.		
DR	MIM; 603919; -		
DR	InterPro; IPR0000719; Euk_Pkinase.		
DR	InterPro; IPR002290; Ser_Thr_Pkinase.		
DR	InterPro; IPR001245; Tyr_Pkinase.		
DR	Pfam; PF00069; Pkinase; 1.		
DR	PRINTS; PR00109; TYRKINASE.		
DR	ProDom; PD000001; Euk_Pkinase; 1.		
DR	SMART; SM00220; S_TKc; 1.		
DR	PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.		
DR	PROSITE; PS00108; PROTEIN_KINASE_ST; 1.		
DR	PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.		
RW	Transferase; Serine/threonine-protein kinase; ATP-binding;		
KW	Phosphorylation; Coiled coil.		
FT	DOMAIN 36 294		
FT	DOMAIN 573 947		
FT	DOMAIN 750 884		
FT	NP_BIND 42 50		
FT	BINDING 65 65		
FT	ACT_SITE 157 157		
FT	BY SIMILARITY.		
SO	SEQUENCE 968 AA; 112134 MW; 15E245193ECC553D CRC64;		
Query Match	29.5%;	Score 495.5;	DB 1; Length 968;
Best Local Similarity	37.2%;	Pred. No. 1e-29;	
Matches 108; Conservative	57;	Mismatches 112;	Indels 13; Gaps 6;

[illegible]

Search completed: November 22, 2002, 12:24:14  
Job time : 6.96 secs

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OM protein - protein search, using sw model

Run on: November 22, 2002, 12:21:10 : Search time 8.96 Seconds  
(without alignments)  
3433.372 Million cell updates/sec

Title: US-09-686-346a-4\_COPY\_1\_320

Perfect score: 1678

Sequence: 1 MPAGRGAGSLKDPVAVLELF.....VRELDNLQYRKMKKILFQEA 320

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1529	91.1	1001	2 T17365	serine/threonine p
2	1008	60.1	982	2 T18576	serine-threonine k
3	631.5	37.6	836	2 B96716	probable serine/th
4	576	34.3	426	2 S71886	ste20-like protein
5	565	33.7	653	2 T34356	hypothetical prote
6	541.5	32.3	829	2 T29372	hypothetical prote
7	530	31.6	819	2 A53714	protein kinase (EC
8	528	31.5	1062	2 T46444	hypothetical prote
9	524.5	31.3	1233	2 T30989	serine/threonine p
10	523.5	31.2	1102	2 JC6316	probable protein k
11	523	31.2	690	2 C96572	protein F12M16.4 l
12	510.5	30.4	1231	2 T18532	serine/threonine p
13	510	30.4	544	2 S40482	serine/threonine s
14	508	30.3	545	2 G01773	p21-activated prot
15	507.5	30.2	1206	2 T34021	protein kinase SK2
16	505.5	30.1	1233	2 T14157	serine/threonine p
17	505	30.1	544	2 A57597	beta-p21-activated
18	500	29.8	544	2 I49376	p21 activated kina
19	495.5	29.5	490	2 S47946	protein kinase hom
20	490.5	29.2	525	2 S58682	protein kinase, p2
21	487.5	29.1	312	2 T38525	serine/threonine p
22	470.5	28.0	471	2 T39232	probable serine th
23	463	27.6	378	2 T26684	hypothetical prote
24	463	27.6	622	2 T15467	hypothetical prote
25	461	27.5	1080	2 S48944	hypothetical prote
26	450.5	26.8	1230	2 T18256	probable serine/th
27	450.5	26.8	1230	2 T18259	serine/threonine p
28	449	26.8	658	2 T39500	serine/threonine-s
29	445.5	26.5	652	2 T39722	serine/threonine p

30	441	26.3	1062	2 S46367	protein kinase CDC
31	440	26.2	939	2 S28394	probable serine/th
32	439.5	26.2	561	2 T51417	protein kinase-lik
33	436	26.0	589	2 T38086	serine/threonine-p
34	432.5	25.8	1075	2 T27623	hypothetical prote
35	432.5	25.8	1080	2 T27622	hypothetical prote
36	431	25.4	658	2 S60170	protein kinase Pak
37	425.5	25.4	608	2 G96575	probable MEK kinas
38	419.5	25.0	553	2 T01479	hypothetical prote
39	418.5	24.9	883	2 A96662	hypothetical prote
40	418	24.9	655	2 S51884	probable protein k
41	415	24.7	710	2 T13458	hypothetical prote
42	415	24.7	842	2 S60402	protein kinase CIA
43	413	24.6	693	2 B85112	hypothetical prote
44	411	24.5	1228	2 T18897	hypothetical prote
45	408	24.3	651	2 A96591	NPK1-related prote

## ALIGNMENTS

```
RESULT 1
T17365
serine/threonine protein kinase TA01 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T17365
R:Hutchinson, M.; Berman, K.S.; Cobb, M.H.
J. Biol. Chem. 273, 28625-28632, 1998
A:Title: Isolation of TA01, a protein kinase that activates MEKs in stress-activated
A:Reference number: Z18730; MUID:99003202; PMID:9786855
A:Accession: T17365
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1001 <HUT>
A:Cross-references: EMBL:AF084205; NID:g3452472; PID:g3452473; PIDN:AMC71014.1
C:Function:
A:Description: probably implicated in the regulation of the p38-containing stress-res
```

Query Match 91.1%; Score 1529; DB 2; Length 1001;  
Best local Similarity 88.8%; Pred. No. 2.7e-68;  
Matches 284; Conservative 22; Mismatches 14; Indels 0; Gaps 0;

QY	1	MPAGRGAGSLKDPVAVLELFKDDPEKLFSDLRREHGHSFGAVYFARVRYRSEVVAIKMS	60
DB	1	MPSTNRAGSLKDPVIAELFFKDEPEKLFDTLREHGHSFGAVYFARVRYRSEVVAIKMS	60
QY	61	YSGKOSNEKMODIIKEVRFLOKLRHPTIYRGQYLRHRTAMLVMEYCLGSASDLFEVHK	120
DB	61	YSGKOSTEKMODIIKEVRFLOKLRHPTIYRGQYLRHRTAMLVMEYCLGSASDLFEVHK	120
QY	121	KPLQEVIAAVTHGALOGGLAVLHSHNMIRHDVKNITLSEPGVLKGDGSGASIMAPAN	180
DB	121	KPLQEVIAAITHGALOGGLAVLHSHMTIHRDIAKAGNITLREPQGVKADGSGASIMAPAN	180
QY	181	SFGTPTPWMAPEVYLANDEQYDGKVDVWSLGITCITELARRKPLPFMMNMSALYHTAQN	240
DB	181	SFGTPTPWMAPEVYLANDEQYDGKVDVWSLGITCITELARRKPLPFMMNMSALYHTAQN	240
QY	241	ESPLQSGHWESEYFRNVDSCLOKIPDRPTSEVLTKHREVLRRPPTVIMDLIQRTKDA	300
DB	241	ESPTLQSGHWESEYFRNVDSCLOKIPDRPTSEVLTKHREVLRRPPTVIMDLIQRTKDA	300
QY	301	VRELDNLQYRKMKKILFQEA 320	
DB	301	VRELDNLQYRKMKKILFQEA 320	

RESULT 2  
T18576  
serine-threonine kinase - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999





A:Molecule type: mRNA  
 A:Residues: 1-1062 <AA>  
 A:Cross-references: EMBL:AL137701  
 A:Experimental source: adult testis; clone DKFZp434N1427  
 C:Genetics:  
 A:Note: DKFZp434N1427.1

Query Match 31.5%; Score 528; DB 2; Length 1062;  
 Best Local Similarity 98.1%; Pred. No. 4.1e-19;  
 Matches 101; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 218 LARRKRPFLFMNMSALYHAQNESPALOSGHSEYFRNFVDSCLQIKPDRPTSEVLK 277  
 DB 45 VARRKRPFLFMNMSALYHAQNESPVLOSGHSEYFRNFVDSCLQIKPDRPTSEVLK 104  
 QY 278 HREVLREPPVYIMDLQRTKDAVRELDNQLQYRKMKILFQEA 320  
 DB 105 HREVLREPPVYIMDLQRTKDAVRELDNQLQYRKMKILFQEA 147

RESULT 9  
 T30989

serine/threonine protein kinase NIK - mouse  
 N:Alternate names: Nck interacting kinase  
 C:Species: Mus musculus (house mouse)  
 C:Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 22-Oct-1999

C:Accession: T30989  
 R:Su, Y.C.; Han, J.; Xu, S.; Cobb, M.; Skolnik, E.Y.  
 EMBL J. 16, 1279-1290, 1997

A:Title: NIK is a new Ste20-related kinase that binds NCK and MEK1 and activates the SH  
 A:Reference number: Z20954; MUID:97280817; PMID:9135144

A:Accession: T30989

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-1233 <SV>

A:Cross-references: EMBL:U88984; NID:q1872545; PID:q1872546; PIDN:AA053165.1

C:Keywords: protein kinase

Query Match 31.3%; Score 524.5; DB 2; Length 1233;  
 Best Local Similarity 40.4%; Pred. No. 7e-19;  
 Matches 131; Conservative 59; Mismatches 103; Indels 31; Gaps 13;

QY 7 ASLRKPPVLAELFFKDDPEKLSDSLREIGHSGFAGVAFADVRNSEVAIKKMSYSGKOS 66  
 DB 7 ASLSVDIDISL---RDPAGIFELVEVNGTYGVYKGRHVK-TVTAIKVMVY----1 58  
 QY 67 NEKMODIIKEVRFLQKL-RHPMTIOYRGCYLR-----EHTAMLVMEYC-LGSASDLLEY 118  
 DB 59 EDEEETITIEIMLKKYSHHRNATYYGAFIKKSPGHDDQMLVMEYCGAGSITDLVKN 118  
 QY 119 HK-KPLQVEYIAAVTHGALQGLAYLHSHNMHRDVKAGNILLSEPLVRLGDFG-SAST- 175  
 DB 119 TKGNTLKEWMYAYSREILRGALHCHIHVYHRDINGQVALLTENAEVRLVDFGVSQD 178  
 QY 176 --MAPANSVGVPPYMAPEVILAMDE---GQYDGKVDVSLGTCIELAEKRPFLFMNMA 230  
 DB 179 RTVGRNRTFICGPPYMAPEVI-ACDENPDATYDYSRDLMSCGTALTEMAEGCPPLCDMP 237  
 QY 231 MSALYHAQNESPALOSGHSEYFRNFVDSCLQIKPDRPTSEVLKHKFVLRERP----- 286  
 DB 238 MALFLITPNPPRLKSKKWSKFFSFIGCLVKNMORPSTQDLKHPTI-RDQPNERO 296  
 QY 287 -PTVIMDLQRTKDAVRELDNQLQY 309  
 DB 297 VRIQLKDHIDRTIRKKRKGKDETEY 320

RESULT 10

JC6316

proteob protein kinase (EC 2.7.1.-) - fruit fly (Drosophila melanogaster)

C:Species: Drosophila melanogaster

C:Date: 21-May-1999 #sequence\_revision 21-May-1999 #text\_change 21-May-1999

C:Accession: JC6316

R:Treisman, J.E.; Ito, N.; Rubin, G.M.

Gene 186, 119-125, 1997

A:Title: mishapen encodes a protein kinase involved in cell shape control in drosoph

A:Reference number: JC6316; MUID:97199378; PMID:9047354

A:Accession: JC6316

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-1102 <TR>

A:Experimental source: third instar eye-antennal disk cosmid library

A:Note: the cited accession number, 1076485, is not in Genbank release 111.0

C:Genetics:

A:Gene: msn

C:Keywords: phosphotransferase

Query Match 31.2%; Score 523.5; DB 2; Length 1102;  
 Best Local Similarity 39.5%; Pred. No. 7.1e-19;  
 Matches 122; Conservative 60; Mismatches 100; Indels 27; Gaps 11;

QY 23 DPEKFLSDREIGHSGFAGVAFADVRNSEVAIKKMSYSGKOSNEKMODIIKEVRFLQK 82  
 DB 27 DPAGIFELVEVNGTYGVYKGRHKTQGLAIAKVMY----TEDEEELKLEIVLKK 82  
 QY 83 L-RHPMTIOYRGCYL-----EHTAMLVMEYC-LGSASDLLEYVK-KPLQVEYIAAVTH 133  
 DB 83 YSNHRNATYYGAFIKKSPGKDDQMLVMEYCGAGSVTLVKSTGOSLKEEMIAVYICR 142  
 QY 134 GALQGLAYLHSHNMHRDVKAGNILLSEPLVRLGDFG-SAST---MAPANSVGVPPYMA 189  
 DB 143 ELIRGLSYLHSHNMHRDVKAGNILLSEPLVRLGDFG-SAST---MAPANSVGVPPYMA 202  
 QY 190 APEVILAMDE---GQYDGKVDVSLGTCIELAEKRPFLFMNMSALYHAQNESPALO 246  
 DB 203 APEVI-ACDENPDATYDYSRDLMSLGTALTEMAESQPLCDLHPMRLFLIRNSPRLK 261  
 QY 247 SGHWSYFRNFVDSCLQIKPDRPTSEVLKHKFVLRERP-----TVIMDLQRTKDAV 301  
 DB 262 SKRMSKRFHGFIDVYLVKDYHORPTENLLKHGFI-KDQPTDQYRIQLKDHIDRCKRK 320  
 QY 302 RELDNQLQY 310  
 DB 321 QEKREDDYR 329

RESULT 11

C96572

protein F12M16.4 (imported) - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001

C:Accession: C96572

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon

Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dwyer,

ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Matli, R.; Marzia

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A6141; MUID:21016719; PMID:11130712

A:Accession: C96572

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-690 <STO>

A:Cross-references: GB:AE005173; NID:q7769851; PIDN:AAF69529.1; GSPDB:GN00141

A:Gene: F12M16.4

A:Map position: 1

Query Match 31.2%; Score 523; DB 2; Length 690;  
 Best Local Similarity 42.5%; Pred. No. 5e-19;  
 Matches 124; Conservative 48; Mismatches 98; Indels 22; Gaps 10;







GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: November 22, 2002, 12:21:31 ; Search time 7.04 Seconds  
(without alignments)  
1337.406 Million cell updates/sec

Title: US-09-686-346A-4\_COPY\_1\_320

Perfect score: 1678  
Sequence: 1 MPAGGRAGSLKDPDVAFELFF.....VRELNDLQYRKMKILFQEA 320

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

Issued\_Patents\_AA:\*  
1: /cgn2\_6/prodata/1/iaa/5A\_COMB.pep:\*  
2: /cgn2\_6/prodata/1/iaa/5B\_COMB.pep:\*  
3: /cgn2\_6/prodata/1/iaa/6A\_COMB.pep:\*  
4: /cgn2\_6/prodata/1/iaa/6B\_COMB.pep:\*  
5: /cgn2\_6/prodata/1/iaa/PTOS\_COMB.pep:\*  
6: /cgn2\_6/prodata/1/iaa/backfills1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1678	100.0	993	4	US-09-060-410-4 Sequence 4, App11
2	1529	91.1	1001	4	US-09-060-410-2 Sequence 2, App11
3	873.5	52.1	278	4	US-09-060-410-17 Sequence 17, App11
4	594	35.4	431	2	US-09-211-930-5 Sequence 5, App11
5	594	35.4	431	3	US-09-340-993-5 Sequence 5, App11
6	594	35.4	431	4	US-09-152-406-3 Sequence 3, App11
7	594	35.4	431	4	US-09-468-442-5 Sequence 5, App11
8	576	34.3	426	2	US-08-852-743-2 Sequence 2, App11
9	576	34.3	426	2	US-09-211-930-4 Sequence 4, App11
10	576	34.3	426	3	US-09-340-993-4 Sequence 4, App11
11	576	34.3	426	3	US-09-185-370-2 Sequence 2, App11
12	576	34.3	426	4	US-09-152-406-4 Sequence 4, App11
13	576	34.3	426	4	US-09-468-442-4 Sequence 4, App11
14	569	33.9	487	2	US-08-712-709-8 Sequence 8, App11
15	569	33.9	487	3	US-09-111-444-8 Sequence 8, App11
16	569	33.9	487	4	US-09-541-228-8 Sequence 8, App11
17	567	33.8	416	2	US-09-211-930-3 Sequence 3, App11
18	567	33.8	416	2	US-09-211-930-11 Sequence 11, App11
19	567	33.8	416	3	US-09-340-993-3 Sequence 3, App11
20	567	33.8	416	3	US-09-340-993-11 Sequence 11, App11
21	567	33.8	416	4	US-09-468-442-3 Sequence 3, App11
22	567	33.8	416	4	US-09-468-442-11 Sequence 11, App11
23	565	33.7	1360	4	US-09-393-569-2 Sequence 2, App11
24	555	33.1	270	2	US-08-852-743-5 Sequence 5, App11
25	555	33.1	270	3	US-09-185-370-5 Sequence 5, App11
26	550	32.8	403	2	US-08-712-709-3 Sequence 3, App11
27	550	32.8	403	3	US-09-111-444-3 Sequence 3, App11

28	550	32.8	403	4	US-09-541-228-3 Sequence 3, App11
29	516	30.8	276	2	US-08-852-743-7 Sequence 7, App11
30	516	30.8	276	3	US-09-185-370-7 Sequence 7, App11
31	505	30.1	545	2	US-08-935-760-4 Sequence 4, App11
32	503	30.0	465	2	US-08-114-555A-2 Sequence 2, App11
33	503	30.0	544	2	US-08-935-760-2 Sequence 2, App11
34	499	29.7	465	3	US-08-559-397A-2 Sequence 2, App11
35	497	29.6	544	3	US-08-559-397A-19 Sequence 19, App11
36	491	29.3	506	1	US-08-369-780-2 Sequence 2, App11
37	491	29.3	506	1	US-08-475-682-2 Sequence 2, App11
38	491	29.3	506	1	US-08-780-833-2 Sequence 2, App11
39	491	29.3	506	1	US-08-636-036-2 Sequence 2, App11
40	491	29.3	506	1	US-08-918-509-2 Sequence 2, App11
41	491	29.3	506	3	US-09-108-262-2 Sequence 2, App11
42	491	29.3	524	2	US-08-615-942A-2 Sequence 2, App11
43	489	29.1	268	2	US-08-852-743-3 Sequence 3, App11
44	489	29.1	268	3	US-09-185-370-3 Sequence 3, App11
45	487.5	29.1	272	2	US-08-852-743-6 Sequence 6, App11

#### ALIGNMENTS

```
RESULT 1
US-09-060-410-4
; Sequence 4, Application US/09060410
; Patent No. 6165461
;
GENERAL INFORMATION:
; APPLICANT: Cobb, Melanie
; APPLICANT: Hutchinson, Michele
; APPLICANT: Chen, Zhu
; APPLICANT: Berman, Kevin
; TITLE OF INVENTION: TAO PROTEIN KINASES AND METHODS OF USE
; TITLE OF INVENTION: THEREFOR
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED AND BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
;
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/060,410
; FILING DATE: 14-APR-1998
;
CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Maki, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 860098,421
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 993 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
;
US-09-060-410-4
;
Query Match 100.0%; Score 1678; DB 4; Length 993;
Best Local Similarity 100.0%; Pred. No. 4, 7e-157;
Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
OY 1 MPAGGRAGSLKDPDVAFELFFKDPDEKLFSDREIGHSGFGAYVFARDVRSEVVAIKKMS 60
Db 1 MPAGGRAGSLKDPDVAFELFFKDPDEKLFSDREIGHSGFGAYVFARDVRSEVVAIKKMS 60
```

QY	61	YSGKSNKKMODIIKEVYFLOKLRHPNTIOYRGCYLREHNTAMLYMEYCLGASADLLEVHK	120
Db	61	YSGKSNKKMODIIKEVYFLOKLRHPNTIOYRGCYLREHNTAMLYMEYCLGASADLLEVHK	120
QY	121	KPLQVEIAAVTGALOGSLAYLHSHNNIHRDKAGNILLSEPGVLKLGDFGSASIMAPAN	180
Db	121	KPLQVEIAAVTGALOGSLAYLHSHNNIHRDKAGNILLSEPGVLKLGDFGSASIMAPAN	180
QY	181	SFVCGPYMAAEVILLADEGGOYDCKVYVWSLGTICELAEKRPPLPYMNASALYHNAON	240
Db	181	SFVGTPIYMAAEVILLADEGGOYDCKVYVWSLGTICELAEKRPPLPYMNASALYHNAON	240
QY	241	ESPALQSGHWSYFRNMFVDSCLQKIPDRPTSEVLLKHREVLREBRPTVIMDLIQRTKDA	300
Db	241	ESPALQSGHWSYFRNMFVDSCLQKIPDRPTSEVLLKHREVLREBRPTVIMDLIQRTKDA	300
QY	301	VRELDNIQYRKMKKILLFOEA 320	
Db	301	VRELDNIQYRKMKKILLFOEA 320	

```

1      RESULT 2
2      US-09-060-410-2
3      ; Sequence 2, Application US/09060410
4      ; Patent No. 6165461
5      ; GENERAL INFORMATION:
6      ; APPLICANT: Cobb, Melanie
7      ; APPLICANT: Hutchinson, Michele
8      ; APPLICANT: Chen, Zhu
9      ; APPLICANT: Berman, Kevin
10     ; TITLE OF INVENTION: TWO PROTEIN KINASES AND METHODS OF USE
11     ; TITLE OF INVENTION: THEREFOR
12     ; NUMBER OF SEQUENCES: 26
13     ; CORRESPONDENCE ADDRESS:
14     ; ADDRESSEE: SEED AND BERRY LLP
15     ; STREET: 6300 Columbia Avenue, 701 Fifth Avenue
16     ; CITY: Seattle
17     ; STATE: Washington
18     ; COUNTRY: USA
19     ; ZIP: 98104
20     ; COMPUTER READABLE FORM:
21     ; MEDIUM TYPE: Floppy disk
22     ; COMPUTER: IBM PC compatible
23     ; OPERATING SYSTEM: PC-DOS/MS-DOS
24     ; SOFTWARE: PatentIn Release #1.0, Version #1.30
25     ; CURRENT APPLICATION DATA:
26     ; APPLICATION NUMBER: US/09/060,410
27     ; FILING DATE: 14-APR-1998
28     ; CLASSIFICATION:
29     ; ATTORNEY/AGENT INFORMATION:
30     ; NAME: Makl, David J.
31     ; REGISTRATION NUMBER: 31,392
32     ; REFERENCE/DOCKET NUMBER: 860098.421
33     ; TELECOMMUNICATION INFORMATION:
34     ; TELEPHONE: (206) 622-4900
35     ; TELEFAX: (206) 682-6031
36     ; INFORMATION FOR SEQ ID NO: 2:
37     ; SEQUENCE CHARACTERISTICS:
38     ; LENGTH: 1001 amino acids
39     ; TYPE: amino acid
40     ; TOPOLOGY: linear
41     ; MOLECULE TYPE: protein
42     ; US-09-060-410-2

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Query Match	91.1%;	Score 1529;	DB 4;	Length 1001;
Best Local Similarity	88.8%;	Pred. No. 2.5e-142;		
Matches 284;	Conservative 22;	Mismatches 14;	Indels 0;	Gaps 0;

[illegible]

QY	61	YSGKSNKMODIIKEVYFLORIKHPNTIOYRGCYLREHNTAMLYMEYCLASADLLEVHK	120
Db	61	YSGKSNKMODIIKEVYFLORIKHPNTIOYRGCYLREHNTAMLYMEYCLASADLLEVHK	120
QY	121	KPLDVEIAAVTGALOGGLAYLHSHNNIHRDVKAGNTLLSEPGVLKIDFGSASIMAPAN	180
Db	121	KPLDVEIAAVTGALOGGLAYLHSHNNIHRDVKAGNTLLSEPGVLKIDFGSASIMAPAN	180
QY	181	SFVGTPYMAAEVILLADDEGOYDKYVWMSLGITCIELAEKRPFLFMNMSALYHNAON	240
Db	181	SFVGTPYMAAEVILLADDEGOYDKYVWMSLGITCIELAEKRPFLFMNMSALYHNAON	240
QY	241	ESPALQSGHWSYFRNRFVDSCLQKIPODRPTSEVLLKHRFVLRERPPYVIMDLIQRTKDA	300
Db	241	ESPALQSGHWSYFRNRFVDSCLQKIPODRPTSEVLLKHRFVLRERPPYVIMDLIQRTKDA	300
QY	301	VRELDNLOYRKMKKILFOEA 320	
Db	301	VRELDNLOYRKMKKILFOEA 320	

```

1      RESULT 3
2      US-09-060-410-17
3      Sequence 17, Application US/09060410
4      Patent No. 6165461
5      GENERAL INFORMATION:
6      APPLICANT: Cobb, Melanie
7      APPLICANT: Hutchinson, Michele
8      APPLICANT: Chen, Zhu
9      APPLICANT: Berman, Kevin
10     TITLE OF INVENTION: TWO PROTEIN KINASES AND METHODS OF USE
11     TITLE OF INVENTION: THEREFOR
12     NUMBER OF SEQUENCES: 26
13     CORRESPONDENCE ADDRESS:
14     ADDRESSEE: SEED AND BERRY LLP
15     STREET: 6300 Columbia Avenue, 701 Fifth Avenue
16     CITY: Seattle
17     STATE: Washington
18     COUNTRY: USA
19     ZIP: 98104
20     COMPUTER READABLE FORM:
21     MEDIUM TYPE: Floppy disk
22     COMPUTER: IBM PC compatible
23     OPERATING SYSTEM: PC-DOS/MS-DOS
24     SOFTWARE: PatentIn Release #1.0, Version #1.30
25     CURRENT APPLICATION DATA:
26     APPLICATION NUMBER: US/09/060,410
27     FILING DATE: 14-Apr-1998
28     CLASSIFICATION:
29     ATTORNEY/AGENT INFORMATION:
30     NAME: MakI, David J.
31     REGISTRATION NUMBER: 31,392
32     REFERENCE/DOCKET NUMBER: 860098.421
33     TELECOMMUNICATION INFORMATION:
34     TELEPHONE: (206) 622-4900
35     TELEFAX: (206) 682-6031
36     INFORMATION FOR SEQ ID NO: 17:
37     SEQUENCE CHARACTERISTICS:
38     LENGTH: 278 amino acids
39     TYPE: amino acid
40     STRANDEDNESS:
41     TOPOLOGY: linear
42     US-09-060-410-17

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Query Match	52.1%;	Score 873.5;	DB 4.;	Length 278;
Best Local Similarity	59.1%;	Pred. No. 2.2e-78;		
Matches 162;	Conservative 47;	Mismatches 56;	Indels 9;	Gaps 2;

```

0Y      6 RAGSLKPDVAELFEFKDDPEKLSDLREIGHSGGANYFAPDVRNSWVAIKKMSYSGQ 65
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
      8 KPGYIKPSTIALESNNKDPED---DLREIGHSGGANYFAYDKKNEGYVAIKKMFPSGQ 64

0Y      66 SNEKMODIKEVRELQKLRHNNTIQYRGCVLREHTTAMLVMEYCLGASDLDLEVHKRPDQ 125

```

[illegible]

```

RESULT 4
US-09-211-930-5
Sequence 5, Application US/09211930
Patent No. 5962265
GENERAL INFORMATION:
APPLICANT: Tyrell E. No. 5962265ris
APPLICANT: William Craig Moore
APPLICANT: David Shay Silberstein
TITLE OF INVENTION: HUMAN SIGNAL TRANSDUCTION
FILE REFERENCE: PHM.70296
CURRENT APPLICATION NUMBER: US/09/211,930
EARLIER FILING DATE: 1998-12-15
EARLIER APPLICATION NUMBER: GB 9726851.0
NUMBER OF SEQ ID NOS: 14
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 5
LENGTH: 431
TYPE: PRF
ORGANISM: Homo sapiens
US-09-211-930-5

```

```

Query Match 35.4%: Score 594; DB 2: Length 431;
Best Local Similarity 45.8%: Pred. NO. 1.7e-50;
Matches 130; Conservative 48; Mismatches 92; Indels 14; Gaps
7;

QY 21 KDDEKPLSFDSREIGHGSGFGAAYFAPADVNRNSEVNAIKKMSYSGKOSNEKMODIKKEVRL 80
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 17 KADPEELFTKLEKIGKSGFGEYFKRIDNRKQKVAIKIIDL--EEADEDEDIOQDEIYVL 74
QY 81 QKLRHPNTIOYRGCTLRKHTAMLYMEYC-LGSASDLLEVHKKPDLQVEETAAVTHGALQGL 139
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 75 SQCSPPYTKKYYGSLKJCDTKLMIIMEYLGSGSALDILLE--PGDLDETOIATLRREIKGL 132
QY 140 AYLSHHNHIIHDVKNAGNILLSPGUYKTLGDPGSSASIMAPA---NSFPGTPVWMAPEVYL 195
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 133 DYLSHEKKIHDRIKAAVNLSEHGKVLADRGVAGQLDTQIKRNTFVGTPWMAPEVYL 191
QY 196 AMDEQYDGNKYVWVSLGTCIELAEKRPPLFMNMAASALYHIAQNEPSALOSGHSEYER 255
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 192 --KQSAVDSKADIMSLGITAIELANGEPHSLHMKVYFLIPKNNPYLE-GNISKPLK 248
QY 256 NFVDSCLKIQRDPTSEVLKHKRFVLRERPRPT-VIMDLIQRTK 298
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : : |
Db 249 EFVEACLNKKEPSFRYAKELKHKKILNNAKTSYLETIDIRYK 292

RESULT 5
US-09-340-993-5
; Sequence 5, Application US/09340993
; Patent No. 6034228
; GENERAL INFORMATION:
; APPLICANT: Tyrell E. No. 6034228R1S
; APPLICANT: William Craig Moore
; APPLICANT: David Shay Silberstein
; TITLE OF INVENTION: HUMAN SIGNAL TRANSDUCTION SERINE/THREONINE KINASE

```

```

? FILE REFERENCE: PHM.70296.N1
? CURRENT APPLICATION NUMBER: US/09/340.993
? CURRENT FILING DATE: 1999-06-25
? EARLIER APPLICATION NUMBER: GB 9726851.0 & US 09/211,930
? EARLIER FILING DATE: 1997-12-19 & 1998-12-15
? NUMBER OF SEQ ID NOS: 14
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 5
? LENGTH: 431
? TYPE: PR1
? ORGANISM: Homo sapiens
? US-09-340-993-5

```

[illegible]

```

RESULT 6
US-09-152-406-3
; Sequence 3, Application US/09152406
; Patent No. 6265560
; GENERAL INFORMATION:
; APPLICANT: William Craig Moore
; APPLICANT: Tyrrell E. No. 6265560ris
; APPLICANT: David Shay Silberstein
; TITLE OF INVENTION: HUMAN STE20-LIKE STRESS ACTIVATED
; TITLE OF INVENTION: SERINE/THREONINE KINASE
; FILE REFERENCE: PHM.70272
; CURRENT APPLICATION NUMBER: US/09/152.406
; CURRENT FILING DATE: 1998-09-14
; EARLIER APPLICATION NUMBER: 9719920.2
; EARLIER FILING DATE: 1997-09-19
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 431
; TYPE: PRF
; ORGANISM: Homo Sapiens
US-09-152-406-3

Query Match          35.4%; Score 594; DB 4; Length 431;
Best Local Similarity 45.8%; Pred. No. 1.7e-50.
Matches 130; Conservative 48; Mismatches 92; Indels 14; Gaps 7;

QY      21 KDDPEKFLSDIREIGHSGFGAVFYFARDYRNSEVVAIKRMYSKGKSNKKMODIIKEVREL 80
      | | | | | : | | | | | : | | | | | : : : : : | | : |
Db       17 KADPEELFTLEKIGKSGFEVGEFKIDNRQKVAAIKTIID--EEADEIEDIQGEITVL 74

OY      81 QKLRHPNTIQRCGLRHTMALVMEYC-LGSASDLLEVHKKPLDQEVIAATGACALGGL 139
      | : | | | | : | | | | | | | | | | | | | | : | | |
Db       75 SQQCSPPVTKYGVSLKPKTKLMIIMEYVGGGSADLLD--PGPDDTQIATLREILKGL 132

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QY 140 ATLSHNMTHRDVKAAGNIIISLSEGLVKLDFGASATMAPA---NSFVGTPTWMAPEVIL 195
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 133 DYLHSEKKTTHRIKANKANVILSEHGEVKLADFGVAGQLTDTQIKRNTFVGTPTWMAPEVIL- 191
QY 196 AMDEGOYDGKVDVWSLIGITCIELAEKRPPLFNMMNSALYHIAQNSPALQSGHSEYFR 255
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 192 --KQSAVDKADIMSLGITAELARGEPPHSELPKRVFLIPKNNPPTLE-GNYSKPLK 248
QY 256 NFVDSCLQKIPDRPTSEVLKHKRFVLRERPT-VIMDLIORTK 298
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 249 EFVEACLKNEPSPRPTAKELLKHKFLLRNAAKTSYLTLEIDRYK 292

```

# RESULT 7

```

US-09-468-442-5
; Sequence 5, Application US/09468442
; Patent No. 6300098
; GENERAL INFORMATION:
; APPLICANT: Tyrell E. No. 6300098frs
; APPLICANT: William Craig Moore
; APPLICANT: David Shay Silberstein
; TITLE OF INVENTION: HUMAN SIGNAL TRANSDUCTION SERINE/THREONINE KINASE
; FILE REFERENCE: PHM.70296.N1
; CURRENT APPLICATION NUMBER: US/09/468,442
; CURRENT FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: US 09/340,993
; EARLIER FILING DATE: 1999-06-25
; EARLIER APPLICATION NUMBER: GB 9726851.0
; EARLIER FILING DATE: 1997-12-19
; EARLIER APPLICATION NUMBER: US 09/211,930
; EARLIER FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-468-442-5

```

```

Query Match          35.4%; Score 594; DB 4; Length 431;
Best Local Similarity 45.8%; Pred. No. 1.7e-50;
Matches 130; Conservative 48; Mismatches 92; Indels 14; Gaps 7;

```

```

QY 21 KDDPEKLSDLREIGHSGFGAAYFARDVRNSEVVAIKMSYSGKQSNKEMODIIKEVREL 80
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 17 KADPEELFTKLEIKGSGFEVFKGIDNRTQYVAIKIIDL--EEADEIEDIQEITVL 74
QY 81 QKLRHPTIQYRGCIYLRHTAMLVMEYC-LGSASDILEVHKRPLOEVEIAVTHGALQGLAY 139
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 75 SCQDSPYVYKRYGSLKDKIMTMEYLGGSALDLE--PGPLDETQIATILREILKGL 132
QY 140 ATLSHNMTHRDVKAAGNIIISLSEGLVKLDFGASATMAPA---NSFVGTPTWMAPEVIL 195
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 133 DYLHSEKKTTHRIKANKANVILSEHGEVKLADFGVAGQLTDTQIKRNTFVGTPTWMAPEVIL- 191
QY 196 AMDEGOYDGKVDVWSLIGITCIELAEKRPPLFNMMNSALYHIAQNSPALQSGHSEYFR 255
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 192 --KQSAVDKADIMSLGITAELARGEPPHSELPKRVFLIPKNNPPTLE-GNYSKPLK 248
QY 256 NFVDSCLQKIPDRPTSEVLKHKRFVLRERPT-VIMDLIORTK 298
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 249 EFVEACLKNEPSPRPTAKELLKHKFLLRNAAKTSYLTLEIDRYK 292

```

## RESULT 8

```

US-08-852-743-2
; Sequence 2, Application US/08852743
; Patent No. 5830699
; GENERAL INFORMATION:
; APPLICANT: Force, Thomas
; APPLICANT: Kyriakis, John M.
; APPLICANT: Pombo, Celia M.
; APPLICANT: Bonventre, Joseph

```

```

; TITLE OF INVENTION: SOK-1 AND METHODS OF USE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson, P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: US
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/852,743
; FILING DATE: 7-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/016,774
; FILING DATE: 7-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Fraser, Janis K.
; REGISTRATION NUMBER: 34,819
; REFERENCE/DOCKET NUMBER: 00786/327001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 426 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: Internal
US-08-852-743-2

```

```

Query Match          34.3%; Score 576; DB 2; Length 426;
Best Local Similarity 45.4%; Pred. No. 9.9e-49;
Matches 128; Conservative 48; Mismatches 92; Indels 14; Gaps 7;

```

```

QY 23 DEKLFESDLREIGHSGFGAAYFARDVRNSEVVAIKMSYSGKQSNKEMODIIKEVREL 82
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 15 DEEELFTKLRIGKSGFEVYKGINHTKEVVAIKIIDL--BEADEIEDIQEITVL 72
QY 83 LKHPNTIQYRGCIYLRHTAMLVMEYC-LGSASDILEVHKRPLOEVEIAVTHGALQGLAY 141
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 73 CDSPYTRFYGSLKSTKIMTMEYLGGSALDLE--PGPLETYIATILREILKGLDY 130
QY 142 LSHNMTHRDVKAAGNIIISLSEGLVKLDFGASATMAPA---NSFVGTPTWMAPEVIL 197
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 131 LHSEKKTTHRIKANKANVILSEHGEVKLADFGVAGQLTDTQIKRNTFVGTPTWMAPEVIL- 187
QY 198 DEGOYDGKVDVWSLIGITCIELAEKRPPLFNMMNSALYHIAQNSPALQSGHSEYFRNF 257
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 188 KQSAVDKADIMSLGITAELARGEPPHSDLPKRVFLIPKNNPPTLEGGH-SKPFKEF 246
QY 258 VDSCLQKIPDRPTSEVLKHKRFVLR-ERPTVIMDLIORTK 298
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 247 VEACLKNEPSPRPTAKELLKHKFLLRNAAKTSYLTLEIDRYK 288

```

## RESULT 9

```

US-09-211-930-4
; Sequence 4, Application US/09211930
; Patent No. 5962265
; GENERAL INFORMATION:
; APPLICANT: Tyrell E. No. 5962265frs
; APPLICANT: William Craig Moore
; APPLICANT: David Shay Silberstein
; TITLE OF INVENTION: HUMAN SIGNAL TRANSDUCTION
; FILE OF INVENTION: SERINE/THREONINE KINASE

```



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Db 131 LHSERKIHNDIKAAVNLSEQDVKLADGVAGQLTDQIKRNTFVGTFFMAPEVI--- 187
Qy 198 DEGOYDGKVDVMSLGTICTELAEKRPPLFNMMASALYHIAQNESPALOSGHMSEYFRNF 257
Db 188 KOSAYDFKADIMSLGTTAIELAKGEPNPSDLHPMRVLFILPKNSPPTLEGQH-SKPFKEF 246
Qy 258 VDSCLQKIPQDRPTSEVLKHKRFVL-ERRPTVIMDLQRTK 298
Db 247 VEACLKNDPRFRPTAKELKHKFTTRYTKTSTFLELIDRYK 288

RESULT 12
US-09-152-406-4
; Sequence 4, Application US/09152406
; Patent No. 6265560
; GENERAL INFORMATION:
; APPLICANT: William Craig Moore
; APPLICANT: Tyrell E. No. 6265560r1s
; APPLICANT: David Shay Silberstein
; TITLE OF INVENTION: HUMAN STE20-LIKE STRESS ACTIVATED
; FILE REFERENCE: PHM.70272
; CURRENT APPLICATION NUMBER: US/09/152,406
; EARLIER FILING DATE: 1998-09-14
; EARLIER APPLICATION NUMBER: 9719920.2
; EARLIER FILING DATE: 1997-09-19
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-152-406-4

Query Match 34.3%; Score 576; DB 4; Length 426;
Best Local Similarity 45.4%; Pred. No. 9.9e-49;
Matches 128; Conservative 48; Mismatches 92; Indels 14; Gaps 7;

Qy 23 DEKLFSDREIGHSGFAGVYFARDVRNSEVVAIKKMSYSGKOSNEKMODIKEVFLQK 82
Db 15 DEELFTKIDRIKSGSFQVYKGINHTKEVVAIKIIDL--EEAEIEDIDIOEITVLSQ 72
Qy 83 LHPNTIOYRGCYLREHTAMLYMEYC-LGSASDLEVHKRPLOEVEIAVTHGALQGLAY 141
Db 73 CSPTYTRFGSLKSTKMTIMEYLGGSALDLK--PGPLETYIATILREILKGLDY 130
Qy 142 LHSNMHHRDVKAGNLLSEPGVLKLGDFGSASIMAPA-----NSFYGTPYMAPEVILAM 197
Db 131 LHSERKIHNDIKAAVNLSEQDVKLADGVAGQLTDQIKRNTFVGTFFMAPEVI--- 187
Qy 198 DEGOYDGKVDVMSLGTICTELAEKRPPLFNMMASALYHIAQNESPALOSGHMSEYFRNF 257
Db 188 KOSAYDFKADIMSLGTTAIELAKGEPNPSDLHPMRVLFILPKNSPPTLEGQH-SKPFKEF 246
Qy 258 VDSCLQKIPQDRPTSEVLKHKRFVL-ERRPTVIMDLQRTK 298
Db 247 VEACLKNDPRFRPTAKELKHKFTTRYTKTSTFLELIDRYK 288

RESULT 13
US-09-468-442-4
; Sequence 4, Application US/09468442
; Patent No. 6300098
; GENERAL INFORMATION:
; APPLICANT: Tyrell E. No. 6300098r1s
; APPLICANT: William Craig Moore
; APPLICANT: David Shay Silberstein
; TITLE OF INVENTION: HUMAN SIGNAL TRANSDUCTION SERINE/THREONINE KINASE
; FILE REFERENCE: PHM.70296.N1
; CURRENT APPLICATION NUMBER: US/09/468,442
; EARLIER FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: US 09/340,993
; EARLIER FILING DATE: 1999-06-25
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; EARLIER APPLICATION NUMBER: GB 9726851.0
; EARLIER FILING DATE: 1997-12-19
; EARLIER APPLICATION NUMBER: US 09/211,930
; EARLIER FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-468-442-4

Query Match 34.3%; Score 576; DB 4; Length 426;
Best Local Similarity 45.4%; Pred. No. 9.9e-49;
Matches 128; Conservative 48; Mismatches 92; Indels 14; Gaps 7;

Qy 23 DEKLFSDREIGHSGFAGVYFARDVRNSEVVAIKKMSYSGKOSNEKMODIKEVFLQK 82
Db 15 DEELFTKIDRIKSGSFQVYKGINHTKEVVAIKIIDL--EEAEIEDIDIOEITVLSQ 72
Qy 83 LHPNTIOYRGCYLREHTAMLYMEYC-LGSASDLEVHKRPLOEVEIAVTHGALQGLAY 141
Db 73 CSPTYTRFGSLKSTKMTIMEYLGGSALDLK--PGPLETYIATILREILKGLDY 130
Qy 142 LHSNMHHRDVKAGNLLSEPGVLKLGDFGSASIMAPA-----NSFYGTPYMAPEVILAM 197
Db 131 LHSERKIHNDIKAAVNLSEQDVKLADGVAGQLTDQIKRNTFVGTFFMAPEVI--- 187
Qy 198 DEGOYDGKVDVMSLGTICTELAEKRPPLFNMMASALYHIAQNESPALOSGHMSEYFRNF 257
Db 188 KOSAYDFKADIMSLGTTAIELAKGEPNPSDLHPMRVLFILPKNSPPTLEGQH-SKPFKEF 246
Qy 258 VDSCLQKIPQDRPTSEVLKHKRFVL-ERRPTVIMDLQRTK 298
Db 247 VEACLKNDPRFRPTAKELKHKFTTRYTKTSTFLELIDRYK 288

RESULT 14
US-08-712-709-8
; Sequence 8, Application US/08712709
; Patent No. 5863780
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Guegler, Karl J.
; APPLICANT: Hawkins, Phillip R.
; TITLE OF INVENTION: NOVEL HUMAN PROTEIN KINASES
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/712,709
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0118 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-4166
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 487 amino acids
; TYPE: amino acid
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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 22, 2002, 12:18:00 ; Search time 19.52 Seconds  
(without alignments)  
2184.436 Million cell updates/sec

Title: US-09-686-346a-4\_COPY\_1\_320

Perfect score: 1678

Sequence: 1 MPAGGRAGSLKDPVAELFF.....VRELDNLOYRKMKILFOEA 320

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

A.Geneseq-101002:\*

1: /SID2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:\*  
2: /SID2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*  
3: /SID2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*  
4: /SID2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:\*  
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18: /SID2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:\*  
19: /SID2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:\*  
20: /SID2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:\*  
21: /SID2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:\*  
22: /SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*  
23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1678	100.0	993	20	AAV49897
2	1674	99.8	1235	21	AAAB4163
3	1665	99.2	1049	22	AAE04366
4	1639	97.7	758	20	AAW97677
5	1529	91.1	1001	20	AAV49896
6	1527	91.0	1001	20	AAV55942
7	1527	91.0	1001	23	ABW97326
8	1467	87.4	748	20	AAV55938
9	1392	83.0	899	21	AAAB43191
10	1389	82.8	898	20	AAW97676

11	1384	82.5	898	21	AAV44244
12	1383	82.4	898	20	AAV55936
13	1239.5	73.9	1039	22	ABB69116
14	1158	69.0	323	22	AAU87114
15	1092	65.1	265	22	AAU87435
16	1092	65.1	265	22	AAU17256
17	1008	60.1	982	20	AAV55955
18	703	41.9	398	22	AAW5890
19	660	39.3	163	22	AAW25383
20	596	35.5	431	22	AAW97069
21	594	35.4	431	20	AAV55950
22	594	35.4	431	20	AAV04473
23	594	35.4	431	21	AAW82276
24	594	35.4	443	23	AAO20953
25	591	35.2	413	20	AAV21672
26	588	35.0	431	21	AAW68771
27	581	34.6	458	22	ABG04990
28	576	34.3	426	18	AAW31603
29	576	34.3	426	20	AAV55949
30	576	34.3	426	21	AAW82275
31	574.5	34.2	596	22	ABB65561
32	574	34.2	487	20	AAV21674
33	567	33.8	392	22	AAW93576
34	567	33.8	416	20	AAV55927
35	567	33.8	416	20	AAV22648
36	567	33.8	416	20	AAV22651
37	567	33.8	416	20	AAV21673
38	567	33.8	416	21	AAW82274
39	567	33.8	416	21	AAW82277
40	567	33.8	416	22	AAW40348
41	567	33.8	416	22	AAW71958
42	567	33.8	416	22	AAW66607
43	565	33.7	443	20	AAV55951
44	565	33.7	1269	22	AAW68823
45	565	33.7	1277	22	AAW68820

#### ALIGNMENTS

RESULT 1  
AAV49897  
AAV49897 standard; Protein; 993 AA.  
XX  
AC AAV49897;  
XX  
DT 27-JAN-2000 (first entry)  
XX  
DE Rat TAO2 kinase.  
XX  
XX TAO1, TAO2; MEK3; mitogen activated protein kinase; phosphorylation;  
KW p38; protein kinase; cancer; inflammation; autoimmune disease;  
KW degeneration; insulin-resistant diabetes; metabolic disorder;  
KW neurodegeneration; MAP kinase; MAP/ERK kinase.  
XX  
OS Rattus sp.  
XX  
PN WO953076-A1.  
XX  
PD 21-OCT-1999.  
XX  
PF 14-APR-1999; 99WO-US08165.  
XX  
PR 14-APR-1998; 98OS-0060410.  
XX  
PA (TEXA ) UNIV TEXAS SYSTEM.  
XX  
PI Cobb M, Hutchison M, Chen Z, Berman K;  
XX  
DR WPI; 1999-633831/54.  
XX  
DR N-PSDB; AA232436.  
XX  
PT New polypeptides that phosphorylate kinase, used to screen for

PT modulators for treating e.g. cancer or inflammation -

XX Claim 7, Page 84-87; 95pp; English.

XX The present sequence represents rat TAO2 protein kinase, which is capable

XX of phosphorylating MEK3 (a MAP/ERK kinase). TAO kinases, and related

XX polypeptides, are used to screen for modulators of stress-responsive

XX mitogen activated protein (MAP) kinase pathways. These modulators are

XX potentially useful for treating or preventing: (1) inflammation,

XX autoimmune disease, cancer and degeneration (inhibitors of

XX phosphorylation); or (2) insulin-resistant diabetes, metabolic disorders

XX and neurodegeneration (enhancers of phosphorylation). TAO kinases are

XX also used to raise specific antibodies, useful therapeutically as

XX modulators and as immunoassay reagents for detecting TAO kinases.

XX TAO kinase polynucleotides can be used: (a) for recombinant expression

XX of TAO kinases; and (b) in the form of fragments, for detecting TAO

XX kinase polynucleotides in standard hybridisation and amplification

XX tests. TAO kinases are highly specific for MEK3.

SQ Sequence 993 AA:

Query Match 100.0%; Score 1678; DB 20; Length 993;

Best Local Similarity 100.0%; Pred. No. 1.3e-162;

Matches 320; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MPAGRAGSLKDPDAELFFKDDPEKLFSDLEIGHSGFAGYFARDVNSSEVAIKKMS 60

DB 1 MPAGRAGSLKDPDAELFFKDDPEKLFSDLEIGHSGFAGYFARDVNSSEVAIKKMS 60

QY 61 YSGKSNKEMWODIIEKVRFLQKLRHNTIOYRGCTLRHTAMLVMEYICGSASDLEEVHK 120

DB 61 YSGKSNKEMWODIIEKVRFLQKLRHNTIOYRGCTLRHTAMLVMEYICGSASDLEEVHK 120

QY 121 KPLOEVEIAAVTHGALOGIAYLHSHNMIRHDKAGNIIISSEGLVKLDFGSASIMAPAN 180

DB 121 KPLOEVEIAAVTHGALOGIAYLHSHNMIRHDKAGNIIISSEGLVKLDFGSASIMAPAN 180

QY 181 SFVGGPYMAPEVILLAMDEGOYDGKVDVWSLGTCTIELAEKRPPLFNMMASALYHIAON 240

DB 181 SFVGGPYMAPEVILLAMDEGOYDGKVDVWSLGTCTIELAEKRPPLFNMMASALYHIAON 240

QY 241 ESPALOSGHWSEYFRNFVDSCLQKIPDRPTSEVLLKHFVLRERPPYIMDLIORTKDA 300

DB 241 ESPALOSGHWSEYFRNFVDSCLQKIPDRPTSEVLLKHFVLRERPPYIMDLIORTKDA 300

QY 301 VRELDMLOYRKMKKILFQEA 320

DB 301 VRELDMLOYRKMKKILFQEA 320

RESULT 2

AAB41663

XX AAB41663 standard; Protein; 1235 AA.

XX AAB41663;

DT 08-FEB-2001 (first entry)

XX Human ORFX ORF1427 polypeptide sequence SEQ ID NO:2854.

XX Human; open reading frame; ORFX; detection; cytosolic; hepatotropic;

XX vulnerability; antiparasitic; antiparkinsonian; neurotrophic; neuroprotective;

XX anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;

XX immunostimulant; thrombolytic; coagulant; vasotropic; antiatheric;

XX hypotensive; dermatological; immunosuppressive; antiinflammatory;

XX antiviral; antibacterial; antifungal; antirheumatic; antithyroid;

XX antianaemic; gene therapy; cancer; proliferative disorder; hypertension;

XX neurodegenerative disorder; osteoarthritis; graft vs host disease;

XX cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;

XX cholesterol ester storage; systemic lupus erythematosus; infection;

XX severe combined immunodeficiency; malaria; autoimmune disorder; asthma;

XX allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;

XX bone damage; cartilage damage; antiinflammatory disease; coagulation;

KW thrombosis; contraceptive.

XX Homo sapiens.

OS WO200058473-A2.

XX 05-OCT-2000.

PD 31-MAR-2000; 2000WO-US08621.

PE 31-MAR-1999; 99US-0127607.

PR 02-APR-1999; 99US-0127636.

PR 05-APR-1999; 99US-0127728.

PR 30-MAR-2000; 2000US-0540763.

XX (CUBA-) CUBAGEN CORP.

PA Shinkets RA, Leach M;

PI WPI; 2000-602362/57.

DR N-PSDB; AAC75872.

XX Novel nucleic acids and peptides derived from open reading frame X,

PT useful for treating e.g. cancers, proliferative disorders,

PT neurodegenerative disorders and cardiovascular disease -

Claim 11; Page 2092-2095; 5507pp; English.

CC AAC7446 to AAC7606 encode the proteins given in AAB40237 to AAB43397,

CC which represent the human ORFX open reading frames 1 to 3161. The ORFX

CC sequences have activities such as: cytosolic; hepatotropic; vulnerability;

CC antiparasitic; antiparkinsonian; neurotrophic; neuroprotective;

CC osteopathic; anticonvulsant; antiarthritic; immunosuppressant;

CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;

CC antidiabetic; hypotensive; dermatological; immunosuppressive;

CC antinflammatory; antibacterial; antiviral; antifungal; antirheumatic;

CC antithyroid; and antianaemic. The sequences can be used for determining

CC the presence of or predisposition to, or preventing or treating

CC pathological conditions associated with an ORFX-associated disorder. The

CC nucleic acids can be used to express ORFX proteins in gene therapy

CC vectors. The proteins and nucleic acids may be used to treat cancers,

CC proliferative disorders, neurodegenerative disorders, osteoarthritis,

CC graft vs host disease, cardiovascular disease, diabetes mellitus,

CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus

CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,

CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,

CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,

CC nocturnal haemoglobinuria, antiinflammatory disease, to enhance

CC coagulation; to inhibit thrombosis; and as a contraceptive.

XX Sequence 1235 AA:

Query Match 99.8%; Score 1674; DB 21; Length 1235;

Best Local Similarity 99.7%; Pred. No. 4.5e-162;

Matches 319; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MPAGRAGSLKDPDAELFFKDDPEKLFSDLEIGHSGFAGYFARDVNSSEVAIKKMS 60

DB 1 MPAGRAGSLKDPDAELFFKDDPEKLFSDLEIGHSGFAGYFARDVNSSEVAIKKMS 60

QY 61 YSGKSNKEMWODIIEKVRFLQKLRHNTIOYRGCTLRHTAMLVMEYICGSASDLEEVHK 120

DB 61 YSGKSNKEMWODIIEKVRFLQKLRHNTIOYRGCTLRHTAMLVMEYICGSASDLEEVHK 120

QY 121 KPLOEVEIAAVTHGALOGIAYLHSHNMIRHDKAGNIIISSEGLVKLDFGSASIMAPAN 180

DB 121 KPLOEVEIAAVTHGALOGIAYLHSHNMIRHDKAGNIIISSEGLVKLDFGSASIMAPAN 180

QY 181 SFVGGPYMAPEVILLAMDEGOYDGKVDVWSLGTCTIELAEKRPPLFNMMASALYHIAON 240

DB 181 SFVGGPYMAPEVILLAMDEGOYDGKVDVWSLGTCTIELAEKRPPLFNMMASALYHIAON 240

QY 241 ESPALOSGHWSEYFRNFVDSCLQKIPDRPTSEVLLKHFVLRERPPYIMDLIORTKDA 300

```

DB      241 ESPVLOSGHMSEYFRNFVDSCLQKIPDRPTSEVLLKHFVLRERPPVTYIMDLIQRTKDA 300
QY      301 VRELDMLOYRKMKKILFQEA 320
DB      301 VRELDMLOYRKMKKILFQEA 320

RESULT 3
AAE04366
ID      AAE04366 standard; Protein; 1049 AA.
XX
AC      AAE04366;
XX
DT      04-SEP-2001 (first entry)
XX
DE      Human kinase (PKIN)-7.
XX
KW      Human kinase; PKIN-7; therapy; immune disorder; Addison's disease; AIDS;
KW      acquired immune deficiency syndrome; growth and developmental disorder;
KW      arteriosclerosis; mixed connective tissue disease; MCTD; adenocarcinoma;
KW      leukemia; cardiovascular disease; myocardial infarction; hypertension;
KW      lipid disorder; cancer; fatty liver; cholestasis; transgenic animal;
KW      gene therapy; antiallergic; antiasthmatic; antithyroid; dermatological;
KW      antidiabetic; nephrotoxic; antitumor; antiarthritic; antirheumatic;
KW      antipsoriatic; neuroprotective; cytostatic; hepatotrophic; osteopathic;
KW      vasotropic; antianginal; anorectic.
XX
OS      Homo sapiens.
XX
FH      Location/Qualifiers
FT      Domain
FT      28..281
FT      /note="Eukaryotic protein kinase domain"
FT      Domain
FT      30..269
FT      /note="Protein kinase domain"
FT      147..158
FT      /note="Protein kinase ST"
FT      618..777
FT      /note="serine/threonine protein kinase TAO1"
XX
PN      WO200146397-A2.
XX
PD      28-JUN-2001.
XX
PF      20-DEC-2000; 2000WO-US35304.
XX
PR      23-DEC-1999; 9905-0172066.
PR      14-JAN-2000; 2000US-0176107.
PR      21-JAN-2000; 2000US-0177731.
PR      28-JAN-2000; 2000US-0178573.
XX
PA      (INCY-) INCYTE GENOMICS INC.
XX
PI      Yang J, Baughn MR, Burford N, Au-Young J, Lu DAM, Reddy R, Yue H;
PI      Yao MG, Lal P, Khan FA.
XX
DR      MPI: 2001-418059/44.
DR      N-PSDB; AAD08640.
XX
PT      Novel human kinase proteins (PKIN) useful for diagnosing, treating,
PT      preventing immune disorders, cardiovascular diseases and disorders
PT      affecting growth and development associated with abnormal expression of
PT      PKIN
XX
PS      Claim 1, Page 111-113; 128pp; English.
XX
XX
XX      The invention relates to novel human kinase proteins (PKIN) and
XX      nucleic acid molecules encoding them. PKIN is useful for identifying
XX      compounds that modulates its activity. PKIN cDNA is useful for
XX      assessing toxicity of a test compound. PKIN and its cDNA are useful
XX      for diagnosis, prevention and treatment of immune disorders such as
XX      acquired immune deficiency syndrome (AIDS), Addison's disease, anaemia,
XX      adult respiratory distress syndrome, allergies, amyloidosis, psoriasis,
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CC      autoimmune haemolytic anaemia, autoimmune thyroiditis, multiple
CC      sclerosis, asthma, osteoarthritis, osteoporosis, rheumatoid arthritis,
CC      ulcerative colitis and diabetes mellitus; growth and developmental
CC      disorders such as actinic keratosis, arteriosclerosis, atherosclerosis,
CC      bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD),
CC      and myelofibrosis; cancers such as adenocarcinoma and leukaemia,
CC      cardiovascular diseases such as myocardial infarction and hypertension;
CC      and lipid disorders such as fatty liver and cholestasis. PKIN cDNA is
CC      useful to detect upstream sequences such as promoters and regulatory
CC      elements, for creating knock in or knock out in humanised animals or
CC      transgenic animals to model human disease and for somatic or germ-line
CC      gene therapy for treating the above mentioned disorders. The present
CC      sequence is human kinase (PKIN)-7.
XX
SQ      Sequence      1049 AA:
XX
Query Match      99.2%; Score 1665; DB 22; Length 1049;
Best Local Similarity 99.1%; Pred. No. 2,9e-161;
Matches 317; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY      1 MPAGRGAGSLKDPVAVLEFFKDPPEKLFSDRLREIGHSGGAVFPADVNSEVVAIKKMS 60
DB      1 MPAGRGAGSLKDPVAVLEFFKDPPEKLFSDRLREIGHSGGAVFPADVNSEVVAIKKMS 60
QY      61 YSGKQSNEMKQDILIKRFRFLQKLRLHNTIOYRGCVLRHRTAWLVMEYCGASADLLEVHK 120
DB      61 YSGKQSNEMKQDILIKRFRFLQKLRLHNTIOYRGCVLRHRTAWLVMEYCGASADLLEVHK 120
QY      121 KPLQVEYIAAVTHGALQGLAVLHSHNMIRHDYKAGNILLSEPLVRLGDFGSASIMAPAN 180
DB      121 KPLQVEYIAAVTHGALQGLAVLHSHNMIRHDYKAGNILLSEPLVRLGDFGSASIMAPAN 180
QY      181 SFVGTPTWMAPEVILAMDEQYDGKVDVWSLGTTCIEFLAEKRPPLNNMAMSALYHIAQN 240
DB      181 SFVGTPTWMAPEVILAMDEQYDGKVDVWSLGTTCIEFLAEKRPPLNNMAMSALYHIAQN 240
QY      241 ESPVLOSGHMSEYFRNFVDSCLQKIPDRPTSEVLLKHFVLRERPPVTYIMDLIQRTKDA 300
DB      241 ESPVLOSGHMSEYFRNFVDSCLQKIPDRPTSEVLLKHFVLRERPPVTYIMDLIQRTKDA 300
QY      301 VRELDMLOYRKMKKILFQEA 320
DB      301 VRELDMLOYRKMKKILFQEA 320

RESULT 4
AAW97677
ID      AAW97677 standard; Protein; 758 AA.
XX
AC      AAW97677;
XX
DT      10-MAY-1999 (first entry)
XX
DE      Human KDS2 protein kinase.
XX
KW      KDS2, kinase domain related to Ste20; human; serine kinase;
KW      threonine kinase; protein kinase; signal transduction.
XX
OS      Homo sapiens.
XX
PN      MO9902699-A1.
XX
PD      21-JAN-1999.
XX
PF      07-JUL-1998; 98WO-US14231.
XX
PR      08-JUL-1997; 97US-0889518.
XX
PA      (CADU-) CADUS PHARM CORP.
XX
PI      Johnson GL, Pleiman CM;
XX
DR      MPI: 1999-120900/10.
```

DR N-PSDB; AAX07075.  
 XX  
 PT New isolated vertebrate kinase - used to develop products for the  
 PT diagnosis and treatment of disorders involving cellular processes  
 PT such as signal transduction processes  
 XX  
 PS Claim 31: Page 85-88; 100pp: English.  
 CC This polypeptide comprises human protein kinase KDS2, a novel  
 CC protein associated with signal transduction. KDS2 has a  
 CC kinase domain related to that of Ste20 (KDS1 = Kinase Domain  
 CC related to Ste20). KDS2 cDNA (see AAX07075) was isolated from a  
 CC human bone marrow cDNA library. A clone (see AAX07074) encoding the  
 CC highly homologous KDS1 (see AAX97676) was also obtained. Both KDS1  
 CC and KDS2 have Glu/Gln-rich regions at their C-terminus (see also  
 CC AAX97678-79) suggesting an alpha-helical structure that may play a  
 CC role in covalently localising these proteins to a specific site  
 CC within the cells, which may be necessary for function. A method  
 CC for producing KDS polypeptides in host cells is provided. Since  
 CC KDS molecules have kinase activity, they are useful as modulating  
 CC agents in regulating a variety of cellular processes such as signal  
 CC transduction pathways. These pathways may regulate cytoskeleton,  
 CC secretion, growth, apoptosis, superoxide generation, and specific  
 CC gene transcription. KDS polypeptides and polynucleotides can be  
 CC used for treating disorders involving aberrant expression of  
 CC mammalian KDS genes. They can also be used for detection,  
 CC diagnosis and drug screening.  
 CC  
 XX  
 SQ Sequence 758 AA:  
 Query Match 97.7%; Score 1639; DB 20; Length 758;  
 Best Local Similarity 97.8%; Pred. No. 8.4e-159;  
 Matches 313; Conservative 2; Mismatches 5; Indels 0; Gaps 0;  
 QY 1 MAGGAGAGSLKPDVAELFFKDDPEKLFSDLRITGSGAGAYFADVKNSEVVAIKKMS 60  
 DB 1 MPAGGAGSLKPDVAELFFKDDPEKLFSDLRITGSGAGAYFADVKNSEVVAIKKMS 60  
 QY 61 YSGKOSNEKMODIIKEVREFLQRLRHPTIOYRGCYLREHTAWLVMEYCLGSASDLEEVK 120  
 DB 61 YSGKOSNEKMODIIKEVREFLQRLRHPTIOYRGCYLREHTAWLVMEYCLGSASDLEEVK 120  
 QY 121 KPLQVEEIAAVTHGALQGLAYLHSHNMHRDYKAGNIIILSEPGLYKLGFGSASIMAPAN 180  
 DB 121 KPLQVEEIAAVTHGALQGLAYLHSHNMHRDYKAGNIIILSEPGLYKLGFGSASIMAPAN 180  
 QY 181 SFVGTPTWMAPEVILLAMDGOYDKVDVWSLGTICIELAEKRPPLFNNMAMSAALHIAON 240  
 DB 181 SFVGTPTWMAPEVILLAMDGOYDKVDVWSLGTICIELAEKRPPLFNNMAMSAALHIAON 240  
 QY 241 ESPALQSGHMSSEYFRNFVDSCLQKIPQDRPTSEVLKHFVLRERPPYIMDLIORTKDA 300  
 DB 241 ESPVLOSNGHMSSEYFRNFVDSCLQKIPQDRPTSEVLKHFVLRERPPYIMDLIORTKDA 300  
 QY 301 VRELDNLQYRKMKKILFOEA 320  
 DB 301 VRELDNLQYRKMKKILFOEA 320  
 RESULT 5  
 AAY49896  
 ID AAY49896 standard; Protein; 1001 AA.  
 XX  
 AC AAY49896;  
 XX  
 DT 27-JAN-2000 (first entry)  
 XX  
 DE Rat TAO1 kinase.  
 XX  
 KM TAO1; TAO2; MEK3; mitogen activated protein kinase; phosphorylation;  
 KM p38; protein kinase; cancer; inflammation; autoimmune disease;  
 KM degeneration; insulin-resistant diabetes; metabolic disorder;  
 KM neurodegeneration; MAP kinase; MAP/ERK kinase.

XX  
 OS Rattus sp.  
 XX  
 PN W09953076-A1.  
 XX  
 PD 21-OCT-1999.  
 XX  
 PF 14-APR-1999; 99WO-US08165.  
 XX  
 PR 14-APR-1998; 98US-0060410.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Cobb M, Hutchison M, Chen Z, Berman K;  
 XX  
 DR WPI: 1999-633831/54.  
 PT N-PSDB; AA32435.  
 PT  
 PT New polypeptides that phosphorylate kinase, used to screen for  
 PT modulators for treating e.g. cancer or inflammation  
 XX  
 PS Claim 1: Fig 1: 95pp: English.  
 XX  
 CC The present sequence represents rat TAO1 protein kinase, which is capable  
 CC of phosphorylating MEK3 (a MAP/ERK kinase). TAO kinases, and related  
 CC polypeptides, are used to screen for modulators of stress-responsive  
 CC mitogen activated protein (MAP) kinase pathways. These modulators are  
 CC potentially useful for treating or preventing: (1) inflammation,  
 CC autoimmune disease, cancer and degeneration (inhibitors of  
 CC phosphorylation); or (2) insulin-resistant diabetes, metabolic disorders  
 CC and neurodegeneration (enhancers of phosphorylation). TAO kinases are  
 CC also used to raise specific antibodies, useful therapeutically as  
 CC modulators and as immunoassay reagents for detecting TAO kinases.  
 CC TAO kinase polynucleotides can be used: (a) for recombinant expression  
 CC of TAO kinases; and (b) in the form of fragments, for detecting TAO  
 CC kinase polynucleotides in standard hybridisation and amplification  
 CC tests. TAO kinases are highly specific for MEK3.  
 CC  
 XX  
 SQ Sequence 1001 AA:  
 Query Match 91.1%; Score 1529; DB 20; Length 1001;  
 Best Local Similarity 88.8%; Pred. No. 2.4e-147;  
 Matches 284; Conservative 22; Mismatches 14; Indels 0; Gaps 0;  
 QY 1 MPAGGAGSLKPDVAELFFKDDPEKLFSDLRITGSGAGAYFADVKNSEVVAIKKMS 60  
 DB 1 MPSTNAGSLKPDVAELFFKDDPEKLFSDLRITGSGAGAYFADVKNSEVVAIKKMS 60  
 QY 61 YSGKOSNEKMODIIKEVREFLQRLRHPTIOYRGCYLREHTAWLVMEYCLGSASDLEEVK 120  
 DB 61 YSGKOSTEKMODIIKEVREFLQRLRHPTIOYRGCYLREHTAWLVMEYCLGSASDLEEVK 120  
 QY 121 KPLQVEEIAAVTHGALQGLAYLHSHNMHRDYKAGNIIILSEPGLYKLGFGSASIMAPAN 180  
 DB 121 KPLQVEEIAAVTHGALQGLAYLHSHNMHRDYKAGNIIILTEPGYKLVDFGSASIMAPAN 180  
 QY 181 SFVGTPTWMAPEVILLAMDGOYDKVDVWSLGTICIELAEKRPPLFNNMAMSAALHIAON 240  
 DB 181 SFVGTPTWMAPEVILLAMDGOYDKVDVWSLGTICIELAEKRPPLFNNMAMSAALHIAON 240  
 QY 241 ESPALQSGHMSSEYFRNFVDSCLQKIPQDRPTSEVLKHFVLRERPPYIMDLIORTKDA 300  
 DB 241 ESPVLOSNGHMSSEYFRNFVDSCLQKIPQDRPTSEVLKHFVLRERPPYIMDLIORTKDA 300  
 QY 301 VRELDNLQYRKMKKILFOEA 320  
 DB 301 VRELDNLQYRKMKKILFOEA 320  
 RESULT 6  
 AAY55942  
 ID AAY55942 standard; Peptide; 1001 AA.  
 XX

AC AAY55942;  
 XX  
 XX 18-FEB-2000 (first entry)  
 XX  
 DE Human/Murine SULU3 consensus protein sequence.  
 XX  
 XX Antirheumatic; antiarthritic; antiinflammatory; antiallergic; osteopathic;  
 KW antipsoriatic; antiarteriosclerotic; antiasthmatic; immunosuppressive;  
 KW neuroprotective; cardiatic; cerebroprotective; cytoslatic; antidiabetic;  
 KW vulnery; STE20; protein kinase; STLK2; STLK3; STLK4; STLK5; STLK6; STLK7;  
 KW ZC1; ZC2; ZC3; ZC4; KHS2; SULU1; SULU3; GSK2; PAK4; PAK5; antagonists;  
 KW antibody; gene therapy; rheumatoid arthritis; artherosclerosis; asthma;  
 KW inflammatory bowel disease; Crohn's disease; osteoarthritis; psoriasis;  
 KW rhinitis; autoimmunity; organ transplantation; multiple sclerosis;  
 KW myocardial infarction; cardiovascular disease; stroke; renal failure;  
 KW oxidative stress-related neurodegenerative disorder; Parkinson's disease;  
 KW amyotrophic lateral sclerosis; Leigh syndrome; cancer; cardiomyopathy;  
 KW ischemic disorder; inflammation; diabetes mellitus; fibrosis; mitosis;  
 KW mesangial disorder; growth regulation; wound healing; T cell activation;  
 KW immunosuppressant.  
 XX  
 XX Homo sapiens.  
 OS Mus sp.  
 OS  
 XX W09953036-A2.  
 PN  
 XX 21-OCT-1999.  
 PD  
 XX 13-APR-1999; 99WO-US08150.  
 PF  
 XX 14-APR-1998; 98US-0081784.  
 PR  
 XX (SUGE-) SUGEN INC.  
 PA Plozman G, Martinez R, Whyte D;  
 PI WPI; 1999-611301/52.  
 DR  
 XX Novel kinase-related polypeptides used for the diagnosis and treatment  
 PT of kinase-related diseases and disorders -  
 XX  
 PS Claim 11; Page 312-315; 387pp; English.  
 XX  
 CC This sequence represents a consensus peptide sequence conained in novel  
 CC STE20-related protein kinases. The invention relates to a nucleic acid  
 CC molecule encoding a kinase polypeptide selected from STLK2, STLK3, STLK4,  
 CC STLK5, STLK6, STLK7, ZC1, ZC2, ZC3, ZC4, KHS2, SULU1, SULU3, GSK2, PAK4  
 CC and PAK5. The proteins are used to identify agonists and antagonists, and  
 CC to raise antibodies. The polynucleotides are useful in gene therapy  
 CC protocols. The polynucleotides, polypeptides, antibodies, antagonists and  
 CC agonists may be used to treat diseases such as immune-related disorders  
 CC and diseases (e.g. rheumatoid arthritis, artherosclerosis, chronic  
 CC inflammatory bowel disease (e.g. Crohn's disease), asthma,  
 CC osteoarthritis, psoriasis, atherosclerosis, rhinitis, autoimmunity,  
 CC and organ transplantation, chronic inflammatory pelvic disease, multiple  
 CC sclerosis, organ transplantation, myocardial infarction, cardiovascular  
 CC disease, stroke, renal failure, oxidative stress-related  
 CC neurodegenerative disorders (e.g. amyotrophic lateral sclerosis,  
 CC Parkinson's disease and Leigh syndrome), cancer, cardiomyopathies,  
 CC ischemic disorders, inflammatory disorders, diabetes mellitus, fibrotic  
 CC and mesangial disorders. The proteins may also be useful for cell growth  
 CC regulation (e.g. in wound healing), T cell activation, mitosis control,  
 CC and as immunosuppressants.  
 CC  
 XX  
 SQ Sequence 1001 AA:  
 Query Match 91.0%; Score 1527; DB 20; Length 1001;  
 Best Local Similarity 88.8%; Pred. No. 3.9e-147;  
 Matches 284; Conservative 22; Mismatches 14; Indels 0; Gaps 0;  
 QY 1 MPAGAGAGSLKPDVAELFFKDDPEKLFSDLRITGSGGAYVFAADYRNSEVVAIKKMS 60  
 DB 1 MPSTNRAGSLKDPDELALFFKDEPEKLFIDLREIGHGSGAYVFAADYRNSEVVAIKKMS 60

QY 61 YSGKSNSEKMODITKEVRFLOKLRHPTIOYRCGYLRHRTAWLVMKCYGSASDLLEVHK 120  
 DB 61 YSGKSTEMKMODITKEVRFLOKLRHPTISLEYKGCYLRHRTAWLVMKCYGSASDLLEVHK 120  
 QY 121 KPLQVEEIAAVTGAQLGLAYLHSHNMIRHDVAKAGNILLSEPLVYKGDGSGASIMAPAN 180  
 DB 121 KPLQVEEIAAITGALQGLAYLHSHNMIRHDVAKAGNILLSEPLVYKGDGSGASIMAPAN 180  
 QY 181 SFPGTTPYMAPEVILAMDSCQYDGKVDVMSLGITCIELEAKRPPLFNMAASALYHIAQN 240  
 DB 181 SFPGTTPYMAPEVILAMDSCQYDGKVDVMSLGITCIELEAKRPPLFNMAASALYHIAQN 240  
 QY 241 ESPALQSGHSEVFRNFVSCLOKIPDRPTSVLLKHRVLEKRPPTVMDLIQRTKDA 300  
 DB 241 ESPALQSGHSEVFRNFVSCLOKIPDRPTSVLLKHRVLEKRPPTVMDLIQRTKDA 300  
 QY 301 VRELDMLOYRKMKKILFQEA 320  
 DB 301 VRELDMLOYRKMKKILFQEA 320

RESULT 7  
 ABB97326  
 ID ABB97326 standard; Protein; 1001 AA.  
 XX  
 AC ABB97326;  
 XX  
 DT 27-JUN-2002 (first entry)  
 XX  
 DE Novel human protein SEQ ID NO: 594.  
 XX  
 KW Human; antianaemic; vulnery; antiinflammatory; immunomodulator;  
 KW antinfertility; cerebroprotective; cytoslatic; rheumatic; gene therapy;  
 KW neuroprotective; antiparkinsonian; protein therapy; ESR;  
 KW expressed sequence tag.  
 XX  
 OS Homo sapiens.  
 XX  
 PN W0200222660-A2.  
 PD 21-MAR-2002.  
 XX  
 PF 10-SEP-2001; 2001WO-US26015.  
 PR 11-SEP-2000; 2000US-0659671.  
 PA (HYSE-) HYSEQ INC.  
 PI Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;  
 PI Xue AJ, Yang Y, Weinman T, Drmanac RT;  
 DR N-PSDB; AEN32512.  
 DR WPI; 2002-292408/33.  
 PT An isolated polynucleotide for treating diseases associated with its  
 PT encoded polypeptide such as cancer and multiple sclerosis -  
 XX  
 PS Example 2; SEQ ID NO 594; 509pp; English.  
 XX  
 CC The present invention provides the protein and coding sequences of 444  
 CC novel human proteins. These were isolated from expressed sequences tags  
 CC (ESTs). They can be used to stimulate cell growth, to help tissue regrowth  
 CC e.g. in burn treatment, to regulate the immune system e.g. to treat  
 CC multiple sclerosis, to regulate activin or inhibin e.g. to treat  
 CC infertility, to regulate haemostasis or thrombolysis e.g. to treat  
 CC stroke and cancer, to screen for drugs, to treat inflammatory conditions  
 CC e.g. rheumatoid arthritis, and to treat nervous system disorders e.g.  
 CC Parkinson's disease. The present sequence is a protein of the invention.  
 CC  
 XX  
 SQ Sequence 1001 AA:



KM cholesterol ester storage; systemic lupus erythematosus; infection;  
 KM severe combined immunodeficiency; malaria; autoimmune disorder; asthma;  
 KM allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;  
 KM bone damage; cartilage damage; antiinflammatory disease; coagulation;  
 KM thrombosis; contraceptive.  
 OS Homo sapiens.  
 XX WO200058473-A2.  
 PN  
 XX  
 PD 05-OCT-2000.  
 PF  
 XX 31-MAR-2000; 2000WO-0508621.  
 XX  
 PR 31-MAR-1999; 99US-0127607.  
 PR 02-APR-1999; 99US-0127636.  
 PR 05-APR-1999; 99US-0127728.  
 PR 30-MAR-2000; 2000US-0540763.  
 XX  
 PA (CURA-) CURAGEN CORP.  
 XX  
 PI Shimkets RA, Leach M;  
 XX  
 DR WPI, 2000-602362/57.  
 DR N-PSDB; AAC77400.  
 XX  
 PT Novel nucleic acids and peptides derived from open reading frame X,  
 PT useful for treating e.g. cancers, proliferative disorders,  
 PT neurodegenerative disorders and cardiovascular disease -  
 PS  
 XX Claim 11; Page 5088-5090; 5507pp; English.  
 CC AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,  
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX  
 CC sequences have activities such as: cytostatic; hepatotropic; vulnerary;  
 CC antipruritic; antiparkinsonian; nootropic; neuroprotective;  
 CC osteopathic; anticoagulant; antiarthritic; immunosuppressive;  
 CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;  
 CC antidiabetic; hypotensive; dermatological; immunosuppressive;  
 CC antiinflammatory; antibacterial; antiviral; antifungal; antineumatic;  
 CC antihypoid; and antinaemic. The sequences can be used for determining  
 CC the presence of or predisposition to, or preventing or treating  
 CC pathological conditions associated with an ORFX-associated disorder. The  
 CC nucleic acids can be used to express ORFX proteins in gene therapy  
 CC vectors. The proteins and nucleic acids may be used to treat cancers,  
 CC proliferative disorders, neurodegenerative disorders, osteoarthritis,  
 CC graft vs host disease, cardiovascular disease, diabetes mellitus,  
 CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus  
 CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,  
 CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,  
 CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,  
 CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance  
 CC coagulation; to inhibit thrombosis; and as a contraceptive.  
 XX  
 SQ Sequence 899 AA;  
 Query Match 83.0%; Score 1392; DB 21; Length 899;  
 Best Local Similarity 81.8%; Pred. No. 2.3e-133;  
 Matches 257; Conservative 31; Mismatches 26; Indels 0; Gaps 0;

DB 182 PYWAPPEVILLAMDEGQYDGVADTWSLGTICIELAERKPPLENNAMASALYHIAQNDSPTL 241  
 QY 246 QSGHWSXEFNFENVDSCLQKIPQDRPTSEVLKRRFVLRERPPYIMLTQRTDAVVELD 305  
 DB 242 QSNEMWDSFERFVDCQKIPQERPTSAELLRHDFVRDRPLRYLIDLQRTDAVVELD 301  
 QY 306 NLOYRKMKKILFOE 319  
 DB 302 NLOYRKMKKILFOE 315  
 RESULT 10  
 ID AAM97676  
 XX AAM97676 standard; Protein; 898 AA.  
 AC AAM97676;  
 XX  
 DT 10-MAY-1999 (first entry)  
 XX  
 DE Human KDS1 serine/threonine kinase.  
 XX  
 KW KDS1; kinase domain related to Ste20; human; serine kinase;  
 KW threonine kinase; protein kinase; signal transduction.  
 XX  
 OS Homo sapiens.  
 PN WO9902699-A1.  
 PD 21-JAN-1999.  
 PF 07-JUL-1998; 98WO-US14231.  
 XX  
 PR 08-JUL-1997; 97US-0889518.  
 XX  
 PA (CADU-) CADUS PHARM CORP.  
 PI Johnson GL, Pleiman CM;  
 DR WPI, 1999-120900/10.  
 DR N-PSDB; AAX07074.  
 XX  
 PT New isolated vertebrate kinase - used to develop products for the  
 PT diagnosis and treatment of disorders involving cellular processes  
 PT such as signal transduction processes  
 PS Claim 30; Page 78-81; 100pp; English.  
 XX  
 CC This polypeptide comprises human serine/threonine kinase KDS1, a  
 CC novel protein associated with signal transduction. KDS1 has a  
 CC kinase domain related to that of Ste20 (KDS1 - Kinase Domain  
 CC related to Ste20). KDS1 cDNA (see AAX07074) was isolated from a  
 CC human bone marrow cDNA library. A clone (see AAX07075) encoding the  
 CC highly homologous KDS2 (see AAM97677) was also obtained. Both KDS1  
 CC and KDS2 have Glu/Gln-rich regions at their C-terminus (see also  
 CC AAM97678-79) suggesting an alpha-helical structure that may play a  
 CC role in covalently localising these proteins to a specific site  
 CC within the cells, which may be necessary for function. A method  
 CC for producing KDS polypeptides in host cells is provided. Since  
 CC KDS molecules have kinase activity, they are useful as modulating  
 CC agents in regulating a variety of cellular processes such as signal  
 CC transduction pathways. These pathways may regulate cytoskeleton,  
 CC secretion, growth, apoptosis, superoxide generation, and specific  
 CC gene transcription. KDS polypeptides and polynucleotides can be  
 CC used for treating disorders involving aberrant expression of  
 CC mammalian KDS genes. They can also be used for detection,  
 CC diagnosis and drug screening.  
 XX  
 SQ Sequence 898 AA;  
 Query Match 82.8%; Score 1389; DB 20; Length 898;  
 Best Local Similarity 81.5%; Pred. No. 4.6e-133;  
 Matches 256; Conservative 32; Mismatches 26; Indels 0; Gaps 0;





Seq	Sequence	898 AA:	82.5%:	Score 1384:	DB 21:	Length 898:
Query Match			81.5%:	Pred. No. 1.5e-132:		
Best Local Similarity			31:	Mismatches 27:	Indels 0:	Gaps 0:
Matches	256:	Conservative				
QY	6	RAGSLKDPVALFPRKDDPEKLFSDIREIGHGSGFAVYFARDVRNSEVAIIRKMSYSGKQ	65			
DB	2	RKGVDLKDEIADLSYKDPPEELFGLHEIGHGSGFAVYFATNAHTSEVAIRKMSYSGKQ	61			
QY	66	SNEKKODIRKEVRFLOKLRHPNTIOYRGCYLREHRAVLMEVCLGSASDLLEVHKKPQIE	125			
DB	62	THEKKODILKEVKEFRQLKHPNTIEYKGCYCLEHRAVLMEVCLGSASDLLEVHKKPQIE	121			
QY	126	VEIAAVTHGALOGIAYLASHNMIRHDVYKAGNILLSEPGIYKIGDGSGASIMAPANSFVGT	185			
DB	122	VEIAAITHGALGLAYLASHALIHMDIKAGNILLLEPGVKIADLADGSGASMAPANSFVGT	181			
QY	186	PYMAAPEVILADEGQYDGVMSLGTICIELAEKRPPLFNMNMSALYHIAQNESPAL	245			
DB	182	PYMAAPEVILADEGQYDGVMSLGTICIELAEKRPPLFNMNMSALYHIAQNDSPIL	241			
QY	246	OSGHSEVFERNVDSCLQIKIPQDRPTSEVLKHKRYLRRPPTVIMDLIQRTKDAVRELD	305			
DB	242	OSNEMTDSRRRFRVDCLOKIPQERTSALLRHDVRDRPRLVILDIQRTKDAVRELD	301			
QY	306	NLOYRKMKILFQE	319			
DB	302	NLOYRKMKILFQE	315			
RESULT 12						
ID	AAV55936					
AAV55936	standard; Protein; 898 AA.					
AC	AAV55936;					
XX	18-FEB-2000 (first entry)					
DT	Human SUD1 protein.					
XX	Antirheumatic; antithrptic; antinflammatory; antiallergic; osteopathic;					
KW	antiprotic; antiarteriosclerotic; antiasthmatic; immunosuppressive;					
KW	neuroprotective; cardiac; cerebroprotective; cytosolic; antidiabetic;					
KW	vulnery; SREBP2; protein kinase; STIK2; STIK3; STIK4; STIK5; STIK6; STIK7;					
KW	ZC1; ZC2; ZC3; ZC4; KHS2; SUD1; SUD3; GER2; PAK4; PAK5; antagonist;					
KW	antibody; gene therapy; rheumatoid arthritis; arteriosclerosis; asthma;					
KW	inflammatory bowel disease; Crohn's disease; osteoarthritis; psoriasis;					
KW	rheitis; autoimmunity; organ transplantation; multiple sclerosis;					
KW	myocardial infarction; cardiovascular disease; stroke; renal failure;					
KW	oxidative stress-related neurodegenerative disorder; Parkinson's disease;					
KW	amyotrophic lateral sclerosis; Leigh syndrome; cancer; cardiomyopathy;					
KW	ischemic disorder; inflammation; diabetes mellitus; fibrosis; mitosis;					
KW	measngial disorder; growth regulation; wound healing; T cell activation;					
KW	immunosuppressant.					
XX						
OS	Homo sapiens.					
XX						
PN	W09953036-A2.					
XX						
PD	21-OCT-1999.					
XX						
PE	13-APR-1999; 99WO-US08150.					
XX						
PR	14-APR-1998; 98US-0081784.					
XX						
PA	(SUGEN-) SUGEN INC.					
PI	Plowman G, Martinez R, Whyte D;					
XX	WPI: 1999-611301/52.					
DR	N-PSDB; AA240488.					
XX						

Novel kinase-related polypeptides used for the diagnosis and treatment of kinase-related diseases and disorders -

Claim 11: Page 293-296; 387pp; English.

This sequence represents a novel STR20-related protein kinase. The invention relates to nucleic acid molecule encoding a kinase polypeptide selected from STLK2, STLK3, STLK4, STLK5, STLK6, STLK7, ZC1, ZC2, ZC3, ZC4, KHS2, S0L0J1, S0L0J3, GEX2, PAK4 and PAK5. The proteins are used to identify agonists and antagonists, and to raise antibodies. The polynucleotides are useful in gene therapy protocols. The polynucleotides, polypeptides, antibodies, antagonists and agonists may be used to treat diseases such as immune-related disorders and diseases (e.g. rheumatoid arthritis, atherosclerosis, chronic inflammatory bowel disease (e.g. Crohn's disease), asthma, osteoarthritis, psoriasis, atherosclerosis, rheinitis, autoimmunity, and organ transplantation, chronic inflammatory pelvic disease, multiple sclerosis, organ transplantation, myocardial infarction, cardiovascular disease, stroke, renal failure, oxidative stress-related neurodegenerative disorders (e.g. amyotrophic lateral sclerosis, Parkinson's disease and Leigh syndrome), cancer, cardiomyopathies, ischemic disorders, inflammatory disorders, diabetes mellitus, fibrotic and mesangial disorders. The proteins may also be useful for cell growth regulation (e.g. in wound healing), T cell activation, mitosis control, and as immunosuppressants.

Query Match	82.4%	Score 1383;	DB 20;	Length 898;
Best Local Similarity	81.2%;	Pred. No. 1.9e-132;		
Matches 255;	Conservative 32;	Mismatches 27;	Indels 0;	Gaps 0;
QY	6	RAGSLKDDVAELPPKDDPEKLFSDLRILGSGSGAVVFADVRNSVEVALIKKMSYSGQ	65	
Db	2	RKGVAKDEIDLEFKDDPEELFGLHEIGHGSGFVAVFATNAHNEVVAIRKMSYSGQ	61	
QY	66	SNEKKMODIKIEVRFLQKIRHNPTIOYRCGYLREHTAMLVMEYCGSASDLEFVHKRPLOE	125	
Db	62	THEKMODILKEVKELRQAKHNPTIEYKCCYLKEHTAMLVMEYCGSASDLEFVHKRPLOE	121	
QY	126	VELAAVTGALOGIAYLISHNMIRHDVAKAGNILLSEPGVLKADFGSASIMAPANSFVGT	185	
Db	122	VELAITGHALGLAYLHSHALIHDDIKAGNILLTEPGQVLADFGSASIMAPANSFVGT	181	
QY	186	PYMAAPEVITLMDSEQYDGVKDVWSLGTICIELAKRPPLFNMMASALYHIAONESPAL	245	
Db	182	PYMAAPEVITLMDSEQYDGVKDVWSLGTICIELAKRPPLFNMMASALYHIAONESPAL	241	
QY	246	QSGHSEVFERNPVDSCLOKIPODRPTSEVLKHNRPVLSREPRYIMDLIORTKQAVRELD	305	
Db	242	QSNEMTDSFRFRVDCLOKIPDRPTSEVLKHNRPVLSREPRYIMDLIORTKQAVRELD	301	
QY	306	NLOYRKMKKILFOE	319	
Db	302	NLOYRKMKKILFOE	315	
RESULT 13				
ABB69116				
ID	ABB69116	standard; Protein; 1039 AA.		
XX	ABB69116;			
XX	AC			
XX	DT	26-MAR-2002 (first entry)		
DE	XX	Drosophila melanogaster polypeptide seq ID NO 34140.		
XX	XX			
KW	XX	Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical.		
XX	XX			
OS	XX	Drosophila melanogaster.		
NN	NN			
XX	NN	W0200171042-A2.		



PR	14-SEP-2000	2000US-02323399
PR	14-SEP-2000	2000US-02334401
PR	14-SEP-2000	2000US-02343400
PR	14-SEP-2000	2000US-02343401
PR	14-SEP-2000	2000US-02330663
PR	14-SEP-2000	2000US-02330634
PR	14-SEP-2000	2000US-02330635
PR	21-SEP-2000	2000US-02343223
PR	21-SEP-2000	2000US-02343224
PR	21-SEP-2000	2000US-02343273
PR	25-SEP-2000	2000US-02343997
PR	25-SEP-2000	2000US-02343998
PR	25-SEP-2000	2000US-02343998
PR	27-SEP-2000	2000US-02358384
PR	27-SEP-2000	2000US-02358384
PR	27-SEP-2000	2000US-02358386
PR	29-SEP-2000	2000US-02363327
PR	29-SEP-2000	2000US-02363367
PR	29-SEP-2000	2000US-02363368
PR	29-SEP-2000	2000US-02363369
PR	29-SEP-2000	2000US-02363370
PR	02-OCT-2000	2000US-02373802
PR	02-OCT-2000	2000US-02373803
PR	02-OCT-2000	2000US-02373807
PR	02-OCT-2000	2000US-02373808
PR	02-OCT-2000	2000US-02373839
PR	02-OCT-2000	2000US-02373839
PR	02-OCT-2000	2000US-02370400
PR	13-OCT-2000	2000US-02393935
PR	13-OCT-2000	2000US-02393937
PR	20-OCT-2000	2000US-02418009
PR	20-OCT-2000	2000US-02418060
PR	20-OCT-2000	2000US-02419211
PR	20-OCT-2000	2000US-02417885
PR	20-OCT-2000	2000US-02417885
PR	20-OCT-2000	2000US-02417887
PR	20-OCT-2000	2000US-02418008
PR	20-OCT-2000	2000US-02418018
PR	20-OCT-2000	2000US-02418019
PR	01-NOV-2000	2000US-02446127
PR	08-NOV-2000	2000US-02464474
PR	08-NOV-2000	2000US-02464475
PR	08-NOV-2000	2000US-02464476
PR	08-NOV-2000	2000US-02464477
PR	08-NOV-2000	2000US-02464478
PR	08-NOV-2000	2000US-02464523
PR	08-NOV-2000	2000US-02465524
PR	08-NOV-2000	2000US-02465525
PR	08-NOV-2000	2000US-02465526
PR	08-NOV-2000	2000US-02465527
PR	08-NOV-2000	2000US-02465528
PR	08-NOV-2000	2000US-02465532
PR	08-NOV-2000	2000US-02466609
PR	08-NOV-2000	2000US-02466610
PR	08-NOV-2000	2000US-02466611
PR	17-NOV-2000	2000US-02492121
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PR	17-NOV-2000	2000US-02492123
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PR	17-NOV-2000	2000US-02492125
PR	17-NOV-2000	2000US-02492126
PR	17-NOV-2000	2000US-02492127
PR	17-NOV-2000	2000US-02492128
PR	17-NOV-2000	2000US-02492144
PR	17-NOV-2000	2000US-02492245
PR	17-NOV-2000	2000US-02492245
PR	17-NOV-2000	2000US-02492265
PR	17-NOV-2000	2000US-02492265
PR	17-NOV-2000	2000US-02492297
PR	17-NOV-2000	2000US-02492299
PR	01-DEC-2000	2000US-02501600
PR	01-DEC-2000	2000US-02501600
PR	05-DEC-2000	2000US-02510300
PR	05-DEC-2000	2000US-02510300
PR	05-DEC-2000	2000US-02519888

PR 05-DEC-2000; 2000US-0256719.  
PR 06-DEC-2000; 2000US-0251479.  
PR 08-DEC-2000; 2000US-0251835.  
PR 08-DEC-2000; 2000US-0251868.  
PR 08-DEC-2000; 2000US-0251865.  
PR 08-DEC-2000; 2000US-0251989.  
PR 08-DEC-2000; 2000US-0251990.  
PR 11-DEC-2000; 2000US-0254097.  
PR 05-JAN-2001; 2001US-0259676.

PT New isolated nucleic acid encoding a protein for diagnosing,  
PT preventing, treating or ameliorating medical conditions and used as  
PT food additives or preservatives -  
XX  
PS Claim 9; SEQ ID No 632; 837bp; English.

The invention describes an isolated nucleic acid molecule (I) encoding a novel central nervous system protein, (I) and polypeptides (II) encoded by (I), are used to treat a medical conditions and in diagnosis of a pathological condition. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g. Alzheimer's disease and amyotrophic lateral sclerosis, infections caused by bacteria, viruses e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders e.g. corneal infection, gastrointestinal disorders e.g. dysphagia, adenocarcinomas and irritable bowel syndrome, reproductive system disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes and pituitary disorders, cancers and disorders at the cellular level e.g. leukaemia, disorders involving neovascularisation e.g. malignancies, respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g. acute kidney failure and blood related disorders e.g. myocardial infarction. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities, fat content, lipid, protein,

Query Match	69.0%	Score 1158;	DB 22;	Length 323;
Best Local Similarity	88.8%	Pred. No. 5e-110;		
Matches 215; Conservative	15;	Mismatches 12;	Indels 0;	Gaps 0;

QY	79	FLOKLRHPNTIOYRCGLREHTAMLYEMXCJLASADLLFEVHKPPLQBEVIAAVTHGALOG	138
Db	1	FLORKHPMSIEYKCCYLYNEHTAMLYEMXCJLASADLLFEVHKPPLQBEVIAAVTHGALOG	60
QY	139	LAVLSHNNHHRDVKAGNILLSEPLVJKLDGCSASIMAPANSFVGTPYMAPEVILAMD	198
Db	61	LAVLSHNNHHRDVKAGNILLSEPLVJKLDGCSASIMAPANSFVGTPYMAPEVILAMD	120
QY	199	EOGYGKDYVWSLGITCIEFLAERKPPLENNMNASALYHIAONESPALOSGHWSEYFRNFV	258
Db	121	EOGYGKDYVWSLGITCIEFLAERKPPLENNMNASALYHIAONESPTLOSNEMSDYFRNFV	180
QY	259	DSCLOKIPODRPTSEVLKHFVLEKRPETVYIMDLIORTKAVRELDNIJOYRKMKILFO	318
Db	181	DSCLOKIPODRPTSEVLKHFVLEKRPETVYIMDLIORTKAVRELDNIJOYRKMKILFO	240
QY	319	EA 320	
Db	241	EA 242	

## RESULT 15

AAU87435  
ID AAU87435 standard; Protein; 265 AA.  
XX  
AC AAU87435;  
XX  
DT 05-JUN-2002 (first entry)  
XX  
DE Novel central nervous system protein #345.  
XX  
KW Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;  
KW hyperproliferative disorder; neoplasm; cardiovascular disorder;  
KW cardiac arrest; cerebrovascular disorder; ischemia; anglogenesis;  
KW nervous system disorder; Alzheimer's disease; ocular disorder;  
KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;  
KW adenocarcinoma; reproductive system disorder; testicular feminisation;  
KW endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;  
KW respiratory disorder; renal disorder; kidney failure; blood disorder;  
KW myocardial infarction; wound healing; cell proliferation; skin aging;  
KW food additive; food preservative; gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN W0200155318-A2.  
XX  
PD 02-AUG-2001.  
XX  
PF 17-JAN-2001; 2001WO-US01332.  
XX  
PR 31-JAN-2000; 2000US-0179065.  
PR 04-FEB-2000; 2000US-0180628.  
PR 24-FEB-2000; 2000US-0184664.  
PR 02-MAR-2000; 2000US-0186350.  
PR 16-MAR-2000; 2000US-0189874.  
PR 17-MAR-2000; 2000US-0190076.  
PR 18-APR-2000; 2000US-0198123.  
PR 19-MAY-2000; 2000US-0205515.  
PR 07-JUN-2000; 2000US-0209467.  
PR 28-JUN-2000; 2000US-0214886.  
PR 30-JUN-2000; 2000US-0215135.  
PR 07-JUL-2000; 2000US-0216647.  
PR 07-JUL-2000; 2000US-0216880.  
PR 11-JUL-2000; 2000US-0217487.  
PR 11-JUL-2000; 2000US-0217496.  
PR 14-JUL-2000; 2000US-0218290.  
PR 26-JUL-2000; 2000US-0220963.  
PR 26-JUL-2000; 2000US-0220964.  
PR 14-AUG-2000; 2000US-0224518.  
PR 14-AUG-2000; 2000US-0224519.  
PR 14-AUG-2000; 2000US-0225213.  
PR 14-AUG-2000; 2000US-0225214.  
PR 14-AUG-2000; 2000US-0225266.  
PR 14-AUG-2000; 2000US-0225267.  
PR 14-AUG-2000; 2000US-0225268.  
PR 14-AUG-2000; 2000US-0225270.  
PR 14-AUG-2000; 2000US-0225447.  
PR 14-AUG-2000; 2000US-0225757.  
PR 14-AUG-2000; 2000US-0225758.  
PR 14-AUG-2000; 2000US-0225759.  
PR 18-AUG-2000; 2000US-0226279.  
PR 22-AUG-2000; 2000US-0226681.  
PR 22-AUG-2000; 2000US-0226868.  
PR 23-AUG-2000; 2000US-0227182.  
PR 23-AUG-2000; 2000US-0227009.  
PR 30-AUG-2000; 2000US-0228924.  
PR 01-SEP-2000; 2000US-0229287.  
PR 01-SEP-2000; 2000US-0229343.  
PR 01-SEP-2000; 2000US-0229344.  
PR 01-SEP-2000; 2000US-0229345.  
PR 05-SEP-2000; 2000US-0229509.  
PR 05-SEP-2000; 2000US-0229513.  
PR 06-SEP-2000; 2000US-0230437.  
PR 06-SEP-2000; 2000US-0230438.  
PR 08-SEP-2000; 2000US-0231242.

PR 08-SEP-2000; 2000US-0231243.  
PR 08-SEP-2000; 2000US-0231244.  
PR 08-SEP-2000; 2000US-0231413.  
PR 08-SEP-2000; 2000US-0231414.  
PR 08-SEP-2000; 2000US-0232080.  
PR 08-SEP-2000; 2000US-0232081.  
PR 12-SEP-2000; 2000US-0231968.  
PR 14-SEP-2000; 2000US-0232397.  
PR 14-SEP-2000; 2000US-0232399.  
PR 14-SEP-2000; 2000US-0232400.  
PR 14-SEP-2000; 2000US-0232401.  
PR 14-SEP-2000; 2000US-0233063.  
PR 14-SEP-2000; 2000US-0233064.  
PR 14-SEP-2000; 2000US-0233065.  
PR 21-SEP-2000; 2000US-0234223.  
PR 21-SEP-2000; 2000US-0234274.  
PR 25-SEP-2000; 2000US-0234997.  
PR 25-SEP-2000; 2000US-0234998.  
PR 26-SEP-2000; 2000US-0235484.  
PR 27-SEP-2000; 2000US-0235834.  
PR 27-SEP-2000; 2000US-0235836.  
PR 29-SEP-2000; 2000US-0236327.  
PR 29-SEP-2000; 2000US-0236367.  
PR 29-SEP-2000; 2000US-0236368.  
PR 29-SEP-2000; 2000US-0236370.  
PR 02-OCT-2000; 2000US-0236802.  
PR 02-OCT-2000; 2000US-0237037.  
PR 02-OCT-2000; 2000US-0237038.  
PR 02-OCT-2000; 2000US-0237039.  
PR 02-OCT-2000; 2000US-0237040.  
PR 13-OCT-2000; 2000US-0239935.  
PR 13-OCT-2000; 2000US-0239937.  
PR 20-OCT-2000; 2000US-0240960.  
PR 20-OCT-2000; 2000US-0241221.  
PR 20-OCT-2000; 2000US-0241785.  
PR 20-OCT-2000; 2000US-0241786.  
PR 20-OCT-2000; 2000US-0241787.  
PR 20-OCT-2000; 2000US-0241809.  
PR 20-OCT-2000; 2000US-0241826.  
PR 01-NOV-2000; 2000US-0244617.  
PR 08-NOV-2000; 2000US-0246474.  
PR 08-NOV-2000; 2000US-0246475.  
PR 08-NOV-2000; 2000US-0246476.  
PR 08-NOV-2000; 2000US-0246477.  
PR 08-NOV-2000; 2000US-0246478.  
PR 08-NOV-2000; 2000US-0246523.  
PR 08-NOV-2000; 2000US-0246524.  
PR 08-NOV-2000; 2000US-0246525.  
PR 08-NOV-2000; 2000US-0246526.  
PR 08-NOV-2000; 2000US-0246527.  
PR 08-NOV-2000; 2000US-0246528.  
PR 08-NOV-2000; 2000US-0246532.  
PR 08-NOV-2000; 2000US-0246609.  
PR 08-NOV-2000; 2000US-0246610.  
PR 08-NOV-2000; 2000US-0246611.  
PR 08-NOV-2000; 2000US-0246613.  
PR 17-NOV-2000; 2000US-0249207.  
PR 17-NOV-2000; 2000US-0249208.  
PR 17-NOV-2000; 2000US-0249209.  
PR 17-NOV-2000; 2000US-0249210.  
PR 17-NOV-2000; 2000US-0249211.  
PR 17-NOV-2000; 2000US-0249212.  
PR 17-NOV-2000; 2000US-0249213.  
PR 17-NOV-2000; 2000US-0249214.  
PR 17-NOV-2000; 2000US-0249215.  
PR 17-NOV-2000; 2000US-0249216.  
PR 17-NOV-2000; 2000US-0249217.  
PR 17-NOV-2000; 2000US-0249218.  
PR 17-NOV-2000; 2000US-0249244.  
PR 17-NOV-2000; 2000US-0249245.

PR 17-NOV-2000; 2000US-0249264.  
 PR 17-NOV-2000; 2000US-0249265.  
 PR 17-NOV-2000; 2000US-0249297.  
 PR 17-NOV-2000; 2000US-0249299.  
 PR 17-NOV-2000; 2000US-0249300.  
 PR 01-DEC-2000; 2000US-0250160.  
 PR 01-DEC-2000; 2000US-0250391.  
 PR 05-DEC-2000; 2000US-0251030.  
 PR 05-DEC-2000; 2000US-0251988.  
 PR 05-DEC-2000; 2000US-0256719.  
 PR 06-DEC-2000; 2000US-0251479.  
 PR 08-DEC-2000; 2000US-0251856.  
 PR 08-DEC-2000; 2000US-0251868.  
 PR 08-DEC-2000; 2000US-0251869.  
 PR 08-DEC-2000; 2000US-0251989.  
 PR 08-DEC-2000; 2000US-0251990.  
 PR 11-DEC-2000; 2000US-0254097.  
 PR 05-JAN-2001; 2001US-0259678.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Rosen CA, Barash SC, Ruben SM;  
 XX  
 DR WPI; 2001-581633/65.  
 DR N-PSDB; ABK43765.  
 XX  
 XX

PT New isolated nucleic acid encoding a protein for diagnosing,  
 PT preventing, treating or ameliorating medical conditions and used as  
 PT food additives or preservatives -  
 XX  
 XX  
 PS Claim 9; SEQ ID No 953; 837pp; English.  
 XX

CC The invention describes an isolated nucleic acid molecule (I) encoding a  
 CC novel central nervous system protein. (I) and polypeptides (II) encoded  
 CC by (I), are used to treat a medical condition and in diagnosis of a  
 CC pathological condition. Disorders which are diagnosed or treated include  
 CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative  
 CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders  
 CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,  
 CC angiogenesis, nervous system disorders e.g. Alzheimer's disease and  
 CC amyotrophic lateral sclerosis, infections caused by bacteria, viruses  
 CC e.g. Acquired immunodeficiency virus (Aids) and fungi, ocular disorders  
 CC e.g. corneal infection, gastrointestinal disorders e.g. dysphagia,  
 CC adenocarcinomas and irritable bowel syndrome, reproductive system  
 CC disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes  
 CC and pituitary dwarfism, cancers and disorders at the cellular level e.g.  
 CC leukaemia, disorders involving neovascularisation e.g. malignancies,  
 CC respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g.  
 CC acute kidney failure and blood related disorders e.g. myocardial  
 CC infarction. The polypeptides can also be used to aid wound healing and  
 CC epithelial cell proliferation, to prevent skin aging due to sunburn, to  
 CC maintain organs before transplantation, for supporting cell culture of  
 CC primary tissues, to regenerate tissues and in chemotaxis. The  
 CC polypeptides can also be used as a food additive or preservative to  
 CC increase or decrease storage capabilities, fat content, lipid, protein,  
 CC

Query Match 65.1%; Score 1092; DB 22; Length 265;  
 Best Local Similarity 89.5%; Pred. No. 2.2e-103;  
 Matches 204; Conservative 11; Mismatches 13; Indels 0; Gaps 0;

QY 91 YRCGYLREHTAMVMEYCYLGSASDLLEVHKRPLOEVEIAVTHGALOGLAYLHSHNMHR 150  
 Db 1 YKGCXLRHXTWVMEYCYLGSASDLLEVHKRPLOEVEIAVTHGALOGLAYLHSHNMHR 60  
 QY 151 DVKAGNILLSEPLVKGDFGSASIMAPNSFVGTPTWMAPEVILAMDEGQYDGKVDVWS 210  
 Db 61 DIKAGNILLTEPQOVYLAFGSASMAPNSFVGTPTWMAPEVILAMDEGQYDGKVDVWS 120  
 QY 211 LGITTELEAKRPPLFNMMNSALYHIAQNESPALOSGHMSEYFRNFVDSCLQIPQDRP 270  
 Db 121 LGITTELEAKRPPLFNMMNSALYHIAQNESPALOSGHMSEYFRNFVDSCLQIPQDRP 180  
 QY 271 TSEVLLKHFVLRERPPVIMDLIQRTKDAVRELDNLYRKMKKILFQ 318

Db 181 TSEVLLKHFVLRERPPVIMDLIQRTKDAVRELDNLYRKMKKILFQ 228

Search completed: November 22, 2002, 12:23:37  
 Job time : 24.52 secs

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: November 22, 2002, 12:18:00 ; Search time 16.531 Seconds  
(without alignments)  
2184.436 Million cell updates/sec

Title: US-09-686-346a-4\_COPY\_15\_285  
Perfect score: 1428  
Sequence: 1 VAELFFKDDPEKLFSDLRRI.....PDQRTSEVLLKHFVLRER 271

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

A\_Geneseq\_101002:\*

- 1: /SID2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:\*
- 2: /SID2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*
- 3: /SID2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*
- 4: /SID2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:\*
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- 6: /SID2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:\*
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- 22: /SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*
- 23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1428	100.0	993	20	AAV49897
2	1424	99.7	1235	21	AAAB4163
3	1420	99.4	1049	22	AAE04366
4	1396	97.8	758	20	AAW97677
5	1316	92.2	1001	20	AAV49896
6	1314	92.0	1001	20	AAV55942
7	1314	92.0	1001	23	ABB97326
8	1254	87.8	748	20	AAV55938
9	1211	84.8	899	21	AAAB43191
10	1208	84.6	898	20	AAW97676

11	1203	84.2	898	21	AAV44244	Human cell signal
12	1202	84.2	898	20	AAV55936	Human SUI1 protei
13	1086	76.1	1039	22	AAAB69116	Drosophila melanog
14	1032	70.9	323	22	AA087114	Novel central nerv
15	946	66.2	265	22	AA087435	Novel central nerv
16	946	66.2	265	22	AA017256	Novel signal trans
17	883	61.8	982	20	AAV55955	Nematode STE20-rel
18	660	46.2	163	22	AAV25383	Human protein sequ
19	586.5	41.1	431	22	AA07069	Human polypeptide
20	584.5	40.9	431	20	AAV55950	Human polypeptide
21	584.5	40.9	431	20	AAV04473	Human MST3 protei
22	584.5	40.9	431	21	AAV82276	Human STE20-like s
23	584.5	40.9	443	23	AA020953	Human Ste20-like k
24	581.5	40.7	413	20	AAV21672	Human-N-kinase pro
25	578.5	40.5	431	21	AAV68771	Murine C12.2bs pol
26	571.5	40.0	458	22	ABG04590	Amino acid sequenc
27	568.5	39.8	426	18	AAV31603	Novel human diagno
28	568.5	39.8	426	20	AAV55949	Human protein kina
29	568.5	39.8	426	21	AAV82275	Human MAPK-pathway
30	557.5	39.0	392	22	AAV93576	Human polypeptide
31	557.5	39.0	416	20	AAV55927	Human STK2 protei
32	557.5	39.0	416	20	AAV22648	A human signal tra
33	557.5	39.0	416	20	AAV22651	A murine signal tra
34	557.5	39.0	416	20	AAV21673	Murine 5e.new poly
35	557.5	39.0	416	21	AAV82274	Human ste20-like s
36	557.5	39.0	416	21	AAV82277	Mouse protein sequ
37	557.5	39.0	416	22	AAV40348	Human polypeptide
38	557.5	39.0	416	22	AAV71958	Human TGF-beta rec
39	557.5	39.0	416	22	AAV66607	Human h2252 protei
40	555	38.9	596	22	AAV65561	Drosophila melanog
41	549	38.4	487	20	AAV21674	Human ste20 homolo
42	544	38.1	398	22	AAV55890	Human protein sequ
43	542.5	38.0	403	19	AAV54024	Human protein kina
44	539	37.7	443	20	AAV55951	Nematode STE20-rel
45	537.5	37.6	1269	22	AAV68223	Amino acid sequenc

#### ALIGNMENTS

RESULT 1  
ID AAV49897 standard; Protein; 993 AA.  
AC AAV49897;  
DT 27-JAN-2000 (first entry)  
XX  
DE Rat TAO2 kinase.  
KW TAO1, TAO2, MEK3; mitogen activated protein kinase; phosphorylation;  
KW p38; protein kinase; cancer; inflammation; autoimmune disease;  
KW degeneration; insulin-resistant diabetes; metabolic disorder;  
KW neurodegeneration; MAP kinase; MAP/ERK kinase.  
XX  
OS Rattus sp.  
XX  
PN WO953076-A1.  
XX  
PD 21-OCT-1999.  
XX  
PE 14-APR-1999; 99WO-US08165.  
XX  
PR 14-APR-1998; 98US-0060410.  
XX  
PA (TEXA) UNIV TEXAS SYSTEM.  
XX  
PI Cobb M, Hutchison M, Chen Z, Berman K;  
XX  
DR WPI; 1999-633831/54.  
XX  
DR N-PSDB; AA232436.  
XX  
PT New polypeptides that phosphorylate kinase, used to screen for

PT modulators for treating e.g. cancer or inflammation -  
XX  
PS Claim 7; Page 84-87; 95pp; English.  
XX  
CC The present sequence represents rat TAO2 protein kinase, which is capable  
CC of phosphorylating MEK3 (a MAP/ERK kinase). TAO kinases, and related  
CC polypeptides, are used to screen for modulators of stress-responsive  
CC mitogen activated protein (MAP) kinase pathways. These modulators are  
CC potentially useful for treating or preventing: (1) inflammation,  
CC autoimmune disease, cancer and degeneration (inhibitors of  
CC phosphorylation); or (2) insulin-resistant diabetes; metabolic disorders  
CC and neurodegeneration (enhancers of phosphorylation). TAO kinases are  
CC also used to raise specific antibodies, useful therapeutically as  
CC modulators and as immunoassay reagents for detecting TAO kinases.  
CC TAO kinase polynucleotides can be used: (a) for recombinant expression  
CC of TAO kinases; and (b) in the form of fragments, for detecting TAO  
CC kinase polynucleotides in standard hybridisation and amplification  
CC tests. TAO kinases are highly specific for MEK3.  
XX  
SQ Sequence 993 AA;  
XX  
Query Match 100.0%; Score 1428; DB 20; Length 993;  
Best Local Similarity 100.0%; Pred. No. 1.9e-142;  
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 VALFFKDDPEKLFSDLRIGHSFGAYVFARDVRNSEVAIAIKMSYSGKQSEKMODII 60  
DB 15 VALFFKDDPEKLFSDLRIGHSFGAYVFARDVRNSEVAIAIKMSYSGKQSEKMODII 74  
QY 61 KEVRFQKLRHNPNTIOYRCGYLREHTAMLYMEKCLGSASDLEVHKRPLOEVEIAAVTHG 120  
DB 75 KEVRFQKLRHNPNTIOYRCGYLREHTAMLYMEKCLGSASDLEVHKRPLOEVEIAAVTHG 134  
QY 121 ALQGLAYLHSHNMHRDVAKGNILSEPLVYKLGDFGSASIMAPANSFVGTPTWMAPEVI 180  
DB 135 ALQGLAYLHSHNMHRDVAKGNILSEPLVYKLGDFGSASIMAPANSFVGTPTWMAPEVI 194  
QY 181 LAMDEQYDGKVDVMSLGTICIELAEKRPPLFNMMNMSALYHIAQNESPALOSGHMSEYF 240  
DB 195 LAMDEQYDGKVDVMSLGTICIELAEKRPPLFNMMNMSALYHIAQNESPALOSGHMSEYF 254  
QY 241 RNFVDSCLQKIPDDRPTSEVLLKHRFVLRER 271  
DB 255 RNFVDSCLQKIPDDRPTSEVLLKHRFVLRER 285  
RESULT 2  
AAB41663  
ID AAB41663 standard; Protein: 1235 AA.  
XX  
AC AAB41663;  
XX  
DT 08-FEB-2001 (first entry)  
XX  
DE Human ORFX ORF1427 polypeptide sequence SEQ ID NO:2854.  
XX  
Human; Open reading frame; ORFX; detection; cytosolic; hepatotropic;  
KM vulnerability; antiparasitic; antiparkinsonian; neurotropic; neuroprotective;  
KM anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;  
KM immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;  
KM hypotensive; dermatological; immunosuppressive; antifungal; antihypertensive;  
KM antiviral; antibacterial; antifungal; antineoplastic; antithyroid;  
KM antianemic; gene therapy; cancer; proliferative disorder; hypertension;  
KM neurodegenerative disorder; osteoarthritis; graft vs host disease;  
KM cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;  
KM cholesterol ester storage; systemic lupus erythematosus; infection;  
KM severe combined immunodeficiency; malaria; autoimmune disorder; asthma;  
KM allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;  
KM bone damage; cartilage damage; antiinflammatory disease; coagulation;  
KM thrombosis; contraceptive.  
XX  
OS Homo sapiens.  
XX

PN WO200058473-A2.  
XX  
PD 05-OCT-2000.  
XX  
XX 31-MAR-2000; 2000WO-US08621.  
PF 31-MAR-1999; 99US-0127607.  
PR 02-APR-1999; 99US-0127636.  
PR 05-APR-1999; 99US-0127728.  
PR 30-MAR-2000; 2000US-0540763.  
XX  
PA (CURA-) CURAGEN CORP.  
XX  
PI Shinketsu RA, Leach M;  
XX  
DR WPI: 2000-602362/57.  
DR N-PSDB: AAC75872.  
XX  
PT Novel nucleic acids and peptides derived from open reading frame X,  
PT useful for treating e.g. cancers, proliferative disorders,  
PT neurodegenerative disorders and cardiovascular disease -  
PS Claim 11; Page 2092-2095; 5507pp; English.  
XX  
CC AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,  
CC which represent the human ORFX open reading frames 1 to 3161. The ORFX  
CC sequences have activities such as: cytosolic; hepatotropic; vulnerability;  
CC antiparasitic; antiparkinsonian; neurotropic; neuroprotective;  
CC osteopathic; anticonvulsant; antiarthritic; immunosuppressant;  
CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;  
CC antidiabetic; hypotensive; dermatological; immunosuppressive;  
CC antineoplastic; antibacterial; antifungal; antithyroid; antineoplastic;  
CC antihypertensive; antineoplastic; antineoplastic; antineoplastic;  
CC antihypertensive; antineoplastic; antineoplastic; antineoplastic;  
CC the presence of or predisposition to, or preventing or treating  
CC pathological conditions associated with an ORFX-associated disorder. The  
CC nucleic acids can be used to express ORFX proteins in gene therapy  
CC vectors. The proteins and nucleic acids may be used to treat cancers,  
CC proliferative disorders, neurodegenerative disorders, osteoarthritis,  
CC graft vs host disease, cardiovascular disease, diabetes mellitus,  
CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus  
CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,  
CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,  
CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,  
CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance  
CC coagulation; to inhibit thrombosis; and as a contraceptive.  
XX  
SQ Sequence 1235 AA;  
XX  
Query Match 99.7%; Score 1424; DB 21; Length 1235;  
Best Local Similarity 99.6%; Pred. No. 6.8e-142;  
Matches 270; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 VALFFKDDPEKLFSDLRIGHSFGAYVFARDVRNSEVAIAIKMSYSGKQSEKMODII 60  
DB 15 VALFFKDDPEKLFSDLRIGHSFGAYVFARDVRNSEVAIAIKMSYSGKQSEKMODII 74  
QY 61 KEVRFQKLRHNPNTIOYRCGYLREHTAMLYMEKCLGSASDLEVHKRPLOEVEIAAVTHG 120  
DB 75 KEVRFQKLRHNPNTIOYRCGYLREHTAMLYMEKCLGSASDLEVHKRPLOEVEIAAVTHG 134  
QY 121 ALQGLAYLHSHNMHRDVAKGNILSEPLVYKLGDFGSASIMAPANSFVGTPTWMAPEVI 180  
DB 135 ALQGLAYLHSHNMHRDVAKGNILSEPLVYKLGDFGSASIMAPANSFVGTPTWMAPEVI 194  
QY 181 LAMDEQYDGKVDVMSLGTICIELAEKRPPLFNMMNMSALYHIAQNESPALOSGHMSEYF 240  
DB 195 LAMDEQYDGKVDVMSLGTICIELAEKRPPLFNMMNMSALYHIAQNESPALOSGHMSEYF 254  
QY 241 RNFVDSCLQKIPDDRPTSEVLLKHRFVLRER 271  
DB 255 RNFVDSCLQKIPDDRPTSEVLLKHRFVLRER 285



RESULT 3  
AAE04366  
ID AAE04366 standard; Protein; 1049 AA.  
XX  
AC AAE04366;  
XX  
DT 04-SEP-2001 (first entry)  
XX  
DE Human kinase (PKIN)-7.  
XX  
KW Human kinase; PKIN-7; therapy; immune disorder; Addison's disease; AIDS;  
KW acquired immune deficiency syndrome; growth and developmental disorder;  
KW arteriosclerosis; mixed connective tissue disease; MCTD; adenocarcinoma;  
KW leukaemia; cardiovascular disease; myocardial infarction; hypertension;  
KW lipid disorder; cancer; fatty liver; cholestasis; transgenic animal;  
KW gene therapy; antiallergic; antidiabetic; antihypertensive; dermatological;  
KW antidiabetic; nephroprotective; antitumor; antithrombotic; antineoplastic;  
KW antiproliferative; neuroprotective; cytoskeletal; hepatotrophic; osteopathic;  
KW vasotropic; antiangiogenic; anorectic.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FH Domain 28..281  
FT /note="Eukaryotic protein kinase domain"  
FT Domain 30..269  
FT /note="Protein kinase domain"  
FT Region 147..158  
FT /note="Protein kinase ST"  
FT Region 618..777  
FT /note="Serine/threonine protein kinase TAO1"  
XX  
PN WO200146397-A2.  
XX  
PD 28-JUN-2001.  
XX  
PF 20-DEC-2000; 2000WO-US35304.  
XX  
PR 23-DEC-1999; 99US-0172066.  
PR 14-JAN-2000; 2000US-0176107.  
PR 21-JAN-2000; 2000US-0177731.  
PR 28-JAN-2000; 2000US-0178573.  
XX  
PA (INCY-) INCYTE GENOMICS INC.  
XX  
PI Yang J, Baughn MR, Buford N, Au-Young J, Lu DM, Reddy R, Yue H;  
PI Yao MG, Tai F, Khan FA;  
XX  
DR WPI: 2001-418059/44.  
DR N-PSDB; AAD08640.  
XX  
PT Novel human kinase proteins (PKIN) useful for diagnosing, treating,  
PT preventing immune disorders, cardiovascular diseases and disorders  
PT affecting growth and development associated with abnormal expression of  
PT PKIN  
XX  
PS Claim 1: Page 111-113; 128pp; English.  
XX  
XX The invention relates to novel human kinase proteins (PKIN) and  
CC nucleic acid molecules encoding them. PKIN is useful for identifying  
CC compounds that modulates its activity. PKIN cDNA is useful for  
CC assessing toxicity of a test compound. PKIN and its cDNA are useful  
CC for diagnosis, prevention and treatment of immune disorders such as  
CC acquired immune deficiency syndrome (AIDS), Addison's disease, anaemia,  
CC adult respiratory distress syndrome, allergies, amyloidosis, psoriasis,  
CC autoimmune haemolytic anaemia, autoimmune thyroiditis, multiple  
CC sclerosis, asthma, osteoarthritis, osteoporosis, rheumatoid arthritis,  
CC ulcerative colitis and diabetes mellitus; growth and developmental  
CC disorders such as actinic keratosis, arteriosclerosis, atherosclerosis,  
CC bursitis, cirrhosis, hepatitis, mixed connective tissue disease (MCTD),  
CC and myelofibrosis; cancers such as adenocarcinoma and leukaemia,  
CC cardiovascular diseases such as myocardial infarction and hypertension;  
CC and lipid disorders such as fatty liver and cholestasis. PKIN cDNA is

CC useful to detect upstream sequences such as promoters and regulatory  
CC elements, for creating knock in or knock out in humanised animals or  
CC transgenic animals to model human disease and for somatic or germline  
CC gene therapy for treating the above mentioned disorders. The present  
CC sequence is human kinase (PKIN)-7.  
XX  
SQ Sequence 1049 AA;  
XX  
Query Match 99.4%; Score 1420; DB 22; Length 1049;  
Best Local Similarity 99.3%; Pred. No. 1.4e-141;  
Matches 269; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
XX  
QY 1 VALFFKDDDEKFFSDIREIGHSGFAGVYFAPRVNNEVAIAIKMSYSGQSNKMODII 60  
DB 15 VALFFKDDDEKFFSDIREIGHSGFAGVYFAPRVNNEVAIAIKMSYSGQSNKMODII 74  
QY 61 KEVRFLOKLHNPNTIOYRGCYLRHPTAMLWMEYCLGSASDLLEVHKKPLQEVETIAVTHG 120  
DB 75 KEVRFLOKLHNPNTIOYRGCYLRHPTAMLWMEYCLGSASDLLEVHKKPLQEVETIAVTHG 134  
QY 121 ALQGLAVLHSHNMIHDPVKAGNILLSEPGLYKLGDFCSASIMAPANFVGTPTWMAPEVI 180  
DB 135 ALQGLAVLHSHNMIHDPVKAGNILLSEPGLYKLGDFCSASIMAPANFVGTPTWMAPEVI 194  
QY 181 LAMDEGQYDGKVDVWVSLGTCIELAEKRPPLFNNMNSALYHIAQNESPALQSGHWSEYF 240  
DB 195 LAMDEGQYDGKVDVWVSLGTCIELAEKRPPLFNNMNSALYHIAQNESPALQSGHWSEYF 254  
QY 241 RNFVDSCLQKIPDRPTSEVLKHPYLRER 271  
DB 255 RNFVDSCLQKIPDRPTSEVLKHPYLRER 285  
XX  
RESULT 4  
AAW97677  
ID AAW97677 standard; Protein; 758 AA.  
XX  
AC AAW97677;  
XX  
DT 10-MAY-1999 (first entry)  
XX  
DE Human KDS2 protein kinase.  
XX  
KW KDS2; Kinase domain related to Ste20; human; serine kinase;  
KW threonine kinase; protein kinase; signal transduction.  
XX  
OS Homo sapiens.  
XX  
PN WO9902699-A1.  
XX  
PD 21-JAN-1999.  
XX  
PF 07-JUL-1998; 98WO-US14231.  
XX  
PR 08-JUL-1997; 97US-0889518.  
XX  
PA (CADU-) CADUS PHARM CORP.  
XX  
PI Johnson GL, Pleiman CM;  
XX  
DR WPI: 1999-120900/10.  
DR N-PSDB; AAX07075.  
XX  
PT New isolated vertebrate kinase - used to develop products for the  
PT diagnosis and treatment of disorders involving cellular processes  
PT such as signal transduction processes  
XX  
PS Claim 31: Page 85-88; 100pp; English.  
XX  
XX This polypeptide comprises human protein kinase KDS2, a novel  
CC protein associated with signal transduction. KDS2 has a  
CC kinase domain related to that of Ste20 (KDS1 = Kinase Domain  
CC related to Ste20). KDS2 cDNA (see AAX07075) was isolated from a

CC human bone marrow cDNA library. A clone (see AAX07074) encoding the  
CC highly homologous KDS1 (see AAW97676) was also obtained. Both KDS1  
CC and KDS2 have Glu/Gln-rich regions at their C-terminus (see also  
CC AAW97678-79) suggesting an alpha-helical structure that may play a  
CC role in covalently localising these proteins to a specific site  
CC within the cells, which may be necessary for function. A method  
CC for producing KDS polypeptides in host cells is provided. Since  
CC KDS molecules have kinase activity, they are useful as modulating  
CC agents in regulating a variety of cellular processes such as signal  
CC transduction pathways. These pathways may regulate cytoskeleton  
CC secretion, growth, apoptosis, superoxide generation, and specific  
CC gene transcription. KDS polypeptides and polynucleotides can be  
CC used for treating disorders involving aberrant expression of  
CC mammalian KDS genes. They can also be used for detection,  
CC diagnosis and drug screening.

CC Sequence 758 AA:

Query Match 97.8%; Score 1396; DB 20; Length 758;  
Best Local Similarity 97.8%; Pred. No. 3.2e-139;  
Matches 265; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 VAELEFKDPEKLFSDLRREIGHSGFAGVYFARDVRNSEVVAIKMYSKQSKNEKMODII 60  
DB 15 VAELEFKDPEKLFSDLRREIGHSGFAGVYFARDVRNSEVVAIKMYSKQSKNEKMODII 74  
QY 61 KEVRFLOKLRHPNTIOYRCYLRREHTAMLVMEYCLGSASDLEVHKRPQVEVIAVTHG 120  
DB 75 KEVRFLOKLRHPNTIOYRCYLRREHTAMLVMEYCLGSASDLEVHKRPQVEVIAVTHG 134  
QY 121 ALQGLAYLHSHMIRHDVAKAGNLLSEPGVLKIDFGSASIMAPANSFVGTPLYMAPEVI 180  
DB 135 AVQGLAYLHSHMIRHDVAKAGNLLSEPGVLKIDFGSASIMAPANSFVGTPLYMAPEVI 194  
QY 181 LAMDEQGYGKVDVMSLGTTCIELEAKRPPLFNMANMSALYHIAQNESPVLOSNGHSEYF 240  
DB 195 LAMDEQGYGKVDVMSLGTTCIELEAKRPPLFNMANMSALYHIAQNESPVLOSNGHSEYF 254  
QY 241 RNFVDSCLQKIPDRPTSEVLKHKRFVLRER 271  
DB 255 RNFVDSCLQKIPDRPTSEVLKHKRFVLRER 285

RESULT 5

AA49896  
ID AAY49896 standard; Protein; 1001 AA.

AC AAY49896;

DT 27-JAN-2000 (first entry)

DE Rat TAO1 kinase.

KM TAO1; TAO2; MEK3; mitogen activated protein kinase; phosphorylation;  
KM p38; protein kinase; cancer; inflammation; autoimmune disease;  
KM degeneration; insulin-resistant diabetes; metabolic disorder;  
KM neurodegeneration; MAP kinase; MAP/ERK kinase.

OS Rattus sp.

PN WO9953076-A1.

PD 21-OCT-1999.

PF 14-APR-1999; 99WO-US08165.

PR 14-APR-1998; 98US-0060410.

PA (TEXA ) UNIV TEXAS SYSTEM.

PI Cobb M, Hutchison M, Chen Z, Berman K;

XX WPI; 1999-633831/54.

DR N-PSDB; AA232435.

XX New polypeptides that phosphorylate kinase, used to screen for  
PT modulators for treating e.g. cancer or inflammation -

PS Claim 1; Fig 1; 95pp; English.

XX The present sequence represents rat TAO1 protein kinase, which is capable  
CC of phosphorylating MEK3 (a MAP/ERK kinase). TAO kinases, and related  
CC polypeptides, are used to screen for modulators of stress-responsive  
CC mitogen activated protein (MAP) kinase pathways. These modulators are  
CC potentially useful for treating or preventing (1) inflammation,  
CC autoimmune disease, cancer and degeneration (inhibitors of  
CC phosphorylation); or (2) insulin-resistant diabetes, metabolic disorders  
CC and neurodegeneration (enhancers of phosphorylation). TAO kinases are  
CC also used to raise specific antibodies, useful therapeutically as  
CC modulators and as immunoassay reagents for detecting TAO kinases.  
CC TAO kinase polynucleotides can be used: (a) for recombinant expression  
CC of TAO kinases; and (b) in the form of fragments, for detecting TAO  
CC kinase polynucleotides in standard hybridisation and amplification  
CC tests. TAO kinases are highly specific for MEK3.

XX Sequence 1001 AA:

Query Match 92.2%; Score 1316; DB 20; Length 1001;  
Best Local Similarity 89.7%; Pred. No. 1.5e-130;  
Matches 243; Conservative 17; Mismatches 11; Indels 0; Gaps 0;

QY 1 VAELEFKDPEKLFSDLRREIGHSGFAGVYFARDVRNSEVVAIKMYSKQSKNEKMODII 60  
DB 15 IAELEFKDPEKLFSDLRREIGHSGFAGVYFARDVRNSEVVAIKMYSKQSKNEKMODII 74  
QY 61 KEVRFLOKLRHPNTIOYRCYLRREHTAMLVMEYCLGSASDLEVHKRPQVEVIAVTHG 120  
DB 75 KEVRFLOKLRHPNTIOYRCYLRREHTAMLVMEYCLGSASDLEVHKRPQVEVIAVTHG 134  
QY 121 ALQGLAYLHSHMIRHDVAKAGNLLSEPGVLKIDFGSASIMAPANSFVGTPLYMAPEVI 180  
DB 135 ALQGLAYLHSHMIRHDVAKAGNLLSEPGVQLADFGSASIMAPANSFVGTPLYMAPEVI 194  
QY 181 LAMDEQGYGKVDVMSLGTTCIELEAKRPPLFNMANMSALYHIAQNESPVLOSNGHSEYF 240  
DB 195 LAMDEQGYGKVDVMSLGTTCIELEAKRPPLFNMANMSALYHIAQNESPVLOSNGHSEYF 254  
QY 241 RNFVDSCLQKIPDRPTSEVLKHKRFVLRER 271  
DB 255 RNFVDSCLQKIPDRPTSEVLKHKRFVLRER 285

RESULT 6

AA55942  
ID AAY55942 standard; Peptide; 1001 AA.

AC AAY55942;

DT 18-FEB-2000 (first entry)

DE Human/Murine SUTU3 consensus protein sequence.

KM Antirheumatic; antiarthritic; antiinflammatory; antiallergic; osteopathic;  
KM antipsoriatic; antiarteriosclerotic; antiasthmatic; immunosuppressive;  
KM neuroprotective; cardiact; cerebroprotective; cytoskeletal; antidiabetic;  
KM vulnery; STE20; protein kinase; STUK2; STUK3; STUK4; STUK5; STUK6; STUK7;  
KM ZC1; ZC2; ZC3; ZC4; KHS2; SUTU3; GEX2; PAK4; PAK5; antagonist;  
KM antibody; gene therapy; rheumatoid arthritis; atherosclerosis; asthma;  
KM inflammatory bowel disease; Crohn's disease; osteoarthritis; psoriasis;  
KM rhinitis; autoimmunity; organ transplantation; multiple sclerosis;  
KM myocardial infarction; cardiovascular disease; stroke; renal failure;  
KM oxidative stress-related neurodegenerative disorder; Parkinson's disease;  
KM amyotrophic lateral sclerosis; Leigh syndrome; cancer; cardiomyopathy;  
KM ischemic disorder; inflammation; diabetes mellitus; fibrosis; mitosis;  
KM mesangial disorder; growth regulation; wound healing; T cell activation;  
KM immunosuppressant.

```
XX Homo sapiens.
OS Mus sp.
XX MO9953036-A2.
XX 21-OCT-1999.
XX
XX 13-APR-1999; 99MO-US08150.
XX
XX 14-APR-1998; 98US-0081784.
XX
XX (SUGC-) SUGEN INC.
XX
XX Plowman G, Martinez R, Whyte D;
XX WPI; 1999-611301/52.
XX
XX Novel kinase-related polypeptides used for the diagnosis and treatment
XX of kinase-related diseases and disorders -
XX
XX Claim 11; Page 312-315; 387pp; English.
XX
XX This sequence represents a consensus peptide sequence contained in novel
XX STE20-related protein kinases. The invention relates to a nucleic acid
XX molecule encoding a kinase polypeptide selected from SULK2, SULK3, SULK4,
XX STIK5, STIK6, STIK7, ZC1, ZC2, ZC3, ZC4, KHS2, SULU1, SULU3, GSK2, PAK4,
XX and PAK5. The proteins are used to identify agonists and antagonists, and
XX to raise antibodies. The polynucleotides are useful in gene therapy
XX protocols. The polynucleotides, polypeptides, antibodies, antagonists and
XX agonists may be used to treat diseases such as immune-related disorders
XX and diseases (e.g. rheumatoid arthritis, atherosclerosis, chronic
XX inflammatory bowel disease (e.g. Crohn's disease), asthma,
XX osteoarthritis, psoriasis, atherosclerosis, rhinitis, autoimmunity,
XX and organ transplantation, chronic inflammatory pelvic disease, multiple
XX sclerosis, organ transplantation, myocardial infarction, cardiovascular
XX disease, stroke, renal failure, oxidative stress-related
XX neurodegenerative disorders (e.g. amyotrophic lateral sclerosis,
XX Parkinson's disease and Leigh syndrome), cancer, cardiomyopathies,
XX ischemic disorders, inflammatory disorders, diabetes mellitus, fibrotic
XX and mesangial disorders. The proteins may also be useful for cell growth
XX regulation (e.g. in wound healing), T cell activation, mitosis control,
XX and as immunosuppressants.
XX
XX Sequence 1001 AA:
SQ
Query Match 92.0%; Score 1314; DB 20; Length 1001;
Best Local Similarity 89.7%; Pred. No. 2.5e-130;
Matches 243; Conservative 17; Mismatches 11; Indels 0; Gaps 0;
QY 1 VALLFFKDEDEKLFSDREIGHSGFGAVYFARDVRNSEVVAIKMSYSGKOSNEKWDII 60
Db 15 IALLFFKDEDEKLFSDREIGHSGFGAVYFARDVRNSEVVAIKMSYSGKOSTEKWDII 74
QY 61 KEVFLQKLRHPNTIOYRGCYLREHTAMLVMEYCLGSASDLEVHKRPLOEVEIAATHG 120
Db 75 KEVFLQRIKHPNSIEYKGCYLREHTAMLVMEYCLGSASDLEVHKRPLOEVEIAATHG 134
QY 121 ALQGLAYLHSHNTHRDYKAGNILLSEPGYVKLGDFGSASIMAPANSFVTPYMAAEVIT 180
Db 135 ALQGLAYLHSHNTHRDYKAGNILLSEPGYVKLGDFGSASIMAPANSFVTPYMAAEVIT 194
QY 181 LAMDEGQYDKVYVWSIGITCIELAEKRPPLFNNMNASALYHTAQNNSPTLQSNEMSDYF 240
Db 195 LAMDEGQYDKVYVWSIGITCIELAEKRPPLFNNMNASALYHTAQNNSPTLQSNEMSDYF 254
QY 241 RNFVDSCLQKIPQDRPTSEVLLKHFVLRER 271
Db 255 RNFVDSCLQKIPQDRPTSEVLLKHFVLRER 285
```

```
XX Homo sapiens.
OS Mus sp.
XX MO9953036-A2.
XX 21-OCT-1999.
XX
XX 13-APR-1999; 99MO-US08150.
XX
XX 14-APR-1998; 98US-0081784.
XX
XX (SUGC-) SUGEN INC.
XX
XX Plowman G, Martinez R, Whyte D;
XX WPI; 1999-611301/52.
XX
XX Novel kinase-related polypeptides used for the diagnosis and treatment
XX of kinase-related diseases and disorders -
XX
XX Claim 11; Page 312-315; 387pp; English.
XX
XX This sequence represents a consensus peptide sequence contained in novel
XX STE20-related protein kinases. The invention relates to a nucleic acid
XX molecule encoding a kinase polypeptide selected from SULK2, SULK3, SULK4,
XX STIK5, STIK6, STIK7, ZC1, ZC2, ZC3, ZC4, KHS2, SULU1, SULU3, GSK2, PAK4,
XX and PAK5. The proteins are used to identify agonists and antagonists, and
XX to raise antibodies. The polynucleotides are useful in gene therapy
XX protocols. The polynucleotides, polypeptides, antibodies, antagonists and
XX agonists may be used to treat diseases such as immune-related disorders
XX and diseases (e.g. rheumatoid arthritis, atherosclerosis, chronic
XX inflammatory bowel disease (e.g. Crohn's disease), asthma,
XX osteoarthritis, psoriasis, atherosclerosis, rhinitis, autoimmunity,
XX and organ transplantation, chronic inflammatory pelvic disease, multiple
XX sclerosis, organ transplantation, myocardial infarction, cardiovascular
XX disease, stroke, renal failure, oxidative stress-related
XX neurodegenerative disorders (e.g. amyotrophic lateral sclerosis,
XX Parkinson's disease and Leigh syndrome), cancer, cardiomyopathies,
XX ischemic disorders, inflammatory disorders, diabetes mellitus, fibrotic
XX and mesangial disorders. The proteins may also be useful for cell growth
XX regulation (e.g. in wound healing), T cell activation, mitosis control,
XX and as immunosuppressants.
XX
XX Sequence 1001 AA:
SQ
Query Match 92.0%; Score 1314; DB 20; Length 1001;
Best Local Similarity 89.7%; Pred. No. 2.5e-130;
Matches 243; Conservative 17; Mismatches 11; Indels 0; Gaps 0;
QY 1 VALLFFKDEDEKLFSDREIGHSGFGAVYFARDVRNSEVVAIKMSYSGKOSNEKWDII 60
Db 15 IALLFFKDEDEKLFSDREIGHSGFGAVYFARDVRNSEVVAIKMSYSGKOSTEKWDII 74
QY 61 KEVFLQKLRHPNTIOYRGCYLREHTAMLVMEYCLGSASDLEVHKRPLOEVEIAATHG 120
Db 75 KEVFLQRIKHPNSIEYKGCYLREHTAMLVMEYCLGSASDLEVHKRPLOEVEIAATHG 134
QY 121 ALQGLAYLHSHNTHRDYKAGNILLSEPGYVKLGDFGSASIMAPANSFVTPYMAAEVIT 180
Db 135 ALQGLAYLHSHNTHRDYKAGNILLSEPGYVKLGDFGSASIMAPANSFVTPYMAAEVIT 194
QY 181 LAMDEGQYDKVYVWSIGITCIELAEKRPPLFNNMNASALYHTAQNNSPTLQSNEMSDYF 240
Db 195 LAMDEGQYDKVYVWSIGITCIELAEKRPPLFNNMNASALYHTAQNNSPTLQSNEMSDYF 254
QY 241 RNFVDSCLQKIPQDRPTSEVLLKHFVLRER 271
Db 255 RNFVDSCLQKIPQDRPTSEVLLKHFVLRER 285
```

```
ID ABB97326 standard; Protein; 1001 AA.
XX
XX ABB97326;
XX
XX 27-JUN-2002 (first entry)
XX
XX Novel human protein SEQ ID NO: 594.
XX
XX Human; anti-naemic; vulnerary; anti-inflammatory; immunomodulator;
XX antifertility; cerebroprotective; cytosstatic; rheumatic; gene therapy;
XX neuroprotective; anti-parkinsonian; protein therapy; EST;
XX expressed sequence tag.
XX
XX Homo sapiens.
XX
XX WO200222660-A2.
XX
XX 21-MAR-2002.
XX
XX 10-SEP-2001; 2001MO-US26015.
XX
XX 11-SEP-2000; 2000US-0659671.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Zhou P, Asundi V, Zhang J, Zhao QA, Ren F;
XX Xue AJ, Yang Y, Wehman T, Drmanac RT;
XX WPI; 2002-292408/33.
XX N-PSDB; ABB97326.
XX
XX An isolated polynucleotide for treating diseases associated with its
XX encoded polypeptide such as cancer and multiple sclerosis -
XX
XX Example 2; SEQ ID NO 594; 509pp; English.
XX
XX The present invention provides the protein and coding sequences of 444
XX novel human proteins. These were isolated from expressed sequences tags
XX (ESTs). They can be used to stimulate cell growth, to regulate
XX haematopoiesis e.g. to treat aplastic anaemia, to help tissue regrowth
XX e.g. in burn treatment, to regulate the immune system e.g. to treat
XX multiple sclerosis, to regulate activin or inhibin e.g. to treat
XX infertility, to regulate haemostasis or thrombolysis e.g. to treat
XX stroke and cancer, to screen for drugs, to treat inflammatory conditions
XX e.g. rheumatoid arthritis, and to treat nervous system disorders e.g.
XX Parkinson's disease. The present sequence is a protein of the invention.
XX
XX Sequence 1001 AA:
SQ
Query Match 92.0%; Score 1314; DB 23; Length 1001;
Best Local Similarity 89.7%; Pred. No. 2.5e-130;
Matches 243; Conservative 17; Mismatches 11; Indels 0; Gaps 0;
QY 1 VALLFFKDEDEKLFSDREIGHSGFGAVYFARDVRNSEVVAIKMSYSGKOSNEKWDII 60
Db 15 IALLFFKDEDEKLFSDREIGHSGFGAVYFARDVRNSEVVAIKMSYSGKOSTEKWDII 74
QY 61 KEVFLQKLRHPNTIOYRGCYLREHTAMLVMEYCLGSASDLEVHKRPLOEVEIAATHG 120
Db 75 KEVFLQRIKHPNSIEYKGCYLREHTAMLVMEYCLGSASDLEVHKRPLOEVEIAATHG 134
QY 121 ALQGLAYLHSHNTHRDYKAGNILLSEPGYVKLGDFGSASIMAPANSFVTPYMAAEVIT 180
Db 135 ALQGLAYLHSHNTHRDYKAGNILLSEPGYVKLGDFGSASIMAPANSFVTPYMAAEVIT 194
QY 181 LAMDEGQYDKVYVWSIGITCIELAEKRPPLFNNMNASALYHTAQNNSPTLQSNEMSDYF 240
Db 195 LAMDEGQYDKVYVWSIGITCIELAEKRPPLFNNMNASALYHTAQNNSPTLQSNEMSDYF 254
QY 241 RNFVDSCLQKIPQDRPTSEVLLKHFVLRER 271
Db 255 RNFVDSCLQKIPQDRPTSEVLLKHFVLRER 285
```

RESULT 8  
AAV55938  
ID AAV55938 standard; Protein: 748 AA.  
XX  
AC AAV55938;  
XX  
DT 18-FEB-2000 (first entry)  
XX  
DE Murine SULU3 protein.  
XX  
KW Antirheumatic; antiarthritic; antiinflammatory; antiallergic; osteopathic;  
KW antipsoriatic; antiarteriosclerotic; antiasthmatic; immunosuppressive;  
KW neuroprotective; cardiact; cerebroprotective; cytosstatic; antidiabetic;  
KW vulnery; SRE20; protein kinase; STK4; STK3; STK4; STK5; STK6; STK7;  
KW ZC1; ZC2; ZC3; ZC4; KHS2; SULU1; SULU3; GSK2; PAK4; PAK5; antagonist;  
KW antibody; gene therapy; rheumatoid arthritis; atherosclerosis; asthma;  
KW inflammatory bowel disease; Crohn's disease; osteoarthritis; psoriasis;  
KW rhinitis; autoimmunity; organ transplantation; multiple sclerosis;  
KW myocardial infarction; cardiovascular disease; stroke; renal failure;  
KW oxidative stress-related neurodegenerative disorder; Parkinson's disease;  
KW amyotrophic lateral sclerosis; Leigh syndrome; cancer; cardiomyopathy;  
KW ischemic disorder; inflammation; diabetes mellitus; fibrosis; mitosis;  
KW mesangial disorder; growth regulation; wound healing; T cell activation;  
KW immunosuppressant.  
XX  
OS Mus sp.  
XX  
PN WO9953036-A2.  
XX  
PD 21-OCT-1999.  
XX  
PF 13-APR-1999; 99WO-US08150.  
XX  
PR 14-APR-1998; 98US-0081784.  
XX  
PA (SUGB-) SUGEN INC.  
XX  
PI Plowman G, Martinez R, Whyte D;  
XX  
DR WPI: 1999-611301/52.  
XX  
DR N-PSDB: AAV40490.  
XX  
PT Novel kinase-related polypeptides used for the diagnosis and treatment  
XX of kinase-related diseases and disorders -  
XX  
PS Claim 11; Page 299-301; 387pp; English.  
XX  
CC This sequence represents a novel SRE20-related protein kinase. The  
CC invention relates to nucleic acid molecule encoding a kinase polypeptide  
CC selected from STK2, STK3, STK4, STK5, STK6, STK7, ZC1, ZC2, ZC3,  
CC ZC4, KHS2, SULU1, SULU3, GSK2, PAK4 and PAK5. The proteins are used to  
CC identify agonists and antagonists, and to raise antibodies. The  
CC polynucleotides are useful in gene therapy protocols. The polynucleotides,  
CC polypeptides, antibodies, antagonists and agonists may be used to treat  
CC diseases such as immune-related disorders and diseases (e.g. rheumatoid  
CC arthritis, atherosclerosis, chronic inflammatory bowel disease (e.g.  
CC Crohn's disease), asthma, osteoarthritis, psoriasis, atherosclerosis,  
CC rhinitis, autoimmunity, and organ transplantation, chronic inflammatory  
CC pelvic disease, multiple sclerosis, organ transplantation, myocardial  
CC infarction, cardiovascular disease, stroke, renal failure, oxidative  
CC stress-related neurodegenerative disorders (e.g. amyotrophic lateral  
CC sclerosis, Parkinson's disease and Leigh syndrome), cancer,  
CC cardiomyopathies, ischemic disorders, inflammatory disorders, diabetes  
CC mellitus, fibrotic and mesangial disorders. The proteins may also be  
CC useful for cell growth regulation (e.g. in wound healing), T cell  
CC activation, mitosis control, and as immunosuppressants.  
XX  
SQ Sequence 748 AA:

Query Match 87.8%; Score 1254; DB 20; Length 748;  
Best Local Similarity 87.1%; Pred. No. 3.9e-124;  
Matches 236; Conservative 16; Mismatches 11; Indels 8; Gaps 1;

QY 1 VAELEFFKDDPEKLFSDLEIGHGSGFCAVYFARDVRNSEVAIAIKMSYSGKOSNEKMODII 60  
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 15 IAELEFFKDEPEKLFDTLREIGHGSGFCAVYFARDVRNEVAIAIKMSYSGKOSNEKMODII 74  
QY 61 KEVRFLOKLRHPNTIOYRCGYLREHFAWLVMEXYCLGASADLLEVHKPLQVEVIAATFHG 120  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 75 KEVRFLOKLRHPNTIOYRCGYLREHFAWLVMEXYCLGASADLLEVHKPLQVEVIAATFHG 134  
QY 121 ALQGLAVLHSHNMIHRDVAGNITLSEPGLYKIGDGSASIMAPSPGTPVMAPEVI 180  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 135 ALQGLAVLHSHNMIHRDVAGNITLSEPGLYKIGDGSASIMAPSPGTPVMAPEVI 194  
QY 181 LAMDEQGYGKVDVWSLGTICIELAEKRPFLFNNMMSALYHIAONEPALOSGHSEYF 240  
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||  
Db 195 LAMDEQGYGKVDVWSLGTICIELAEKRPFLFNNMMSALYHIAONEPALOSGHSEYF 247  
QY 241 RNFVDSCLKIPQDRPTSEVLLKHFVLRER 271  
| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 248 -NMNDSCLKIPQDRPTSEVLLKHFVLRER 277  
RESULT 9  
AAB43191  
ID AAB43191 standard; Protein: 899 AA.  
XX  
XX AAB43191;  
XX  
DT 08-FEB-2001 (first entry)  
XX  
DE Human ORFX ORF2955 polypeptide sequence SEQ ID NO:5910.  
XX  
XX  
KW Human: open reading frame; ORFX: detection; cytosstatic; hepatotropic;  
KW vulnery; antipsoriatic; antiparkinsonian; nocrotropic; neuroprotective;  
KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiact;  
KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;  
KW hypotensive; dermatological; immunosuppressive; antiinflammatory;  
KW antiviral; antibacterial; antifungal; antineumatic; antihypoid;  
KW antinaemic; gene therapy; cancer; proliferative disorder; hypertension;  
KW neurodegenerative disorder; osteoarthritis; graft vs host disease;  
KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;  
KW cholesterol ester storage; systemic lupus erythematosus; infection;  
KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;  
KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;  
KW bone damage; cartilage damage; antiinflammatory disease; coagulation;  
KW thrombosis; contraceptive.  
XX  
OS Homo sapiens.  
XX  
XX  
PN WO200058473-A2.  
XX  
PD 05-OCT-2000.  
XX  
PF 31-MAR-2000; 2000WO-US08621.  
XX  
PR 31-MAR-1999; 99US-0127607.  
XX  
PR 02-APR-1999; 99US-0127636.  
XX  
PR 05-APR-1999; 99US-0127728.  
XX  
PR 30-MAR-2000; 2000US-0540763.  
XX  
PA (CURA-) CURAGEN CORP.  
XX  
PI Shinkets RA, Leach M;  
XX  
DR WPI: 2000-602362/57.  
XX  
DR N-PSDB: AAC77400.  
XX  
PT Novel nucleic acids and peptides derived from open reading frame X,  
XX useful for treating e.g. cancers, proliferative disorders,  
XX neurodegenerative disorders and cardiovascular disease -  
XX  
PS Claim 11; Page 5088-5090; 5507pp; English.



[illegible]

Query Match	84.2%;	Score 1203;	DB 21;	Length 898;
Best Local Similarity	81.2%;	Pred. No. 1.4e-118;		
Matches 220;	Conservative 28;	Mismatches 23;	Indels 0;	Gaps 0
QY	1	VALFLPKDPEKLEFSDLRFTGHGSGFAYVFARDVRNSEVYAIKKMSYSGKOSNEKKMODII	60	
DB	11	INDLSKDPDEELFTGLHETIGHGSGFAYVFATYAAHSEVYAIKKMSYSGKOTHEKKMODII	70	
QY	61	KEVFLQKLRHPNTIORYGCVYLREHTAWLYMEYCLGSASDLLEVHKKRPLQDEVETAAVTHG	120	
DB	71	KEVFLQKLRHPNTIERYKGVLYKEHTAWLYMEYCLGSASDLLEVHKKRPLQDEVETAAVTHG	130	
QY	121	ALQGLAYLHSHNKHNDVYKAGNILLSEPGLYKIGDRGSGASIMAPANSFVGTPIYMAPEVI	180	
DB	131	ALHGLAYLHSHALIHNDIRAGNILLTEPGQVYKLADGSGASMASPANSFVGTPIYMAPEVI	190	
QY	181	LAMDGOYGVKDVWSLGTCTICELARKKPPLFPMNMSALYHIAONSPALQSHWSEYF	240	
DB	191	LAMDGOYGVKDVWSLGTCTICELARKKPPLFPMNMSALYHIAONSPALQSHWSEYF	250	
QY	241	RNFVDSCLQIKIPQDRPTSEVLLKHFRELRER	271	
DB	251	RNFVDSCLQIKIPQDRPTSEVLLKHFRELRER	281	
RESULT 12				
AAV55936				
ID	AAV55936	standard; Protein; 898 AA.		
AC	AAV55936;			
XX				
DT	18-FEB-2000	(first entry)		
XX				
DE	Human SUVU1 protein.			
XX				
KW	Antirheumatic; antiarthritic; antiinflammatory; antiallergic; osteopathic;			
KW	antipsoriatic; antiarteriosclerotic; antiasthmatic; immunosuppressive;			
KW	neuroprotective; cardiac; cerebroprotective; cytostatic; antidiabetic;			



Db 134 VLSGLSTLHSLGRIRHDIKAGNILLTDNGVKLADEGSAICNPANSEVGTYYMAPEVI 193  
QY 181 IAMDGGQYDGKVDVMSIGITTCIEIAERKPPLEFNMAALYHIAONESPALOSGHMSEYF 240  
Db 194 IAMDGGQYDGKVDVMSIGITTCIEIAERKPPYFNMAALYHIAONESPTLRKNMDSAF 253  
QY 241 RNFVDSCLQIKIDRPTSEVLKHFVLRER 271  
Db 254 CSFEVLCILKKMPAERPSAKLLTHAVTRPR 284  
RESULT 14  
AAU87114  
ID AAU87114 standard; Protein: 323 AA.  
XX  
AC AAU87114;  
XX  
DT 05-JUN-2002 (first entry)  
XX  
DE Novel central nervous system protein #24.  
XX  
KW Central nervous system; CNS; autoimmune disease; rheumatoid arthritis;  
KW hyperproliferative disorder; neoplasm; cardiovascular disorder;  
KW cardiac arrest; cerebrovascular disorder; ischemia; angiogenesis;  
KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;  
KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;  
KW adenocarcinoma; reproductive system disorder; testicular feminisation;  
KW endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;  
KW respiratory disorder; renal disorder; kidney failure; blood disorder;  
KW myocardial infarction; wound healing; cell proliferation; skin aging;  
KW food additive; food preservative; gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN WO20015318-A2.  
XX  
PD 02-AUG-2001.  
XX  
PF 17-JAN-2001; 2001WO-US01332.  
XX  
PR 31-JAN-2000; 2000US-0179065.  
PR 04-FEB-2000; 2000US-0180628.  
PR 24-FEB-2000; 2000US-0184664.  
PR 02-MAR-2000; 2000US-0186350.  
PR 16-MAR-2000; 2000US-0189874.  
PR 17-MAR-2000; 2000US-0190076.  
PR 18-APR-2000; 2000US-0198123.  
PR 19-MAY-2000; 2000US-020515.  
PR 07-JUN-2000; 2000US-0209467.  
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XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Rosen CA, Barash SC, Ruben SM;  
PI WPI; 2001-581633/65.  
DR N-PSDB; ABR43444.  
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XX New isolated nucleic acid encoding a protein for diagnosing,  
PT preventing, treating or ameliorating medical conditions and used as  
PT food additives or preservatives -  
XX  
XX  
PS Claim 9; SEQ ID NO 632; 837pp; English.  
XX  
XX The invention describes an isolated nucleic acid molecule (I) encoding a  
CC novel central nervous system protein. (I) and polypeptides (II) encoded  
CC by (I), are used to treat a medical conditions and in diagnosis of a  
CC pathological condition. Disorders which are diagnosed or treated include  
CC autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative  
CC disorders e.g. neoplasms of the breast or liver, cardiovascular disorders  
CC e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,  
CC angiodenesis, nervous system disorders e.g. Alzheimer's disease and  
CC amyotrophic lateral sclerosis, infections caused by bacteria, viruses  
CC e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders  
CC e.g. corneal infection, gastrointestinal disorders e.g. dysphagia,  
CC adenocarcinomas and irritable bowel syndrome, reproductive system  
CC disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes  
CC and pituitary dwarfism, cancers and disorders at the cellular level e.g.  
CC leukaemia, disorders involving neovascularisation e.g. malignancies,  
CC respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g.  
CC acute kidney failure and blood related disorders e.g. myocardial  
CC infarction. The polypeptides can also be used to aid wound healing and  
CC epithelial cell proliferation, to prevent skin aging due to sunburn, to  
CC maintain organs before transplantation, for supporting cell culture of  
CC primary tissues, to regenerate tissues and in Chemotaxis. The  
CC polypeptides can also be used as a food additive or preservative to  
CC increase or decrease storage capabilities, fat content, lipid, protein,

Query Match 70.9%; Score 1012; DB 22; Length 323;  
Best Local Similarity 89.9%; Pred. No. 6.3e-99;  
Matches 186; Conservative 12; Mismatches 9; Indels 0; Gaps 0;

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DB 1 FLQRIKHPNISTEYKGGYLTREHTAMLVMEYCLGSASDLLEVNKKRPLQEVETIAVTGHALQG 60  
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DB 61 LAYLSHTMTIHRDIKAGNLTLLTEPGCVKLADGSGASMAPANSFVGTPTVMAPEVILLAD 120  
QY 185 EGYDQKVDVWSLGTICIELAEKRPPLFMNMMASALYHIAONSSPALQSGHSEYFRNFV 244  
DB 121 EGYDQKVDVWSLGTICIELAEKRPPLFMNMMASALYHIAONSSPALQSGHSEYFRNFV 180  
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DT 05-JUN-2002 (first entry)  
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KW hyperproliferative disorder; neoplasm; cardiovascular disorder;  
KW cardiac arrest; cerebrovascular disorder; ischaemia; angiodenesis;  
KW nervous system disorder; Alzheimer's disease; AIDS; ocular disorder;  
KW acquired immunodeficiency virus; dysphagia; gastrointestinal disorder;  
KW adenocarcinoma; reproductive system disorder; testicular feminisation;  
KW endocrine disorder; diabetes; cancer; leukaemia; neovascularisation;  
KW respiratory disorder; renal disorder; kidney failure; blood disorder;  
KW myocardial infarction; wound healing; cell proliferation; skin aging;  
KW food additive; food preservative; gene therapy.  
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PN WO200155318-A2.  
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(HUMA-) HUMAN GENOME SCI INC.  
PA  
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N-PSDB; ABR43765.  
WPI: 2001-581633/65.  
Rosen CA, Barash SC, Ruben SM;  
  
New isolated nucleic acid encoding a protein for diagnosing,  
preventing, treating or ameliorating medical conditions and used as  
food additives or preservatives -  
PI  
XX  
PS  
Clam 9; SEQ ID NO 953; 837bp; English.  
  
The invention describes an isolated nucleic acid molecule (I) encoding a  
novel central nervous system protein. (I) and polypeptides (II) encoded  
by (I), are used to treat a medical conditions and in diagnosis of a  
pathological condition. Disorders which are diagnosed or treated include  
autoimmune diseases e.g. Rheumatoid arthritis, hyperproliferative  
disorders e.g. neoplasms of the breast or liver, cardiovascular disorders  
e.g. cardiac arrest, cerebrovascular disorders e.g. cerebral ischaemia,  
angiogenesis, nervous system disorders e.g. Alzheimer's disease and  
amyotrophic lateral sclerosis, infections caused by bacteria, viruses  
e.g. Acquired immunodeficiency virus (AIDS) and fungi, ocular disorders  
e.g. corneal infection, gastrointestinal disorders e.g. dysphagia,  
adenocarcinomas and irritable bowel syndrome, reproductive system  
disorders e.g. testicular feminisation, endocrine disorders e.g. diabetes  
and pituitary dwarfism, cancers and disorders at the cellular level e.g.  
leukemia, disorders involving neovascularisation e.g. malignancies,  
respiratory disorders e.g. nonallergic rhinitis, renal disorders e.g.  
acute kidney failure and blood related disorders e.g. myocardial  
infarction. The polypeptides can also be used to aid wound healing and  
epithelial cell proliferation, to prevent skin aging due to sunburn, to  
maintain organs before transplantation, for supporting cell culture of  
primary tissues, to regenerate tissues and in chemotaxis. The  
polypeptides can also be used as a food additive or preservative to  
increase or decrease storage capabilities, fat content, lipid, protein,

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Query Match          66.2%; Score 946; DB 22; Length 265;
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QY 137 DVKAGNILLSEPLVTLGDFGSASIMAPANSFVGTPTWMAPEVILAMDEGQYDGKVDWS 196
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QY 197 LGITCIELAERKPPLEFNMNAMSALYHIAQNESPALQSGHWSSEYFRNFVDSCLQIPQDRP 256
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Db 121 LGITCIELAERKPPLEFNMNAMSALYHIAQNESPTLQSNEMSDYFRNFVDSCLQIPQDRP 180
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QY 257 TSEVLKHKRFVLRER 271
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Db 181 TSEELKHKIFXRER 195
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 Job time : 20.531 secs

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: November 22, 2002, 12:21:31 ; Search time 5.962 Seconds  
(without alignments)  
1337.406 Million cell updates/sec

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Perfect score: 1428  
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Scoring table: BLOSUM62  
Gap 10.0 , Gapext 0.5

Searched: 262574 segs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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6	584.5	40.9	431	4	US-09-152-406-3
7	584.5	40.9	431	4	US-09-468-442-5
8	568.5	39.8	426	2	US-08-852-743-2
9	568.5	39.8	426	2	US-09-211-930-4
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21	542.5	38.0	403	3	US-09-111-444-3
22	542.5	38.0	403	4	US-09-541-228-3
23	542	38.0	270	2	US-08-852-743-5
24	541	37.9	487	2	US-09-185-370-5
25	541	37.9	487	2	US-08-712-709-8
26	541	37.9	487	3	US-09-111-444-8
27	541	37.9	487	4	US-09-541-228-8

28	537.5	37.6	1360	4	US-09-393-569-2	Sequence 2, Appl1
29	505	35.4	276	2	US-08-852-743-7	Sequence 7, Appl1
30	505	35.4	276	3	US-09-185-370-7	Sequence 7, Appl1
31	487.5	34.1	272	2	US-08-852-743-6	Sequence 6, Appl1
32	487.5	34.1	272	3	US-09-185-370-6	Sequence 6, Appl1
33	487	34.1	545	2	US-08-935-760-4	Sequence 4, Appl1
34	486	34.0	268	2	US-08-852-743-3	Sequence 3, Appl1
35	486	34.0	268	3	US-09-185-370-3	Sequence 3, Appl1
36	482	33.8	544	2	US-08-114-555A-2	Sequence 2, Appl1
37	482	33.8	544	2	US-08-935-760-2	Sequence 2, Appl1
38	478	33.5	465	3	US-08-559-397A-2	Sequence 2, Appl1
39	476	33.3	544	3	US-08-559-397A-19	Sequence 19, Appl1
40	470	32.9	506	1	US-08-369-780-2	Sequence 2, Appl1
41	470	32.9	506	1	US-08-475-682-2	Sequence 2, Appl1
42	470	32.9	506	1	US-08-780-833-2	Sequence 2, Appl1
43	470	32.9	506	1	US-08-636-036-2	Sequence 2, Appl1
44	470	32.9	506	3	US-08-918-509-2	Sequence 2, Appl1
45	470	32.9	506	3	US-09-108-262-2	Sequence 2, Appl1

## ALIGNMENTS

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RESULT 1
US-09-060-410-4
; Sequence 4, Application US/09060410
; Patent No. 6165461
; GENERAL INFORMATION:
; APPLICANT: Cobb, Melanie
; APPLICANT: Hutchinson, Michele
; APPLICANT: Chen, Zhu
; APPLICANT: Bertram, Kevin
; TITLE OF INVENTION: TAO PROTEIN KINASES AND METHODS OF USE
; TITLE OF INVENTION: THEREFOR
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/060,410
; FILING DATE: 14-Apr-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Makl, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 860098.421
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 993 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-060-410-4

Query Match      100.0%; Score 1428; DB 4; Length 993;
Best local Similarity 100.0%; Pred. No. 2.1e-134;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VALLEFKDDPEKLFSDLEI...PDQRTSEVILKHFVLRER 271
Db 15 VALLEFKDDPEKLFSDLEI...PDQRTSEVILKHFVLRER 271
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QY 61 KEVRFLOKLRHPNTIOYRCGYLREHTAMLVMEYCLGSASDLLEVHKKPLOEVEIAAVTHG 120  
 DB 75 KEVRFLOKLRHPNTIOYRCGYLREHTAMLVMEYCLGSASDLLEVHKKPLOEVEIAAVTHG 134  
 QY 121 ALQGLAYLHSHNMIRHDVYAGNILLSEPGLYKLGDFGSASIMAPANSFVGTPLYMAPEVI 180  
 DB 135 ALQGLAYLHSHNMIRHDVYAGNILLSEPGLYKLGDFGSASIMAPANSFVGTPLYMAPEVI 194  
 QY 181 LAMDEGOYDGKDVVWSLIGTICIELAERKRPPLFNMNMSALYHIAQNESPALQSGHSEYF 240  
 DB 195 LAMDEGOYDGKDVVWSLIGTICIELAERKRPPLFNMNMSALYHIAQNESPALQSGHSEYF 254  
 QY 241 RNFVDSCLKIPDRPTSEVLLKHFVLRER 271  
 DB 255 RNFVDSCLKIPDRPTSEVLLKHFVLRER 285

RESULT 2  
 US-09-060-410-2  
 ; Sequence 2, Application US/09060410  
 ; Patent No. 6165461  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cobb, Melanie  
 ; APPLICANT: Hutchinson, Michele  
 ; APPLICANT: Chen, Zhu  
 ; APPLICANT: Berman, Kevin  
 ; TITLE OF INVENTION: TAO PROTEIN KINASES AND METHODS OF USE  
 ; TITLE OF INVENTION: THEREFOR  
 ; NUMBER OF SEQUENCES: 26  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: SEED AND BERRY LLP  
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue  
 ; CITY: Seattle  
 ; STATE: Washington  
 ; COUNTRY: USA  
 ; ZIP: 98104  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; OPERATING SYSTEM: IBM PC compatible  
 ; SOFTWARE: Patent Release #1.0, Version #1.30  
 ; CURRENT APPLICATION NUMBER: US/09/060,410  
 ; FILING DATE: 14-APR-1998  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Makl, David J.  
 ; REGISTRATION NUMBER: 31,392  
 ; REFERENCE/DOCKET NUMBER: 860098.421  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (206) 622-4900  
 ; TELEFAX: (206) 682-6031  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 1001 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-09-060-410-2

Query Match 92.2%; Score 1316; DB 4; Length 1001;  
 Best Local Similarity 89.7%; Pred. No. 3,6e-123;  
 Matches 243; Conservative 17; Mismatches 11; Indels 0; Gaps 0;

QY 1 VALFFKDDPEKLFSDLREIGHSGFAYVFARDVNSEVAIAIKMSYSGKOSNEKMODII 60  
 DB 15 IALFFKDDPEKLFSDLREIGHSGFAYVFARDVNSEVAIAIKMSYSGKOSNEKMODII 74  
 QY 61 KEVRFLOKLRHPNTIOYRCGYLREHTAMLVMEYCLGSASDLLEVHKKPLOEVEIAAVTHG 120  
 DB 75 KEVRFLOKLRHPNTIOYRCGYLREHTAMLVMEYCLGSASDLLEVHKKPLOEVEIAAVTHG 134

QY 121 ALQGLAYLHSHNMIRHDVYAGNILLSEPGLYKLGDFGSASIMAPANSFVGTPLYMAPEVI 180  
 DB 135 ALQGLAYLHSHNMIRHDVYAGNILLSEPGLYKLGDFGSASIMAPANSFVGTPLYMAPEVI 194  
 QY 181 LAMDEGOYDGKDVVWSLIGTICIELAERKRPPLFNMNMSALYHIAQNESPALQSGHSEYF 240  
 DB 195 LAMDEGOYDGKDVVWSLIGTICIELAERKRPPLFNMNMSALYHIAQNESPALQSGHSEYF 254  
 QY 241 RNFVDSCLKIPDRPTSEVLLKHFVLRER 271  
 DB 255 RNFVDSCLKIPDRPTSEVLLKHFVLRER 285

RESULT 3  
 US-09-060-410-17  
 ; Sequence 17, Application US/09060410  
 ; Patent No. 6165461  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Cobb, Melanie  
 ; APPLICANT: Hutchinson, Michele  
 ; APPLICANT: Chen, Zhu  
 ; APPLICANT: Berman, Kevin  
 ; TITLE OF INVENTION: TAO PROTEIN KINASES AND METHODS OF USE  
 ; TITLE OF INVENTION: THEREFOR  
 ; NUMBER OF SEQUENCES: 26  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: SEED AND BERRY LLP  
 ; STREET: 6300 Columbia Center, 701 Fifth Avenue  
 ; CITY: Seattle  
 ; STATE: Washington  
 ; COUNTRY: USA  
 ; ZIP: 98104  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; OPERATING SYSTEM: IBM PC compatible  
 ; SOFTWARE: Patent Release #1.0, Version #1.30  
 ; CURRENT APPLICATION NUMBER: US/09/060,410  
 ; FILING DATE: 14-APR-1998  
 ; CLASSIFICATION:  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Makl, David J.  
 ; REGISTRATION NUMBER: 31,392  
 ; REFERENCE/DOCKET NUMBER: 860098.421  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (206) 622-4900  
 ; TELEFAX: (206) 682-6031  
 ; INFORMATION FOR SEQ ID NO: 17:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 278 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS:  
 ; TOPOLOGY: linear  
 ; US-09-060-410-17

Query Match 59.4%; Score 848.5; DB 4; Length 278;  
 Best Local Similarity 59.6%; Pred. No. 4e-77; Indels 9; Gaps 2;  
 Matches 158; Conservative 45; Mismatches 53;

QY 1 VALFFKDDPEKLFSDLREIGHSGFAYVFARDVNSEVAIAIKMSYSGKOSNEKMODII 60  
 DB 17 IALFFKDDPEKLFSDLREIGHSGFAYVFARDVNSEVAIAIKMSYSGKOSNEKMODII 73  
 QY 61 KEVRFLOKLRHPNTIOYRCGYLREHTAMLVMEYCLGSASDLLEVHKKPLOEVEIAAVTHG 120  
 DB 74 KEVRFLOKLRHPNTIOYRCGYLREHTAMLVMEYCLGSASDLLEVHKKPLOEVEIAAVTHG 133  
 QY 121 ALQGLAYLHSHNMIRHDVYAGNILLSEPGLYKLGDFGSASIMAPANSFVGTPLYMAPEVI 180  
 DB 134 TIDALRYLHSLKRIHNDVYAGNILLSEPGLYKLGDFGSASIMAPANSFVGTPLYMAPEVI 193  
 QY 181 LAMDEGOYDGKDVVWSLIGTICIELAERKRPPLFNMNMSALYHIAQNESPALQSGHSEYF 240



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QY      242 NFVDSCLQIKPQDRPTSEVLKHFVLR 269
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Db      249 EFVEACLNKESFRPTAKELKHKFILR 276

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RESULT 7
US-09-468-442-5
; Sequence 5, Application US/09468442
; Patent No. 6300098
; GENERAL INFORMATION:
; APPLICANT: Tyrell E. No. 6300098rfs
; APPLICANT: William Craig Moore
; APPLICANT: David Shay Silberstein
; TITLE OF INVENTION: HUMAN SIGNAL TRANSDUCTION SERINE/THREONINE KINASE
; FILE REFERENCE: PHM.70296.N1
; CURRENT APPLICATION NUMBER: US/09/468,442
; CURRENT FILING DATE: 1999-12-21
; EARLIER APPLICATION NUMBER: US 09/340,993
; EARLIER FILING DATE: 1999-06-25
; EARLIER APPLICATION NUMBER: GB 9726851.0
; EARLIER FILING DATE: 1997-12-19
; EARLIER APPLICATION NUMBER: US 09/211,930
; EARLIER FILING DATE: 1998-12-15
; NUMBER OF SEQ. ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-468-442-5

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Query Match	40.9%;	Score 584.5;	DB 4;	Length 431;
Best Local Similarity	46.6%;	Pred. No. 2e-50;		
Matches 125;	Conservative 46;	Mismatches 84;	Indels 13;	Gaps 6

QY	67	OKLHNPNTIOYRGCVLSEHNTAMLEWXC--LGSASDLELVHKKPLQOEVEIAVTHGALQGL	125
Db	75	SQCSPPYTKYGGSYLKDQTKIMTMEELGGSSALDLE--PGPLDETQITILREILIKGL	132
QY	126	AYLHSHNNIHRDVAKAGNILLSEPLVRLGDFGSASIAAPA---NSFVGTGYWMAPEVIL	181
Db	133	DYLHSEKKIHRDIAKANVLLSEHEVYKLDADPGVAGQLTLDQIKNTFTVGGPFWMAPPEVI-	191
QY	182	AMDESGQTDGKAVDWSLGTICTELAEKRPPLFNMAKMSALYHIAONESPALQSGHSEYFR	241
Db	192	--KQSAVDKSKADIMSLGITAIELARGPPSESLHPMKVELFLIPANNPTE--GVYSKPLK	248
QY	242	NFVDSCLKITPDQDRPTEGVLLKHAFFVR	269
Db	249	EVEVACLNKESFRTAKELLKHAFFILR	276

RESULT 8  
US-08-852-743-2  
; Sequence 2, Application US/08852743

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1 ZIP: 02110-2804
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3 COMPUTER READABLE FORM:
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5 MEDIUM TYPE: Diskette
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7 COMPUTER: IBM Compatible
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9 OPERATING SYSTEM: Windows95
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11 SOFTWARE: FASTSEQ for Windows Version 2.0
12
13 CURRENT APPLICATION DATA:
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15 APPLICATION NUMBER: US/08/852,743
16
17 FILING DATE: 7-MAY-1997
18
19 CLASSIFICATION: 435
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21 PRIOR APPLICATION DATA:
22
23 APPLICATION NUMBER: 60/016,774
24
25 FILING DATE: 7-MAY-1996
26
27 ATTORNEY/AGENT INFORMATION:
28
29 NAME: Fraser, Janis K.
30
31 REGISTRATION NUMBER: 34,819
32
33 REFERENCE/DOCKET NUMBER: 00786/327001
34
35 TELECOMMUNICATION INFORMATION:
36
37 TELEPHONE: 617/542-5070
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39 TELEFAX: 617/542-8906
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41 TELEX: 200154
42
43 INFORMATION FOR SEQ ID NO: 2:
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45 SEQUENCE CHARACTERISTICS:
46
47 LENGTH: 426 amino acids
48
49 TYPE: amino acid
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51 TOPOLOGY: linear
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53 MOLECULE TYPE: protein
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55 FRAGMENT TYPE: Internal
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Query Match	39.8%;	Score 568.5;	DB 2;	Length 426;
Best Local Similarity	46.6%;	Pred. No. 8e-49;		
Matches 124;	Conservative 44;	Mismatches 85;	Indels 13;	Gaps 6

[illegible]

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RESULT 8
US-08-852-743-2
: Sequence 2, Application US/08852743
: Patent No. 5830699
:
GENERAL INFORMATION:
:
APPLICANT: Force, Thomas
APPLICANT: Kyriakis, John M.
APPLICANT: Pombo, Celia M.
APPLICANT: Bonventre, Joseph
: TITLE OF INVENTION: SOK-1 AND METHODS OF USE
: NUMBER OF SEQUENCES: 10
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Fish & Richardson, P.C.
: STREET: 225 Franklin Street
: CITY: Boston
: STATE: MA
: COUNTRY: US

RESULT 9
US-09-211-930-4
: Sequence 4, Application US/09211930
: Patent No. 596265
:
GENERAL INFORMATION:
:
APPLICANT: Tyrell E. No. 5962265r1s
APPLICANT: William Craig Moore
APPLICANT: David Shay Silberstein
: TITLE OF INVENTION: HUMAN SIGNAL TRANSDUCTION
: TITLE OF INVENTION: SERINE/THREONINE KINASE
: FILE REFERENCE: PHM.70296
: CURRENT APPLICATION NUMBER: US/09/211,930
: CURRENT FILING DATE: 1998-12-15
: EARLIER APPLICATION NUMBER: GB 9726851.0
: EARLIER FILING DATE: 1997-12-19
: NUMBER OF SEQ ID NOS: 14
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 4

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; LENGTH: 426
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-211-930-4

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[illegible]

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RESULT 10
US-09-340-993-4
: Sequence 4, Application US/09340993
: Patent No. 603428
: GENERAL INFORMATION:
: APPLICANT: TYRELL E. NO. 6034228r1s
: APPLICANT: William Craig Moore
: APPLICANT: David Shay Silberstein
: TITLE OF INVENTION: HUMAN SIGNAL TRANSDUCTION SERINE/THREONINE KINASE
: FILE REFERENCE: PHM.70296.N1
: CURRENT APPLICATION NUMBER: US/09/340,993
: CURRENT FILING DATE: 1999-06-25
: EARLIER APPLICATION NUMBER: GB 9726651.0 & US 09/211,930
: EARLIER FILING DATE: 1997-12-19 & 1998-12-15
: NUMBER OF SEQ ID NOS: 14
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 4
: LENGTH: 426
: TYPE: PRT
: ORGANISM: Homo sapiens
: IS-09-340-993-4

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Query Match	39.8%	Score 568.5	DB 3	Length 426
Best Local Similarity	46.6%	Pred. No. 8e-49		
Matches 124	Conservative 44	Mismatches 85	Indels 13	Gaps 6

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Db      247 VEACLNKDPRFRPTAKELLKHKFTR 272
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Query Match	39.8%	Score	568.5	DB	3	Length	426
Best Local Similarity	46.6%	Pred. No.	8e+49				
Matches	124	Conservative	44	Mismatches	85	Indels	13
						Gaps	6

[illegible]

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QY 3 DPELEFLKRLBRIGGSGGEVYKGDJNHTKEVAIKIDL--EEAEDEIDIEDIOEETVLSQ 72
Db 15 DPELEFLKRLBRIGGSGGEVYKGDJNHTKEVAIKIDL--EEAEDEIDIEDIOEETVLSQ 72
QY 69 LRHENTIOYRGCYRREHTAMLVMEYC-LGSADLLEVHKRPLOVEVLAATNGALGLAY 127
Db 73 CDSPIIRIRFGSYLKRKIMIMYLOGGSALDLK--PGRPLETTYIATITIRELTKELDY 130
QY 128 LHSINMTHRDVYKAGNIIILSEBGLVKLDFGSASIMADA---NSFVGPYVMAAEVITLAM 183
Db 131 LHSERKTHRDIKANVLLISBQGDVLDLFCVAGQGLDTQIKRNFVETPTPMMAEVIT-- 187
QY 184 DEGYDSDKVVWVMSLGTICIEIAERKRPFLPMNMAISALYHIAONESPATLOGSHSEYRNF 243
Db 188 KQSAIYDKPAIMVLSGITAIETLAKGEPNSDUIHPRKVLFLIPKNSPPLBEOH-SKPKKEF 246
QY 244 VDSCLKIIPQDRPTSEVLLKRRFVLR 269

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QY 3 DPELEFLKRLBRIGGSGGEVYKGDJNHTKEVAIKIDL--EEAEDEIDIEDIOEETVLSQ 72
Db 15 DPELEFLKRLBRIGGSGGEVYKGDJNHTKEVAIKIDL--EEAEDEIDIEDIOEETVLSQ 72
QY 69 LRHENTIOYRGCYRREHTAMLVMEYC-LGSADLLEVHKRPLOVEVLAATNGALGLAY 127
Db 73 CDSPIIRIRFGSYLKRKIMIMYLOGGSALDLK--PGRPLETTYIATITIRELTKELDY 130
QY 128 LHSINMTHRDVYKAGNIIILSEBGLVKLDFGSASIMADA---NSFVGPYVMAAEVITLAM 183
Db 131 LHSERKTHRDIKANVALLSEGGVDLDFGAGOLDTDTQIKRNFVEVTPPMMAEVI--- 187
QY 184 DEGYDCKVYVMSLGTICIEIAERKRPFLPMNMAASALYHIAONESPATLOGHSEYRNF 243
Db 188 KQSAIYDKPAIMSLGTITAIELAKGEPNSDJIHPKRVFLPIPKNSPPLBEOH-SKPKKEF 246
QY 244 VDSCLKIIPQDRPTSEVLLKRRFVLR 269

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Db 251 IDACLNKDPFSRPTAKELKHKFIYK 276

RESULT 15  
US-09-211-930-11  
; Sequence 11, Application US/09211930  
; Patent No. 5962265  
; GENERAL INFORMATION:  
; APPLICANT: Tyrell E. No. 5962265r1s  
; APPLICANT: William Craig Moore  
; APPLICANT: David Shay Silberstein  
; TITLE OF INVENTION: HUMAN SIGNAL TRANSDUCTION  
; TITLE OF INVENTION: SERINE/THREONINE KINASE  
; FILE REFERENCE: PHM 70296  
; CURRENT APPLICATION NUMBER: US/09/211,930  
; CURRENT FILING DATE: 1998-12-15  
; EARLIER APPLICATION NUMBER: GB 9726851.0  
; EARLIER FILING DATE: 1997-12-19  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 11  
; LENGTH: 416  
; TYPE: PR1  
; ORGANISM: Mus musculus  
US-09-211-930-11

Query Match 39.0%; Score 557.5; DB 2; Length 416;  
Best Local Similarity 45.1%; Pred. No. 9.7e-48;  
Matches 120; Conservative 46; Mismatches 87; Indels 13; Gaps 6;

QY 9 DPEKLSDLREIGHSGFAYFARDVNSSEVAIKKMSYSGKSNKKMODIKKEVRELQK 68  
Db 19 DPEELFTKLERIGKSGFGEYFKGIDNRTQOVAIKIIDL--EEAEDEIEDIQOEITVLSQ 76  
QY 69 LRHPNTIQYRGCYLREHTAWLVMEYC-IGSASDLEVHKKPLQEVETIAVTHGALQGLAY 127  
Db 77 CDSSTYTKYGYSLKSGSKLWIMEYLGSGSALDLRA--GPDEFOIATMLKEILKGLDY 134  
QY 128 LHSNMIHRDYKAGNILLSPGLVKLGDFGSASIMAPA---NSFVGTPYMAPEVILAM 183  
Db 135 LHSEKKIHRDIKAAVLLSEQGVKLADFGVAGQLTDTQIKRNTFVGTPYMAPEVI--- 191  
QY 184 DEGOYDGKVDVMSLGTICIELAEKRPFLFNMMASALYHIAONESPALQSGHMSVEFRNF 243  
Db 192 QQSAIYDSKADIMSLGITATLAKGEPNDSMDHPRVFLIPKNNPTL-IGDFTKSFKEF 250  
QY 244 VDSCLQKIPQDRPTSEVLLKHFVLR 269  
Db 251 IDACLNKDPFSRPTAKELKHKFIYK 276

Search completed: November 22, 2002, 12:28:09  
Job time : 9.212 secs

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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 22, 2002, 12:21:10 ; Search time 7.588 Seconds  
(without alignments)  
3433.372 Million cell updates/sec

Title: US-09-686-346a-4\_COPY\_15\_285  
Perfect score: 1428  
Sequence: 1 VAELEFKDDPEKLFSDLEI.....PODRPSEVLKHFVLRER 271

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1316	92.2	1001	2 T17365	serine/threonine p
2	883	61.8	982	2 T18576	serine-threonine k
3	631.5	44.2	836	2 B96716	probable serine/th
4	568.5	39.8	426	2 S71886	Ste20-like protein
5	539	37.7	653	2 T34356	hypothetical prote
6	527.5	36.9	829	2 T29372	hypothetical prote
7	512.5	35.9	690	2 C96572	protein F12M16.4 l
8	511	35.8	819	2 A53714	protein kinase (EC
9	510.5	35.7	1102	2 JC6316	probable protein k
10	502.5	35.2	1231	2 T18532	serine/threonine p
11	500.5	35.0	1206	2 T34021	protein kinase SK2
12	498.5	34.9	1233	2 T14157	serine/threonine p
13	498	34.9	1233	2 T30989	serine/threonine p
14	492	34.5	544	2 S40482	serine/threonine p
15	490	34.3	545	2 G01773	p21-activated prot
16	489.5	34.3	490	2 S47946	protein kinase hom
17	484	33.6	544	2 A57597	beta-p21-activated
18	480	33.6	544	2 T49376	p21 activated kina
19	476.5	33.4	312	2 T38525	serine/threonine p
20	469.5	32.9	525	2 S58682	protein kinase, p2
21	469	32.8	471	2 T39232	probable serine/th
22	450.5	31.5	1230	2 T18256	serine/threonine p
23	450.5	31.5	1230	2 T18256	serine/threonine p
24	447	31.3	1080	2 S48944	hypothetical prote
25	446	31.2	378	2 T26684	hypothetical prote
26	444	31.1	622	2 T15467	hypothetical prote
27	441.5	30.9	652	2 T39722	serine/threonine p
28	440	30.8	939	2 S28394	probable serine/th
29	439	30.7	658	2 T39500	serine/threonine-s

30	433	30.3	589	2 T38086	serine/threonine-p
31	430.5	30.1	1062	2 S46367	protein kinase CDC
32	428.5	30.0	561	2 T51417	protein kinase-lik
33	425.5	29.8	608	2 G96575	probable MEK kinas
34	425.5	29.8	1075	2 T27623	hypothetical prote
35	425.5	29.8	1080	2 T27622	hypothetical prote
36	421	29.5	658	2 T01479	protein kinase Pak
37	418.5	29.3	553	2 T01479	hypothetical prote
38	416	29.1	655	2 S51884	probable protein k
39	413	28.9	842	2 S60402	protein kinase CLA
40	409.5	28.7	883	2 A96652	hypothetical prote
41	403	28.2	710	2 T13458	hypothetical prote
42	402.5	28.2	651	2 A96591	NEK1-related prote
43	401.5	28.1	1228	2 T18897	myosin IIT - Atlan
44	399.5	28.0	1014	2 T31109	hypothetical prote
45	398	27.9	693	2 B85112	hypothetical prote

## ALIGNMENTS

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RESULT 1
T17365
serine/threonine protein kinase TA01 - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T17365
R:Hutchinson, M.; Berman, K.S.; Cobb, M.H.
J. Biol. Chem. 273, 28625-28632, 1998
A:Title: Isolation of TA01, a protein kinase that activates MEKs in stress-activated
A:Reference number: Z18730; MUID:99003202; PMID:9786855
A:Accession: T17365
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1001 <HUT>
A:Cross-references: EMBL:AF084205; NID:g3452472; PID:g3452473; PIDN:AC71014.1
A:Function:
A:Description: probably implicated in the regulation of the p38-containing stress-res
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Query Match	92.2%	Score 1316;	DB 2;	Length 1001;
Best Local Similarity	89.7%	Pred. No. 3.6e-59;		
Matches 243;	Conservative 17;	Mismatches 11;	Indels 0;	Gaps 0;

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QY 1 VAELEFKDDPEKLFSDLEIGHSGGAYVFARDVANSSEVVAIKKMSYSGKOSNEKWDII 60
DB 15 IAELEFKDDPEKLFSDLEIGHSGGAYVFARDVANSSEVVAIKKMSYSGKOSTEKWDII 74
QY 61 KEVRFLOKLRHPTTOYRGCYLREHTAMLVMEYCLGSASDLEEVKRPLOEVEIAAVTHG 120
DB 75 KEVKELQRIKHPNSEYRGCYLREHTAMLVMEYCLGSASDLEEVKRPLOEVEIAAVTHG 134
QY 121 ALQGLAYVSHNMTHRDYKAGNILLSEPGLVKLGDFGSASIMAPANSFVGTPYMAPEVI 180
DB 135 ALQGLAYVSHNMTHRDYKAGNILLSEPGLVKLGDFGSASIMAPANSFVGTPYMAPEVI 194
QY 181 LAMDGQYDGVKVDVSLITGCELAERKPLFNNAMASALYHIANESPAQSGMSYEF 240
DB 195 LAMDGQYDGVKVDVSLITGCELAERKPLFNNAMASALYHIANESPAQSGMSYEF 254
QY 241 RNFVDSCLQKIPDRPTEVLLKHFVLRER 271
DB 255 RNFVDSCLQKIPDRPTEVLLKHFVLRER 285
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RESULT 2
T18576
serine-threonine kinase - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T18576
R:Cope, M.J.T.V.; Kendrick-Jones, A.
submitted to the EMBL Data Library, July 1995
A:Reference number: Z18984
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A:Accession: F118576  
A:Status: preliminary; translated from GB/EMBL/DBD  
A:Molecule\_type: mRNA  
A:Residues: 1982 <BAR>  
A:Cross-references: EMBL:U32275; PID:AAA75370.1; GSPDB:GN00021; CESP:Su1u  
A:Experimental\_source: strain NZ Bristol  
C:Genetics:  
A:Gene: CESP:Su1u  
A:Map\_position: 3

Query Match	61.8%;	Score 883;	DB 2;	Length 982;
Best Local Similarity	58.5%;	Pred. No. 1.8e-37;		
Matches 162;	Conservative 48;	Mismatches 61;	Indels 6;	Gaps 1;

[illegible]

RESULT 3  
B96716  
Probable serine/threonine kinase F23010.20 [Imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
C:Accession: B96716  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso  
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.  
ansen, N.F.; Hughes, B.; Huizart, L.  
N:Native 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.  
A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Marziali  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719; PMID:11130712  
A:Accession: B96716  
A:Status: Preliminary  
A:Molecule type: DNA  
A:Residues: 1-836 <STO>  
A:Cross-references: GB:AE005173; NID:g7705100; PIDN:AA677779.1; GSPDB:GM00141  
C:Genetics:  
A:Gene: F23010.20  
A:Map position: 1

Query Match	44.28;	Score 631.5;	DB 2;	Length 836;
Best Local Similarity	47.28;	Pred. No. 6.1e-25;		
Matches 127; Conservative	54;	Mismatches 77;	Indels 11;	Gaps 5

[illegible][illegible]

RESULT 4  
S71886

C:Date: 29-Jan-1998 #sequence\_revision 06-Feb-1998 #text\_change 21-Jul-2000  
 C:Accession: S71886; G01022  
 R:Pombo, C.M.; Bonventure, J.V.; Molnar, A.; Kyriakis, J.; Force, T.  
 EMBO J. 15, 4537-4546, 1996  
 A:Title: Activation of a human Ste20-like kinase by oxidant stress defines a novel stress-activated pathway  
 A:Reference number: S71886; MUID:97042345; PMID:8887545  
 A:Accession: S71886  
 A:Molecule type: mRNA  
 A:Residues: 1-426 <POM>  
 A:Cross-references: EMBL:X93325; NID:g1430821; PIDN:CAA67700.1; PID:g1430822  
 A:Experimental source: cell type B cell  
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homology  
 C:Keywords: ATP; autophosphorylation; phosphotransferase; protein kinase; stress-inducible  
 I:18-270/Domain: protein kinase homology <KIN>

Query Match	39.8%	Score 568.5	DB 2	Length 426
Best Local Similarity	46.6%	Pred. No. 4.9e22		
Matches 124	Conservative 44	Mismatches 85	Indels 13	Gaps 6

[illegible]

RESULT 5  
T34356  
hypothetical protein T19A5.2 - *Caenorhabditis elegans*  
C;Species: *Caenorhabditis elegans*  
C;Date: 29-Oct-1999 #sequence  
C;Accession: T34356  
R;Bradshaw, H.

submitted to the EMBL Data Library, March 1996  
A:Description: The sequence of C. elegans cosmid T19A5.  
A:Reference number: Z21512  
A:Accession: T34356  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-653 (BBA>  
A:Cross-references: EMBL:U53153; PIDN:AAC69038.1; GSPDB:GN00023; CESP:T19A5.2  
A:Experimental source: strain Bristol N2; clone T19A5







```

QY 127 YLHSHNMHRDVKAGNILLSEPLVRLGDFG---SASIMAPANSFVGTPTWMAPEVIL- 181
      |||:|||||:|||||:|:|||||:|:|||||:|||||:|||||:|||||:|||||:
Db 145 YLHDNKHHRDLKAGNILLFTLDDIKLADPGVSAKNTRTIGRDSFICGPTWMAPEVVMC 204

QY 182 -AMDEQYDGKVDVMSLGTICIELAEKRPPLFNMMASALYHIAQNESPAL-OSGHMSEX 239
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 205 ETSKDRPYKADVMSLGTILLEMALIEPPHHELPNMRVLKIAKSEPTLAPSRSSN 264

QY 240 FRNFVDSCLQIKIPDRPTSEVLKHKRFV 267
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 265 FKDFLKKCLEKNVDARWTTSQLQHPFV 292

RESULT 12
T14157
serine/threonine protein kinase - mouse
C:Species: Mus musculus (house mouse)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T14157
R:Pykowski, B.; Hicklin, D.J.; Kornhaber, G.; Dellaratta, D.V.; Witte, L.
submitted to the EMBL Data Library, December 1997
A:Reference number: Z17894
A:Accession: T14157
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1233 <P>Y>
A:Cross-references: EMBL:AF039574; NID:q2773155; PID:q2773156; PIDN:AAB9682.1

Query Match
Best Local Similarity 34.9%; Score 498.5; DB 2; Length 1233;
Matches 107; Conservative 53; Mismatches 95; Indels 13; Gaps 6;

QY 9 DPEKLSDLREIGHSGFGAVYFARDVNSEVAIKKMSYSGKOSNEKWDIIEVRFLOK 68
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 29 NPEEFWEIIGELDGAFGKVKYKQNKETNYLAAKYID--TKSELELDYVWEIDILAS 85

QY 69 LRHPNTIYRGCTLRHTAMLVMEYCLGSASD--LLEVHKKPLQVEEIAVTHGALQGLA 126
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 86 CHRPNTYKLLDAFYENNMIILEFCAAGAVDAVLEL-ERPLTESQIOYVCKQITLALN 144

QY 127 YLHSHNMHRDVKAGNILLSEPLVRLGDFG---SASIMAPANSFVGTPTWMAPEVIL- 181
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 145 YLHDNKHHRDLKAGNILLFTLDDIKLADPGVSAKNTRTIGRDSFICGPTWMAPEVVMC 204

QY 182 -AMDEQYDGKVDVMSLGTICIELAEKRPPLFNMMASALYHIAQNESPAL-OSGHMSEX 239
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 205 ETSKDRPYKADVMSLGTILLEMALIEPPHHELPNMRVLKIAKSEPTLAPSRSSN 264

QY 240 FRNFVDSCLQIKIPDRPTSEVLKHKRFV 267
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 265 FKDFLKKCLEKNVDARWTTSQLQHPFV 292

RESULT 13
T30989
serine/threonine protein kinase NIK - mouse
N:Alternate names: Nck interacting kinase
C:Species: Mus musculus (house mouse)
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
C:Accession: T30989
R:Su, Y.C.; Han, J.; Xu, S.; Cobb, M.; Skolnik, E.Y.
EMBO J. 16, 1279-1290, 1997
A:Title: NIK is a new Ste20-related kinase that binds NCK and MEK1 and activates the SA
A:Reference number: Z20954; MUID:97280817; PMID:9135144
A:Accession: T30989
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1233 <SU>
A:Cross-references: EMBL:088984; NID:q1872545; PID:q1872546; PIDN:AAC53165.1
C:Keywords: protein kinase

Query Match 34.9%; Score 498; DB 2; Length 1233;

```

```

Best Local Similarity 42.2%; Pred. No. 4,1e-18;
Matches 116; Conservative 52; Mismatches 85; Indels 22; Gaps 10;

QY 9 DPEKLSDLREIGHSGFGAVYFARDVNSEVAIKKMSYSGKOSNEKWDIIEVRFLOK 68
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 20 DPAIEFELVEVNGTGGYGVYKGRHV-KYTAIKYMDV---TEDEEBEITLIEIMLKK 74

QY 69 L-RHPNTIYRGCTLRHTAMLVMEYCLGSASDLLEVHK-KPLQVEEIAVTH 119
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 75 YSHHRIATYGAFFIKKSPGHDDQLMVLWFEFGASITDLVANTGNTIKEMITAYISR 134

QY 120 GALQGLAYLHSHNMHRDVKAGNILLSEPLVRLGDFG-SASI---MAPANSFVGTPTWMA 175
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 135 EILRGALHLHHVHRDVGQVLLTENAEVLTVPFGVSAQIDRTYGRNTEFTGPTWMA 194

QY 176 APEVILAMDE---GQYDGKVDVMSLGTICIELAEKRPPLFNMMASALYHIAQNESPALQ 232
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 195 APEVIL-ACDENPDATYDRSDLMSCGITAEMAEGGPFLDMDHMPRALFLIPNPPRLK 253

QY 233 SGHMSEFRNFVDSCLQIKIPDRPTSEVLKHKRFV 267
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 254 SKKSKKFFSFIEGCLVKNYMQRPSTEQLKHPFI 288

RESULT 14
S40482
serine/threonine-specific protein kinase (EC 2.7.1.-) - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 17-Mar-1999
C:Accession: S40482
R:Ransier, E.; Leung, T.; Saltuddin, H.; Zhao, Z.; Lim, L.
Nature 367, 40-46, 1994
A:Title: A brain serine/threonine protein kinase activated by Cdc42 and Rac1.
A:Reference number: S40482; MUID:94150588; PMID:8107774
A:Accession: S40482
A:Molecule type: mRNA
A:Residues: 1-544 <MAN>
A:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase hom
C:Keywords: ATP; phosphotransferase; serine/threonine-specific protein kinase
F;267-520/Domain: protein kinase homology <Kin>
F;275-283/Region: protein kinase ATP-binding motif

Query Match 34.5%; Score 492; DB 2; Length 544;
Best Local Similarity 42.3%; Pred. No. 4,1e-18;
Matches 112; Conservative 47; Mismatches 92; Indels 14; Gaps 6;

QY 9 DPEKLSDLREIGHSGFGAVYFARDVNSEVAIKKMSYSGKOSNEKWDIIEVRFLOK 68
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 264 DPKKKTTRFEKIGQASGVYITAMDVATGQEVAKQKML---QQQPKKELIIEILVMRE 320

QY 69 LRHPNTIYRGCTLRHTAMLVMEYCL-GSASDLLEVHKKPLQVEEIAVTHGALQGLAY 127
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 321 NKNPNIVNYLDSTYLVGDELMVWVEYLAGGSLTDV--VTETCMDEGOIAACRCCLDALEF 378

QY 128 LHSNMHRDVKAGNILLSEPLVRLGDFGSASIMAPANS---FVGTPTWMAPEVILAM 183
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 379 LHSNOVYHRDIKSDNILLKMDGSKLTFDFEFCQITPEOSKRSTWGTPTWMAPEV--- 435

QY 184 DEQYDGKVDVMSLGTICIELAEKRPPLFNMMASALYHIAQNESPALOSGH-WSEYFRN 242
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 436 TRAYAGKVDVMSLGTILLEMALIEGEPYINENLRALYLATATGTPELQREKLSAIFRD 495

QY 243 FVDSCLQIKIPDRPTSEVLKHKRFV 267
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 496 FLNRCLEMDVEKRSKAKELLQHOFL 520

RESULT 15
G01773
p21-activated protein kinase - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 24-Sep-1999
C:Accession: G01773

```

R:Chernoff, J.  
submitted to the EMBL Data Library, April 1995  
A:Reference number: G08374  
A:Accession: G01773  
A:Status: preliminary; translated from GR/EMBL/DBD  
A:Molecule type: mRNA  
A:Residues: 1-545 <CHE>  
A:Cross-references: EMBL:U24152; NID:G780805; PIDN:AAA65441.1; PID:G780806  
C:Genetics:  
A:Gene: Pak1  
C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homology  
F:266-521/Domain: protein kinase homology <KIN>

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 22, 2002, 12:18:20 ; Search time 4.2005 Seconds

(without alignments)  
2675.892 Million cell updates/sec

Title: US-09-686-346a-4\_COPY\_15\_285

Perfect score: 1428

Sequence: 1 VALFFKDDPEKLFSDRLREI.....PDQDPTSEYLLKHFVLRER 271

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	883	61.8	982	1	SUDU_CAEEL
2	584.5	40.9	443	1	ST24_HUMAN
3	572.5	40.1	426	1	ST25_MOUSE
4	568.5	39.8	426	1	ST25_HUMAN
5	550	38.5	487	1	STK3_HUMAN
6	538	37.7	491	1	STK3_HUMAN
7	492	34.5	544	1	PAK1_RAT
8	492	34.5	545	1	PAK1_MOUSE
9	490	34.3	545	1	PAK1_HUMAN
10	489.5	34.3	490	1	SPS1_YEAST
11	487.5	34.1	968	1	ST10_HUMAN
12	486.5	34.1	966	1	ST10_MOUSE
13	484	33.9	544	1	PAK3_HUMAN
14	484	33.9	544	1	PAK3_RAT
15	480	33.6	544	1	PAK2_MOUSE
16	470	32.9	524	1	PAK2_HUMAN
17	470	32.9	524	1	PAK2_RABIT
18	470	32.9	524	1	PAK2_RAT
19	450.5	31.5	1230	1	ST20_CANAL
20	447	31.3	1080	1	NRK1_YEAST
21	440	30.8	939	1	ST20_YEAST
22	439	30.7	658	1	PAK1_SCHPO
23	433	30.3	589	1	SHK2_SCHPO
24	430.5	30.1	1062	1	CC7_SCHPO
25	430	29.1	971	1	CLA4_CANAL
26	425.5	29.8	1080	1	MIT5_CAEEL
27	416	29.1	591	1	PAK4_HUMAN
28	416	29.1	655	1	SKM1_YEAST
29	413	28.9	547	1	SPAK_HUMAN
30	413	28.9	553	1	SPAK_RAT
31	413	28.9	556	1	SPAK_MOUSE
32	413	28.9	842	1	CLA4_YEAST
33	412	28.9	719	1	PAK7_HUMAN

34	396	27.7	974	1	CC15_YEAST
35	394.5	27.6	626	1	M3K3_HUMAN
36	394	27.6	1401	1	WIS4_SCHPO
37	388.5	27.2	626	1	M3K3_MOUSE
38	382	26.8	1478	1	BCK1_YEAST
39	378.5	26.5	1501	1	NINC_DROME
40	373.5	26.2	618	1	M3K2_HUMAN
41	372.5	26.1	619	1	M3K2_MOUSE
42	347	24.3	1493	1	M3K1_RAT
43	347	24.3	1495	1	M3K1_HUMAN
44	346	24.2	1493	1	M3K1_MOUSE
45	344.5	24.1	1579	1	SSK2_YEAST

## ALIGNMENTS

```

RESULT 1
ID      SUDU_CAEEL      STANDARD:      PRT:      982 AA.
AC      P46549;
DT      01-NOV-1995 (Rel. 32, Created)
DT      01-NOV-1995 (Rel. 32, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Serine/threonine-protein kinase SUDU (EC 2.7.1.1).
GN      KIN-18 OR SUDU OR T17E9.1.
OS      Caenorhabditis elegans.
OC      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
OX      Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN-Bristol N2;
RA      Du Z.;
RL      Submitted (JUN-1994) to the EMBL/GenBank/DBJ databases.
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN-Bristol N2;
RA      Cope M.J.T.V., Kendrick-Jones A.;
RL      Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
CC      -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC      -----
DR      EMBL: U11280; AAA19437.1; -.
DR      EMBL: U32275; AAA75370.1; -.
DR      WormBep: T17E9.1; CE01405.
DR      InterPro: IPR000719; Euk_Pkinase.
DR      InterPro: IPR002290; Ser_thr_pkinase.
DR      Pfam: PF00069; pkinase.1.
DR      ProDom: PD000001; Euk_Pkinase; 1.
DR      SMART: SM00220; S_TKc; 1.
DR      PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR      PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR      PROSITE: PS00108; PROTEIN_KINASE_ST; FALSE_NG.
KW      Transferase; Serine/threonine-protein kinase; ATP-binding.
FT      DOMAIN      30      289      PROTEIN KINASE.
FT      NF_BIND      36      44      ATP (BY SIMILARITY).
FT      BINDING      59      59      ATP (BY SIMILARITY).
FT      ACT_SITE      153      153      BY SIMILARITY.
SQ      SEQUENCE      982 AA; 112870 MW; 745CE1E2FE90977D CRC64;
Query Match      61.8%; Score 883; DB 1; Length 982;
Best Local Similarity      58.5%; Pred. No. 5,3e-63;
Matches 162; Conservative 48; Mismatches 61; Indels 6; Gaps 1;
OY      1 VALFFKDDPEKLFSDRLREIGHSFGAVVFARVDNRSEVAIAIKMSYSGQSNKKQDII 60

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Cc      17 IAALESNKPEQDYDRLREIGHSGFAGVYFAYDKNEQVVALKKNFSGQAVAEKNDLL 76
Cc      61 KEVRFQKLRHPPTIQRCYLREHTAMVMEYCLASADLLEVHKPLQOEVIATVHG 120
Cc      77 KEVSFLNTVYVHHIYVYKACFLKDTQWLMVEYCISADIDYVLAKGMEVIAAICGQ 136
Cc      121 ALQGLAYLHSHNMHRDVKAGNILLSEPGVLKLGDFGASIMAPANSFVGTPTMAPEVI 180
Cc      137 TLDALRYLHSLKRIHDIKAGNILLSDHAIVKLADFGSASIVDPADQITGTFPMMAPEVI 196
Cc      181 LAMDEGOYGDYVWSLGTCTELAEKRPPLFEMNAMSALYHIAQNSPAL-----QSG 234
Cc      197 LAMDESHYTRADVMSLGTCTELAEKRPPLFEMNAMSALYHIAQNDPPLSPIDTSEQP 256
Cc      235 HMEYFRNFVDSCLQKIPQDRPTSEVLKHKRFYLRR 271
Cc      257 EWSLEFVQFDKCLRKRAEERMSAECCFRHPIQRSR 293

RESULT 2
ST24_HUMAN STANDARD: PRT: 443 AA.
AC 09Y6E0: 014840:
DT 16-OCT-2001 (rel. 40, Created)
DT 16-OCT-2001 (rel. 40, Last sequence update)
DT 16-OCT-2001 (rel. 40, Last annotation update)
DE Serine/threonine protein kinase 24 (EC 2.7.1.37) (STE20-like kinase
MS13) (MST-3) (Mammalian STE20-like protein kinase 3).
GN STRK4 OR MST3 OR STR3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORM A).
RX MEDLINE=98019249; PubMed=9353358;
RA Schinkmann K., Bliens J.;
RT "Cloning and characterization of a human STE20-like protein kinase
RT with unusual cofactor requirements.";
RL J. Biol. Chem. 272:28695-28703(1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM B), AND MUTAGENESIS OF THR-18.
RC TISSUE=Brain;
RX MEDLINE=20112812; PubMed=10644707;
RA Zhou T.-H., Lang K., Guo J., Zhou H., Wu Y.-L., Jing Q., Ma L.,
RA Pei G.;
RT "Identification of a human brain-specific isoform of mammalian
RT STE20-like kinase 3 that is regulated by cAMP-dependent protein
RT kinase.";
RL J. Biol. Chem. 275:2513-2519(2000).
Cc      -1- FUNCTION: PROTEIN KINASE THAT ACT ON BOTH SERINE AND THREONINE
Cc      RESIDUES.
Cc      -1- CATALYTIC ACTIVITY: ATP + a protein -> ADP + a phosphoprotein.
Cc      -1- COFACTOR: ISOFORM A REQUIRES MANGANESE FOR ITS ACTIVITY.
Cc      -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
Cc      -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A AND B (SHOWN HERE); ARE
Cc      PRODUCED BY ALTERNATIVE SPLICING.
Cc      -1- TISSUE SPECIFICITY: ISOFORM A IS UBIQUITOUS. ISOFORM B IS
Cc      EXPRESSED IN BRAIN WITH HIGH EXPRESSION IN HIPPOCAMPUS AND
Cc      CEREBRAL CORTEX.
Cc      -1- PTM: AUTOPHOSPHORYLATED. ISOFORM B IS ACTIVATED BY PHOSPHORYLATION
Cc      BY PKA.
Cc      -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
Cc      STE20 SUBFAMILY.
Cc      -----
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Cc      or send an email to license@sib-sib.ch).

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Cc      -----
Cc      EMBL: AF024636; AAB82560.1; -.
Cc      EMBL: AF083420; AAD42039.1; -.
Cc      HSSP: P24941; 1CRP.
Cc      Genem: HGNC:11403; STRK24.
Cc      MIM: 604984; -.
Cc      InterPro: IP000719; Euk_pkinase.
Cc      InterPro: IP002290; Ser_thr_pkinase.
Cc      InterPro: IP001245; Tyr_pkinase.
Cc      Pfam: PF000069; pkinase; 1.
Cc      PRINTS: PR00109; TYRKINASE.
Cc      ProDom: PD000001; Euk_pkinase; 1.
Cc      SMART: SM00220; S_TKc; 1.
Cc      PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
Cc      PROSITE: PS00108; PROTEIN_KINASE_ST; FALSE_NEG.
Cc      PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
Cc      Trnase: Serine/threonine-protein kinase; ATP-binding;
Cc      Phosphorylation; Alternative splicing.
Cc      DOMAIN
Cc      NP_BIND 36 286 PROTEIN KINASE.
Cc      BINDING 42 50 ATP (BY SIMILARITY).
Cc      ACT_SITE 65 65 ATP (BY SIMILARITY).
Cc      MOD_RES 156 156 BY SIMILARITY.
Cc      VARSPIC 1 26 PHOSPHORYLATION (BY PKA).
Cc      MUTAGEN 18 18 MDSRAQLMGIALAKRRATIPHPGGST -> MAHSFVQSLP
Cc      CONFLICT 414 414 T->A: LOSS OF PHOSPHORYLATION BY PKA.
Cc      FT 414 414 A -> V (IN REF. 2).
Cc      SQ SEQUENCE 443 AA; 49307 MW; 4A9FF1P6B6A8BA97 CRC64;

Query Match 40.9%; Score 584.5; DB 1; Length 443;
Best Local Similarity 46.6%; Pred. No. 1.5e-39;
Matches 125; Conservative 46; Mismatches 84; Indels 13; Gaps 6;

Cc      7 KDDPEKLFSDLRREIGHSGFAGVYFAYDVNSEVVALKKMSYSGKSNEMKODIIKKEVRL 66
Cc      29 KADPEELFTKLEKIGKSGEVEFKGIDNRTQKVAAIKITDL--EEADEIEDIQQETIVL 86
Cc      67 OKLRHPNTIQRCYLREHTAMVMEYC-LGSASDLEVHKRPLOEVIATVHTGALQGL 125
Cc      87 SQGDSPYVYKYYGSYLAKDKRMIMELYLGGSALDLE--PGPLDPTQATILRELKGL 144
Cc      126 AYLSHNMHRDVKAGNILLSEPGVLKLGDFGASIMAPANSFVGTPTMAPEVI 181
Cc      145 DYLSHKKIHRDIKANVLLSEHGEVYKADFGVAGQLPTQIKRNFVGTPTMAPEVI- 203
Cc      182 AMDEGOYGDYVWSLGTCTELAEKRPPLFEMNAMSALYHIAQNSPALQSGHSEYTR 241
Cc      204 --KQSAVDKADIVMSIGITAIELARCEPHSELHPKVYFLIPKNNPILF-GNYSKPLK 260
Cc      242 NFVDSCLQKIPQDRPTSEVLKHKRFYL 269
Cc      261 EFVEACLNKRESPRPYAKELKKHFFILR 288

RESULT 3
ST25_MOUSE STANDARD: PRT: 426 AA.
AC 09Z2M1:
DT 16-OCT-2001 (rel. 40, Created)
DT 16-OCT-2001 (rel. 40, Last sequence update)
DT 16-OCT-2001 (rel. 40, Last annotation update)
DE Serine/threonine protein kinase 25 (EC 2.7.1.37) (Sterile 20/oxidant
DE stress-response kinase 1) (Ste20/oxidant stress response kinase-1)
DE (SOK-1) (Ste20-like kinase).
GN STRK5 OR SOK1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Melnick M.B.;

```

"Genetic mapping of human and mouse PK genes.";  
RT Submitted (May-1997) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: OXIDANT STRESS-ACTIVATED SERINE/THREONINE KINASE THAT  
CC MAY PLAY A ROLE IN THE RESPONSE TO ENVIRONMENTAL STRESS (BY  
CC SIMILARITY).  
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
CC -1- ENZYME REGULATION: ACTIVATED BY PHOSPHORYLATION, PROBABLY  
CC AUTOPHOSPHORYLATION. THE C-TERMINAL NON-CATALYTIC REGION INHIBITS  
CC THE KINASE ACTIVITY (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
CC STE20 SUBFAMILY.  
-----  
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DR EMBL: AF004934; AAD01208.1; -.  
DR MGD: MG1:1891699; STR25.  
DR InterPro: IPR000719; Euk\_pkinase.  
DR InterPro: IPR002290; Ser\_thr\_pkinase.  
DR InterPro: IPR001245; Tyr\_pkinase.  
DR Pfam: PF00069; pkinase.1.  
DR PRINTS: PR00109; TYRKINASE.  
DR ProDom: PD000001; Euk\_pkinase; 1.  
DR SMART: SM00220; S\_ThrKc; 1.  
DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; FALSE\_NEG.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR Transfaser: Serine/threonine-protein kinase; ATP-binding;  
KM Phosphorylation.  
KW DOMAIN 20 270 PROTEIN KINASE.  
FT NP\_BIND 26 34 ATP (BY SIMILARITY).  
FT BINDING 49 49 ATP (BY SIMILARITY).  
FT ACT\_SITE 140 140 BY SIMILARITY.  
SQ SEQUENCE 426 AA; 48175 MW; 6A01916034E26362 CRC64;  
  
Query Match 40.1%; Score 572.5; DB 1; Length 426;  
Best Local Similarity 46.6%; Pred. No. 1.3e-38;  
Matches 124; Conservative 45; Mismatches 84; Indels 13; Gaps 6;  
  
QY 9 DPKLPFSDLREIGHSGFAYFADVNSVVAIKKMSYSGKSNKWDIIKEVRLQK 68  
DB 15 DPBELFTKLDRIKSGSGEYVKGIDNHTKEVNAIKIIDL--EEAEDIEDIQOEITVLSQ 72  
  
QY 69 LRHPNTIOYRGCYLREHTAWLVMEYC-LGSASDLEVHKKKPLQVEVETAAVTHGALGLAY 127  
DB 73 CDSPIYTRVYGSILKSKLMIMEYLGSGSALDLK--PQPLETYTATTLRETLKGLDY 130  
  
QY 128 LHSNMIHRDVKAGNILLSPGLVKLQDFGSASIMAPA---NSFVGTPLYMAPEVILAM 183  
DB 131 LHSERKIHRIKAVNLLSGDGVKMADEFGVAGQLDTQIKRNFVGTPTPMMAPEVI--- 187  
  
QY 184 DEQYDGKLVVWSLGTICILAEKRPFLFMNMANSAIYHIAONESPALQSGHSEYFRNF 243  
DB 188 KQSAYPEKADISLGIYALIELANGEPNSDLHPMRVLEFLIPKNPPLLE-GHHSKPKPEF 246  
  
QY 244 VDSCLKIPQDRPTSEVLLKHFVLR 269  
DB 247 VEACLKNDPFRFPAKELLKHKKFTTR 272

DE Serine/threonine protein kinase 25 (EC 2.7.1.37) (Sterile 20/oxidant  
DE stress-response kinase 1) (Ste20/oxidant stress response kinase-1)  
DE (SOK-1) (Ste20-like kinase).  
GN STR25 OR SOK1 OR YSK1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OX Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
NCBBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97042345; PubMed=8887545;  
RA Pombo C.M., Bonventure J.V., Molnar A., Kyriakis J., Force T.;  
RT "Activation of a human Ste20-like kinase by oxidant stress defines a  
RT novel stress response pathway.";  
RN EMO J. 15:4537-4546(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97304522; PubMed=9160885;  
RA Osada S.-I., Izawa M., Saito R., Mizuno K., Suzuki A., Hirai S.-I.,  
RA Ohno S.;  
RT "YSK1, a novel mammalian protein kinase structurally related to Ste20  
RT and SpSL, but is not involved in the known MAPK pathways.";  
RT Oncogene 14:2047-2057(1997).  
CC -1- FUNCTION: OXIDANT STRESS-ACTIVATED SERINE/THREONINE KINASE THAT  
CC MAY PLAY A ROLE IN THE RESPONSE TO ENVIRONMENTAL STRESS.  
CC -1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.  
CC -1- ENZYME REGULATION: ACTIVATED BY PHOSPHORYLATION, PROBABLY  
CC AUTOPHOSPHORYLATION. THE C-TERMINAL NON-CATALYTIC REGION INHIBITS  
CC THE KINASE ACTIVITY.  
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
CC -1- TISSUE SPECIFICITY: UBICUOUSLY EXPRESSED. HIGHEST LEVELS ARE  
CC FOUND IN TESTIS, LARGE INTESTINE, BRAIN AND STOMACH FOLLOWED BY  
CC HEART AND LUNG.  
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
CC STE20 SUBFAMILY.  
-----  
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-----  
DR EMBL: X99325; CA67700.1; -.  
DR EMBL: D63780; BAA20420.1; -.  
DR HSSP: P12931; IFMK.  
DR Genew: HGNC:11404; STR25.  
DR MIM: 602255; -.  
DR InterPro: IPR000719; Euk\_pkinase.  
DR InterPro: IPR002290; Ser\_thr\_pkinase.  
DR Pfam: PF00069; pkinase.1.  
DR ProDom: PD000001; Euk\_pkinase; 1.  
DR SMART: SM00220; S\_ThrKc; 1.  
DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; FALSE\_NEG.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR Transfaser: Serine/threonine-protein kinase; ATP-binding;  
KW Phosphorylation.  
FT DOMAIN 20 270 PROTEIN KINASE.  
FT NP\_BIND 26 34 ATP (BY SIMILARITY).  
FT BINDING 49 49 ATP (BY SIMILARITY).  
FT ACT\_SITE 140 140 BY SIMILARITY.  
FT CONFLICT 347 348 EP -> DA (IN REF. 1).  
SQ SEQUENCE 426 AA; 48111 MW; 183CE5700FCEA716 CRC64;  
  
Query Match 39.8%; Score 568.5; DB 1; Length 426;  
Best Local Similarity 46.6%; Pred. No. 2.7e-38;  
Matches 124; Conservative 44; Mismatches 85; Indels 13; Gaps 6;  
  
QY 9 DPKLPFSDLREIGHSGFAYFADVNSVVAIKKMSYSGKSNKWDIIKEVRLQK 68  
DB 15 DPBELFTKLDRIKSGSGEYVKGIDNHTKEVNAIKIIDL--EEAEDIEDIQOEITVLSQ 72

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Oy 169 LNHPTMTIQRCGYLSEHNTAMLMWEC-LTSASDLVEHKKRRLQCEVIAVTHOAGLGLAV 127
Db 73 CDSPIYTRFGSYLSTKMTIMTEYLGSSALDLK--FGPLEFYIATITRLIKGLDY 130
Oy 128 LHSNNHHRDVAKAGNLLSEPGVLKLGDFGSASIMAPA---NSFVGTPYMAPEVILAM 183
Db 131 LHSEKRIHRDIAKAMVLLSEGGDVKLADGVAGQLTDTQIKRNTFVGTFPMMAPEVI--- 187
Oy 164 DEGQYDKVWVSLGTCITELAEKRPPLFNMAAMSLYHIAONESALOSGHSEFRNP 243
Db 168 KQASVDFADNIVSLGTTALELAKGEPNSDPLHPMRVLLFIPKNSPTLGGH-SKPFKEF 246
Oy 244 VDSCLQIKIPQDRPTSEVLLKHFVLR 269
Db 247 VEACLNKDRPRFRPTAKELKKHFKFTR 272

RESULT 5
STRK4_HUMAN
ID STRK4_HUMAN STANDARD: PRT: 487 AA.
AC Q13043; Q15802; Q9NTZ4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Serine/threonine protein kinase 4 (EC 2.7.1.37) (SRE20-like kinase
DE MST1) (MST-1) (Mammalian SRE20-like protein kinase 1)
DE (Serine/threonine protein kinase Krs-2).
GN STRK4 OR MST1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid:9606;
[1]
RP SEQUENCE FROM N.A.
RA MEDLINE=95394929; PubMed=7665586;
RX Greasy C.V., Chernoff J.;
RT "Cloning and characterization of a human protein kinase with homology
RT to Ste20.";
RL J. Biol. Chem. 270:21695-21700(1995).
[2]
RP SEQUENCE FROM N.A.
RA MEDLINE=96413604; PubMed=8816758;
RX Taylor L.R., Wang H.C., Erikson R.L.;
RT "Newly identified stress-responsive protein kinases, Krs-1 and Krs-
RT 2.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:10099-10104(1996).
[3]
RP SEQUENCE OF I-435 FROM N.A.
RA Laird G.;
RL Submitted (MAR-2000) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP + a protein -> ADP + a phosphoprotein.
CC -1- ENZYME REGULATION: THE C-TERMINAL NON-CATALYTIC REGION INHIBITS
CC THE KINASE ACTIVITY.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- TISSUE SPECIFICITY: UBICUOUSLY EXPRESSED.
CC -1- PM: AUTOPHOSPHORYLATED ON SERINE AND THREONINE RESIDUES.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC SRE20 SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: U18297; AAA83354.1; -.
DR EMBL: U60207; AAB17262.1; -.
DR EMBL: AL109839; CAB89421.1; -.
DR HSSP: P24941; IHCL.
DR Genew: HGNC:11408; STRK4.

```

DR MIM: 604965; .  
DR InterPro: IPR000719; Euk\_pkinase.  
DR InterPro: IPR002290; Ser\_thr\_pkinase.  
DR InterPro: IPR001245; Tyr\_pkinase.  
DR Pfam: PF00069; Pkinase\_1.  
DR PRINTS: PR00109; TYRKINASE.  
DR ProDom: PD000001; Euk\_pkinase; 1.  
DR SMART: SM00220; S\_TKC; 1.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP\_1.  
DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; FALSE\_NEG.  
DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR Transferase: Serine/threonine-protein kinase; ATP-binding.  
KW TRANSFERASE; 30  
FT NP\_BIND 36 281  
FT BINDING 59 44  
FT ACID\_SITE 149 149  
FT DOMAIN 373 378  
FT CONFLICT 222 222  
FT CONFLICT 312 312  
FT SEQUENCE 487 AA; 55630 MW; 150758BEC5F77D5C CRC64;  
  
Query Match 38.5%; Score 550; DB 1; Length 487;  
Matches 115; Conservative 43; Mismatches 92; Indels 14; Gaps 5;  
  
QY 10 PEKLFSDREIGHGSGFGAVFYARDRVSEVAIKKMYSGRQSNEKMODIKEVFLQKL 69  
Db 26 PEEVFDLEKIEGGISGVYKAHKETQIVAKQVP-----ESDLDEIIRKEISIMQC 80  
QY 70 RHPNTRVRCGLRHRHTAMLVMEYC-LGSADLLEVHKKPLQEVILAVTHGALOGCLAYL 128  
Db 81 DSPHYVKYIGSTFEKPTDIWIMEVCAGASVSDDIRLRNKRTTLEDIAVLLOSTTKGLEYL 140  
QY 129 HSHNNIHHDVNAAGNTLLSEPGLVXLGDGSA----SIAPANSFVGTPYMAPEVILAMD 184  
Db 141 HPMRIHMDIAGNTLLMTTEGHAKLADGVAGQLDTMAKRNTVIGTFFWMAPEVI---Q 197  
QY 185 EGQDGKADVWSLGITTCLEAEKRPPLFNMANMSALYHIAONESPALOSGH-WSEIFYENF 243  
Db 198 EIGNCVADWDIMSLTGTALTEMAEGKPPYADIHPMRAIFEMIPNPPTFFKRLPELSDNFTDF 257  
QY 244 VDSCLOKIPODRPTSEVLLKHREV 267  
Db 258 VKCCLVKSPEQRATRTQLQHFPV 281  
  
RESULT 6  
STRK\_HUMAN STANDARD: PRT: 491 AA.  
AC Q13188; Q15801; Q15445;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Serine/threonine protein kinase 3 (BC 2.7.1.37) (STE20-like kinase MS2) (Msr-2) (Mammalian STE20-like protein kinase 2)  
DE (Serine/threonine protein kinase Krs-1).  
GN STRK OR MST2.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96144292; Pubmed=8566796;  
RA Creasy C.L., Chernoff J.;  
RT "Cloning and characterization of a member of the MST subfamily of Ste20-like kinases.";  
RL Gene 167; :303-306(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96413604; Pubmed=8816758;  
RA Taylor L.K., Wang H.C., Erikson R.L.;  
RT "Newly identified stress-responsive protein kinases, Krs-1 and Krs-







DT 15-JUN-2002 (Rel. 41, last annotation update)  
DE Serine/threonine-protein kinase PAK 1 (EC 2.7.1.1-) (p21-activated  
GN kinase 1) (PAK-1) (P65-PAK) (Alpha-PAK).  
OC PAK1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN (1)  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97199447; PubMed=9395435;  
RA Sells M.A., Knaus U.G., Bagrodia S., Ambrose D.M., Bokoch G.M.,  
RA Cheroff J.;  
RT "Human p21-activated kinase (PAK1) regulates actin organization in  
RT mammalian cells.";  
RL Curr. Biol. 7:202-210(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Placenta;  
RX MEDLINE=96398842; PubMed=8805275;  
RA Brown J.L., Stowers L., Baer M., Trejo J., Coughlin S., Chant J.;  
RT "Human Ste20 homologue hPAK1 links GTPases to the JNK MAP kinase  
RT pathway.";  
RL Curr. Biol. 6:598-605(1996).  
CC -1- FUNCTION: THE ACTIVATED KINASE ACTS ON A VARIETY OF TARGETS.  
CC LIKELY TO BE THE GTPASE EFFECTOR THAT LINKS THE RHO-RELATED  
CC GTPASES TO THE JNK MAP KINASE PATHWAY.  
CC -1- SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND  
CC CDC42/P21 AND RAC1.  
CC -1- PTM: AUTOPHOSPHORYLATED WHEN ACTIVATED BY CDC42/P21.  
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
CC STE20 SUBFAMILY.  
CC -1- SIMILARITY: CONTAINS 1 CRIB DOMAIN.  
CC -----  
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CC -----  
CC EMBL: U24152; AAC65441.1; -;  
CC EMBL: U51120; AAC50590.1; -;  
CC DR HSSP: P24941; ICRP.  
CC DR Genew: HGNC:8590; PAK1.  
CC DR MIM: 602590;  
CC DR InterPro: IPR000719; Euk\_pkinase.  
CC DR InterPro: IPR000095; PAKbox/Rhopndng.  
CC DR InterPro: IPR002290; Ser\_thr\_pkinase.  
CC DR Pfam: PF00069; pkinase; 1.  
CC DR Pfam: PF00786; PBD; 1.  
CC DR Prodom: PD000001; Euk\_pkinase; 1.  
CC DR SMART: SM00285; PBD; 1.  
CC DR SMART: SM00220; S\_TKC; 1.  
CC DR PROSITE: PS50108; CRIB; 1.  
CC DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
CC DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
CC DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
CC KW Transferrase; Serine/threonine-protein kinase; ATP-binding;  
KW phosphorylation.  
FT DOMAIN 75 88 CRIB.  
FT DOMAIN 134 269 LINKER.  
FT DOMAIN 270 521 PROTEIN KINASE.  
FT NP\_BIND 276 284 ATP (BY SIMILARITY).  
FT BINDING 299 299 ATP (BY SIMILARITY).  
FT ACT\_SITE 389 389 BY SIMILARITY.  
FT MOTAFEN 107 107 L->F: CONSTITUTIVELY ACTIVE.  
FT CONFLICT 26 26 V -> A (IN REF. 2).  
FT CONFLICT 237 237 R -> L (IN REF. 2).  
FT CONFLICT 379 379 F -> S (IN REF. 2).  
FT CONFLICT 503 503 D -> E (IN REF. 2).  
SQ SEQUENCE 545 AA; 60661 MW; 14A1E70E6480CD7E CRC64;

Query Match 34.3%; Score 490; DB 1; Length 545;  
Best Local Similarity 42.3%; Pred. No. 6; 9e-32;  
Matches 112; Conservative 46; Mismatches 93; Indels 14; Gaps 6;  
QY 9 DPEKLSDLREIGHGSGAVYFARVNSSEVAIAIKMWSYSGKSNKEMQDIIEVRFQK 68  
DB 265 DPKKKYRFEKIGQASGVYTDVATGQEVAIKQNTL---QQPKKELINEIILVRE 321  
QY 69 LRHPNTIQYRGCYLRHTAALVMEYCL-GSASDLLEHKKRPLEVEVLAATHALQSLAY 127  
DB 322 NKNENIVNYDSTYLVDGELWVMEYLAGSLLTV--VTECMDEGQIAAACRECLQLEF 379  
QY 128 LHSNMIRDPVAKGNILLSEPGVKLGDFGSAIAPANS----FVGTPLYMAPEVILAM 183  
DB 380 LHSNQVYHRDIKDNILLGMDGSVKLDFEFCAGITPEQSKRSTWGTPYMAPEVY--- 436  
QY 184 DEQYDGKVDVWSLGTICIELAERKRPPLFNWMAALYHIAQNESPALQSGH-WSEYFRN 242  
DB 437 TRRAYGKVDIWSIGIMAIEMIGEPYLNENPLRALYLIATNGTPELQPEKLSAIFRD 496  
QY 243 FVDSCLQIKQDRPTSEVLKRFV 267  
DB 497 FLNRCDMDVEKRGSAKELLQHQL 521  
RESULT 10  
SPSL\_YEAST STANDARD; PRT; 490 AA.  
ID SPSL\_YEAST  
AC P08458;  
DT 01-AUG-1988 (Rel. 08, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Sporulation-specific protein 1 (EC 2.7.1.1-).  
GN SPS1 OR YDR523C OR D9719.27.  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Saccharomycetes; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Friesen H., Lunz R., Doyle S., Segall J.;  
RN Submitted (AUG-1994) to the EMBL/GenBank/DBJ databases.  
RL [2]  
RP SEQUENCE FROM N.A.  
RA Dietrich F.S., Mulligan J., Allen E., Araujo R., Aviles E.,  
RA Berno A., Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M.,  
RA Hunkle-Smith S., Hymen R., Komp C., Lashkari D., Lew H., Lin D.,  
RA Mosedale D., Nakahara K., Namath A., Oefner P., Oh C., Petel F.X.,  
RA Roberts D., Schramm S., Schroeder M., Shogren T., Shroff N.,  
RA Winant A., Yelton M., Botstein D., Davis R.W.;  
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE OF 396-490 FROM N.A.  
RX MEDLINE=87064542; PubMed=3029334;  
RA Percival-Smith A., Segall J.;  
RT "Characterization and mutational analysis of a cluster of three genes  
RT expressed preferentially during sporulation of Saccharomyces  
RT cerevisiae.";  
RL Mol. Cell. Biol. 6:2443-2451(1986).  
CC -1- FUNCTION: SERINE/THREONINE PROTEIN KINASE REQUIRED FOR SPORE WALL  
CC DEVELOPMENT.  
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
CC STE20 SUBFAMILY.  
CC -----  
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CC -----

DR	EMBL:	U13018;	AAA64833..1;	-.
DR	EMBL:	U33057;	AAB64963..1;	-.
DR	EMBL:	M13629;	AAA35079..1;	-.
DR	PIR:	B25376;	B25376.	
DR	SGD:	S000293.1;	SPSL.	
DR	InterPro:	IPR000719;	Euk_pkinase.	
DR	InterPro:	IPR002290;	ser_thr_pkinase.	
DR	Pfam:	PF00069;	pkinaase; 1.	
DR	Prodrom:	PD000001;	Euk_Pkinase; 1.	
DR	SMART:	SM00220;	S_TKc; 1.	
DR	PROSITE:	PS00107;	PROTEIN_KINASE_ATP; 1.	
DR	PROSITE:	PS00108;	PROTEIN_KINASE_ST; FALSE_NEG.	
DR	PROSITE:	PS50011;	PROTEIN_KINASE_DOM; 1.	
KW	transferase;	Serine/threonine-protein kinase;	ATP-binding;	
KW	Spurulation;	Melosis.		
FT	DOMAIN	18	272	
FT	NP_BIND	24	32	PROTEIN KINASE.
FT	BINDING	47	47	ATP (BY SIMILARITY).
FT	ACT_SITE	141	141	ATP (BY SIMILARITY).
FT	CONFLICT	454	454	N -> NVN (TN REF. 2).
FT	CONFLICT	469	469	G -> R (TN REF. 2).
SQ	SEQUENCE	490 AA;	55704 MW;	6143055E85BAF4FF CQC64;



FT NP\_BIND 274 282 ATP (BY SIMILARITY).  
 FT BINDING 297 297 ATP (BY SIMILARITY).  
 FT ACT\_SITE 387 387 BY SIMILARITY.  
 SQ SEQUENCE 544 AA: 60692 MW: 230AF6952CB0A9E2 CRC64:

Query Match 33.9%; Score 484; DB 1; Length 544;  
 Best Local Similarity 41.9%; Pred. No. 2.1e-31;  
 Matches 111; Conservative 46; Mismatches 94; Indels 14; Gaps 6;

QY 9 DPEKLFSDLRREIGHSGFAGVAFRDVNRSEVVAIRKMSYSGKOSNKKMODIKKEVFLQK 68  
 DB 263 DPKKKTREKIKGQAGSVYATADATQGEVAIKOMNL---QQPKKLLINELIYVME 319  
 QY 69 LRHPNTIYRGCYLREHTAMLYMEYCL-GSASDLLEVHKPLQVEVIAVTHGALQGLAY 127  
 DB 320 NKNPNVNYLDSYVGLDELMVMEYLAGSLTDV--VFETCMDEGOIAVCRECLOALDF 377  
 QY 128 LHSNMHHRDVKAGNILLSEPLVKLGDFGSASIMAPANS---FVGPPYMAPEVILAM 183  
 DB 378 LHSNOYIHRDIDSDNLLGMDGSKLTDFGCAQITPEOSKSTWVGTPYMAPEV--- 434  
 QY 184 DSGOYDGKDVMSLGTICIELAERKRPLENNMMSALYHIAONESPALOS-GHMSYEFRN 242  
 DB 435 TRKATGPKVDIVSLGIMALEWVEGEPYLNENPLRLYLATNGPELQNPRLSAVFRD 494  
 QY 243 FVDSCLQKIPDRPTSEVLLKHFV 267  
 DB 495 FLNRCLEMDVDRGSAKELLQHPFL 519

## RESULT 14

PAK3\_RAT  
 ID PAK3\_RAT STANDARD: PRT: 544 AA.  
 AC 062829:

DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Serine/threonine-protein kinase PAK 3 (EC 2.7.1.1-) (p21-activated kinase 3) (PAK-3) (Beta-PAK) (P65-PAK).  
 GN PAK3.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE OF 37-56.  
 RC TISSUE=Brain;  
 RA MEDLINE=96027610; PubMed=7559638;  
 RA Manser E., Chong C., Zhao Z.-S., Leung T., Michael G., Hall C., Lim L.;  
 RT "Molecular cloning of a new member of the p21-Cdc42/Rac-activated kinase (PAK) family";  
 RT J. Biol. Chem. 270:25070-25078(1995).  
 CC -1- FUNCTION: THE ACTIVATED KINASE ACTS ON A VARIETY OF TARGETS.  
 CC -1- SUBUNIT: INTERACTS TIGHTLY WITH GTP-BOUND BUT NOT GDP-BOUND CDC42/P21 AND RAC1. SHOWS HIGHLY SPECIFIC BINDING TO THE SH3 DOMAINS OF PHOSPHOLIPASE C-GAMMA AND OF ADAPTER PROTEIN NCK (BY SIMILARITY).  
 CC -1- TISSUE SPECIFICITY: DETECTED AT HIGH LEVELS IN THE BRAIN AND AT LOW LEVELS IN THE TESTIS.  
 CC -1- DEVELOPMENTAL STAGE: FOUND IN THE EMBRYONIC CNS WITH LITTLE EXPRESSION ELSEWHERE.  
 CC -1- PTM: AUTOPHOSPHORYLATED WHEN ACTIVATED BY CDC42/P21.  
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
 CC -1- STR20 SUBFAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 CRIB DOMAIN.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb.ch/announce/>)

CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch).

DR EMBL: U33314; AAC52268.1; -  
 DR HSSP: P24941; ICRP  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR000095; PAKbox/Rhoindg.  
 DR InterPro: IPR002290; Ser\_thr\_pkinase.  
 DR Pfam: PF00069; pkinase; 1.  
 DR Pfam: PF00786; PBD; 1.  
 DR ProDom: PD000001; Euk\_pkinase; 1.  
 DR SMART: SM00285; PBD; 1.  
 DR SMART: SM00220; S\_Tc; 1.  
 DR ProSITE: PS50108; CRIB; 1.  
 DR ProSITE: PS50107; PROTEIN\_KINASE\_ATP; 1.  
 DR ProSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR ProSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW Transferase; Serine/threonine-protein kinase; ATP-binding; Phosphorylation.  
 FT DOMAIN 70 83 CRIB.  
 FT DOMAIN 129 267 LINKER.  
 FT DOMAIN 268 519 PROTEIN\_KINASE.  
 FT NP\_BIND 274 282 ATP (BY SIMILARITY).  
 FT BINDING 297 297 ATP (BY SIMILARITY).  
 FT ACT\_SITE 387 387 BY SIMILARITY.  
 SQ SEQUENCE 544 AA: 60710 MW: 7B940FC204A2B48B CRC64:

Query Match 33.9%; Score 484; DB 1; Length 544;  
 Best Local Similarity 41.9%; Pred. No. 2.1e-31;  
 Matches 111; Conservative 46; Mismatches 94; Indels 14; Gaps 6;

QY 9 DPEKLFSDLRREIGHSGFAGVAFRDVNRSEVVAIRKMSYSGKOSNKKMODIKKEVFLQK 68  
 DB 263 DPKKKTREKIKGQAGSVYATADATQGEVAIKOMNL---QQPKKLLINELIYVME 319  
 QY 69 LRHPNTIYRGCYLREHTAMLYMEYCL-GSASDLLEVHKPLQVEVIAVTHGALQGLAY 127  
 DB 320 NKNPNVNYLDSYVGLDELMVMEYLAGSLTDV--VFETCMDEGOIAVCRECLOALDF 377  
 QY 128 LHSNMHHRDVKAGNILLSEPLVKLGDFGSASIMAPANS---FVGPPYMAPEVILAM 183  
 DB 378 LHSNOYIHRDIDSDNLLGMDGSKLTDFGCAQITPEOSKSTWVGTPYMAPEV--- 434  
 QY 184 DSGOYDGKDVMSLGTICIELAERKRPLENNMMSALYHIAONESPALOS-GHMSYEFRN 242  
 DB 435 TRKATGPKVDIVSLGIMALEWVEGEPYLNENPLRLYLATNGPELQNPRLSAVFRD 494  
 QY 243 FVDSCLQKIPDRPTSEVLLKHFV 267  
 DB 495 FLNRCLEMDVDRGSAKELLQHPFL 519

## RESULT 15

PAK3\_MOUSE  
 ID PAK3\_MOUSE STANDARD: PRT: 544 AA.  
 AC 061036; 088645;

DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Serine/threonine-protein kinase PAK 3 (EC 2.7.1.1-) (p21-activated kinase 3) (PAK-3) (Beta-PAK) (CD42/RAC effector kinase PAK-B).  
 GN PAK3 OR PAK-3 OR STR4 OR PAKB.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Fibroblast;  
 RA MEDLINE=96032693; PubMed=7559398;  
 RA Bagrodia S., Taylor S.J., Creasy C.L., Chernoff J., Cerione R.A.;  
 RT "Identification of a mouse p21Cdc42/Rac activated kinase.";  
 RT J. Biol. Chem. 270:22731-22737(1995).  
 RN [2]



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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 22, 2002, 12:20:50 ; Search time 15.0405 Seconds  
(without alignments)  
3712.561 Million cell updates/sec

Title: US-09-686-346A-4\_COPY\_15\_285  
Perfect score: 1428  
Sequence: 1 VAELEFKDDPEKLEFSDRLREI.....PQDRPTSEVLKHFVLRER 271

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_21:\*  
1: sp-archaea:\*  
2: sp-bacteria:\*  
3: sp-fungi:\*  
4: sp-human:\*  
5: sp-invertebrate:\*  
6: sp-mammal:\*  
7: sp-mhc:\*  
8: sp-organelle:\*  
9: sp-phage:\*  
10: sp-plant:\*  
11: sp-rodent:\*  
12: sp-virus:\*  
13: sp-vertebrate:\*  
14: sp-unclassified:\*  
15: sp-virus:\*  
16: sp-bacteriap:\*  
17: sp-archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1428	100.0	1235	11 Q9JLS3	Q9JLS3 rattus norv
2	1424	99.7	1049	4 Q94957	Q94957 homo sapien
3	1424	99.7	1235	4 Q9JLS4	Q9JLS4 homo sapien
4	1316	92.2	1001	11 Q88664	Q88664 rattus norv
5	1314	92.0	1005	4 Q9P216	Q9P216 homo sapien
6	1306	91.5	1001	4 Q9H2K7	Q9H2K7 homo sapien
7	1211	84.8	898	4 Q9UH67	Q9UH67 homo sapien
8	1211	84.8	898	4 Q9HC79	Q9HC79 homo sapien
9	1210	84.7	898	13 Q919E0	Q919E0 gallus gal1
10	1208	84.6	898	4 Q9NZM9	Q9NZM9 homo sapien
11	1202	84.2	898	4 Q9H2K8	Q9H2K8 homo sapien
12	1086	76.1	1039	5 Q9YWG8	Q9YWG8 drosophila
13	631.5	44.2	836	10 Q24527	Q24527 arabidopsis
14	631.5	44.2	842	10 Q9FNJ3	Q9FNJ3 oryza sativ
15	631.5	44.2	1120	10 Q9LOA1	Q9LOA1 arabidopsis
16	609.5	42.7	825	10 Q9ARL7	Q9ARL7 hordeum vul

17	608.5	42.6	825	10 Q8SAE1	Q8SAE1 tritium mo
18	604	42.3	809	10 Q8VYC1	Q8VYC1 arabidopsis
19	586.5	41.1	431	11 Q99XK8	Q99XK8 mus musculu
20	572	40.1	461	5 Q61125	Q61125 dictyosteli
21	568.5	39.8	426	4 Q6B8A2	Q6B8A2 homo sapien
22	557.5	39.0	416	4 Q9P289	Q9P289 homo sapien
23	557.5	39.0	416	11 Q99J72	Q99J72 mus musculu
24	555	38.9	596	5 Q9V8W4	Q9V8W4 drosophila
25	555	38.9	669	5 Q8T0S6	Q8T0S6 drosophila
26	550	38.5	421	5 Q95ZM5	Q95ZM5 caenorhabdi
27	550	38.5	487	11 Q9J111	Q9J111 mus musculu
28	550	38.5	497	5 Q9NB31	Q9NB31 caenorhabdi
29	550	38.5	523	5 Q966K9	Q966K9 caenorhabdi
30	550	38.5	525	5 Q966K8	Q966K8 caenorhabdi
31	550	38.5	640	5 Q95ZM6	Q95ZM6 caenorhabdi
32	544	38.1	398	4 Q9H7S5	Q9H7S5 homo sapien
33	543	38.0	478	5 Q6Z571	Q6Z571 suberites d
34	541	37.9	445	11 Q60877	Q60877 mus musculu
35	541	37.9	491	11 Q54748	Q54748 rattus norv
36	541	37.9	497	11 Q9J110	Q9J110 mus musculu
37	539	37.7	651	5 Q95ZM6	Q95ZM6 caenorhabdi
38	539	37.7	653	5 Q22553	Q22553 caenorhabdi
39	538	37.7	491	4 Q96F66	Q96F66 homo sapien
40	537.5	37.6	1268	4 Q9UKD8	Q9UKD8 homo sapien
41	537.5	37.6	1276	4 Q9UKD8	Q9UKD8 homo sapien
42	537.5	37.6	1297	4 Q9UKD9	Q9UKD9 homo sapien
43	537.5	37.6	1305	4 Q9UKED	Q9UKED homo sapien
44	537.5	37.6	1323	4 Q9UKED	Q9UKED homo sapien
45	537.5	37.6	1331	4 Q9UKED	Q9UKED homo sapien

#### ALIGNMENTS

RESULT 1  
ID Q9JLS3 PRELIMINARY; PRT; 1235 AA.  
AC Q9JLS3:  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
DE Serine/Chreonine protein kinase TAO2.  
GN TAO2.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=99428563; PubMed=10497253;  
RA Chen Z., Hutchison M., Cobb M.H.;  
RT "Isolation of the protein kinase TAO2 and identification of its  
RT mitogen-activated protein kinase/extracellular signal-regulated kinase  
RT kinase binding domain.";  
RL J. Biol. Chem. 274:28803-28807(1999).  
RN [2]  
RP SEQUENCE FROM N.A.  
RA Chen Z., Hutchison M., Cobb M.;  
RL Submitted (May-2000) to the EMBL/GenBank/DBJ databases.  
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
DR EMBL: AF140556; AMD39480.2; -.  
DR HSSP: P24941; 1B38.  
DR InterPro: IPR000719; Euk\_pkinase.  
DR InterPro: IPR001899; Gram\_pos\_anchor.  
DR InterPro: IPR003006; Ig\_MHC.  
DR InterPro: IPR002290; Ser\_thr\_pkinase.  
DR InterPro: IPR001245; Tyr\_pkinase.  
DR Pfam: PR00069; pkinase.1.  
DR PRINTS: PR00109; TYRKINASE.  
DR ProDom: PD000001; Euk\_pkinase; 1.  
DR SMART: SM00220; S\_TKC; 1.  
DR PROSITE: PS00343; GRAM\_POS\_ANCHORING; UNKNOWN\_1.  
DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_1.

DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 1235 AA; 138750 MW; 426960D0812516AD CRC64;

Query Match 100.0%; Score 1428; DB 11; Length 1235;  
Best Local Similarity 100.0%; Pred. No. 8,3e-121;  
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAELEFKDDPEKLFSDLRIGHSFGAVYFARDVRNSEVVAIKKMSYSGKQSEKMODII 60  
DB 15 VAELEFKDDPEKLFSDLRIGHSFGAVYFARDVRNSEVVAIKKMSYSGKQSEKMODII 74  
QY 61 KEVRFLOKLRHPNTIQRCRCYLREHTAWLMVEYCLGSASADLLEVHKRPLOEVEIAAVTHG 120  
DB 75 KEVRFLOKLRHPNTIQRCRCYLREHTAWLMVEYCLGSASADLLEVHKRPLOEVEIAAVTHG 134  
QY 121 ALQGLAYLHSHNMIRHDYKAGNILLSEPLVKLGDFGSASIMAPANSFVGTPYMAPEVI 180  
DB 135 ALQGLAYLHSHNMIRHDYKAGNILLSEPLVKLGDFGSASIMAPANSFVGTPYMAPEVI 194  
QY 181 LAMDEQYDGYKDVWSLGTCTELAEKRPPLFNMAKMSALYHIAONESPALOSGHMSEYF 240  
DB 195 LAMDEQYDGYKDVWSLGTCTELAEKRPPLFNMAKMSALYHIAONESPALOSGHMSEYF 254  
QY 241 RNFDSCLOKIPODRPTSEVLKHFVLRER 271  
DB 255 RNFDSCLOKIPODRPTSEVLKHFVLRER 285

## RESULT 2

094957 PRELIMINARY: PRT: 1049 AA.

AC 094957:  
DT 01-MAY-1999 (TREMBLrel. 10, Created)  
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
DE KIA00881 protein (STRE20-like kinase).  
GN KIA00881.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-BRAIN:  
RX MEDLINE=99156230; PubMed=10048485;  
RA Nagase T., Ishikawa K., Suyama M., Kikuno R., Hiroseawa M.,  
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;  
RT "Prediction of the coding sequences of unidentified human genes. XII.  
RT The complete sequences of 100 new cDNA clones from brain which code  
RT for large proteins in vitro."  
RL DNA Res. 5:335-364(1998).  
RN [2]  
RN SEQUENCE FROM N.A.  
RA Yuste J.T., Robinson D., Templeton D.J., Kung H.-J.;  
RT "Characterization of a Subfamily of Human STRE20-like Kinases that  
RT Selectively Activate p38 Through MK3 and are Regulated via a p22A-  
RT dependent Mechanism."  
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
DR EMBL: AB020688; BAA74904.1; -  
DR EMBL: AF263313; AAG38503.1; -  
DR HSSP: P24941; 1B38.  
DR InterPro: IPR000719; Euk\_pkinase.  
DR InterPro: IPR002290; Ser\_thr\_pkinase.  
DR Pfam: PF00069; Tyr\_pkinase.  
DR PRINTS: PF00109; TYRKINASE.  
DR ProDom: PD000001; Euk\_pkinase; 1.  
DR SMART: SM00220; S\_TKc; 1.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.

DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 1049 AA; 119280 MW; D6C5062E47794030 CRC64;

Query Match 99.7%; Score 1424; DB 4; Length 1049;  
Best Local Similarity 99.6%; Pred. No. 1.5e-120;  
Matches 270; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VAELEFKDDPEKLFSDLRIGHSFGAVYFARDVRNSEVVAIKKMSYSGKQSEKMODII 60  
DB 15 VAELEFKDDPEKLFSDLRIGHSFGAVYFARDVRNSEVVAIKKMSYSGKQSEKMODII 74  
QY 61 KEVRFLOKLRHPNTIQRCRCYLREHTAWLMVEYCLGSASADLLEVHKRPLOEVEIAAVTHG 120  
DB 75 KEVRFLOKLRHPNTIQRCRCYLREHTAWLMVEYCLGSASADLLEVHKRPLOEVEIAAVTHG 134  
QY 121 ALQGLAYLHSHNMIRHDYKAGNILLSEPLVKLGDFGSASIMAPANSFVGTPYMAPEVI 180  
DB 135 ALQGLAYLHSHNMIRHDYKAGNILLSEPLVKLGDFGSASIMAPANSFVGTPYMAPEVI 194  
QY 181 LAMDEQYDGYKDVWSLGTCTELAEKRPPLFNMAKMSALYHIAONESPALOSGHMSEYF 240  
DB 195 LAMDEQYDGYKDVWSLGTCTELAEKRPPLFNMAKMSALYHIAONESPALOSGHMSEYF 254  
QY 241 RNFDSCLOKIPODRPTSEVLKHFVLRER 271  
DB 255 RNFDSCLOKIPODRPTSEVLKHFVLRER 285

## RESULT 3

09UL54 PRELIMINARY: PRT: 1235 AA.

AC 09UL54:  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
DE Prostate derived STRE20-like kinase PSK.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE-BREAST CARCINOMA:  
RX MEDLINE=20127920; PubMed=10660600;  
RA Moore T.M., Gary R., Johnson C., Copiccoat M.J., Ridley A.J.,  
RA Morris J.D.H.;  
RT "PSK, a novel STRE20-like kinase derived from prostatic carcinoma that  
RT activates the JNK MAPK pathway and regulates actin cytoskeletal  
RT organization."  
RL J. Biol. Chem. 275:4311-4322(2000).  
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
DR EMBL: AF061943; AAD45616.1; -  
DR HSSP: P24941; 1B38.  
DR InterPro: IPR000719; Euk\_pkinase.  
DR InterPro: IPR002290; Ser\_thr\_pkinase.  
DR Pfam: PF00069; Pkinase; 1.  
DR PRINTS: PR00109; TYRKINASE.  
DR ProDom: PD000001; Euk\_pkinase; 1.  
DR SMART: SM00220; S\_TKc; 1.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 1235 AA; 138232 MW; 3AB9E8B690934307 CRC64;

Query Match 99.7%; Score 1424; DB 4; Length 1235;  
Best Local Similarity 99.6%; Pred. No. 1.9e-120;  
Matches 270; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VAELEFKDDPEKLFSDLRIGHSFGAVYFARDVRNSEVVAIKKMSYSGKQSEKMODII 60



```
Db 15 VALLFFKDEPEKLFSDLRREIGHSGFAGVYFARDVRNSEVAIAIKMSYSGKSNKMODII 74
QY 61 KEVRFLOKLRHPPTIOYRGCYLREHTAMLYMEYCLGSASDLELVHKKPDLQEVETIAAVTHG 120
Db 75 KEVRFLOKLRHPPTIOYRGCYLREHTAMLYMEYCLGSASDLELVHKKPDLQEVETIAAVTHG 134
QY 121 ALQGLAYLHSHNMIRHDVAKAGNILLSEPGVLKIGDFGSASIMAPANSFVGTPTWMAPEVI 180
Db 135 ALQGLAYLHSHNMIRHDVAKAGNILLSEPGVLKIGDFGSASIMAPANSFVGTPTWMAPEVI 194
QY 181 LAMDEQGYDGKVDVWSLGTICIELAEKRPPLFNMNMSALYHTAQNESPALQSGHSEYF 240
Db 195 LAMDEQGYDGKVDVWSLGTICIELAEKRPPLFNMNMSALYHTAQNESPALQSGHSEYF 254
QY 241 RNFVDSCLKIPDRPTSEVLKHKRFVLRER 271
Db 255 RNFVDSCLKIPDRPTSEVLKHKRFVLRER 285
```

## RESULT 4

```
088664 PRELIMINARY: PRT: 1001 AA.
AC 088664:
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Serine/threonine protein kinase TAO1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=9003202; PubMed=9786855;
RA Hutchison M., Berman K.S., Cobb M.H.;
RT "Isolation of TAO1, a protein kinase that activates MEKs in stress-
RT activated protein kinase cascades."
RL J. Biol. Chem. 273:28625-28632(1998).
CC 1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AF084203; AAC71014.1; -.
DR HSSP: P24941; 1B38.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Euk_pkinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 1001 AA; 115952 MW; 85511B62DBD62FCC CRC64;
```

Query Match 92.2%; Score 1316; DB 11; Length 1001;

Best local Similarity 89.7%; Pred. No. 9.4e-111;

Matches 243; Conservative 17; Mismatches 11; Indels 0; Gaps 0;

```
QY 1 VALLFFKDEPEKLFSDLRREIGHSGFAGVYFARDVRNSEVAIAIKMSYSGKSNKMODII 60
Db 15 IALLFFKDEPEKLFSDLRREIGHSGFAGVYFARDVRNSEVAIAIKMSYSGKSNKMODII 74
QY 61 KEVRFLOKLRHPPTIOYRGCYLREHTAMLYMEYCLGSASDLELVHKKPDLQEVETIAAVTHG 120
Db 75 KEVRFLOKLRHPPTIOYRGCYLREHTAMLYMEYCLGSASDLELVHKKPDLQEVETIAAVTHG 134
QY 121 ALQGLAYLHSHNMIRHDVAKAGNILLSEPGVLKIGDFGSASIMAPANSFVGTPTWMAPEVI 180
Db 135 ALQGLAYLHSHNMIRHDVAKAGNILLSEPGVLKIGDFGSASIMAPANSFVGTPTWMAPEVI 194
QY 181 LAMDEQGYDGKVDVWSLGTICIELAEKRPPLFNMNMSALYHTAQNESPALQSGHSEYF 240
Db 195 LAMDEQGYDGKVDVWSLGTICIELAEKRPPLFNMNMSALYHTAQNESPALQSGHSEYF 254
```

```
QY 241 RNFVDSCLKIPDRPTSEVLKHKRFVLRER 271
Db 255 RNFVDSCLKIPDRPTSEVLKHKRFVLRER 285
```

## RESULT 5

```
09P216 PRELIMINARY: PRT: 1005 AA.
AC 09P216: 096175;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE KIAA1361 protein (Serine/threonine kinase TAO1) (Fragment).
GN KIAA1361.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE-BRAIN;
RX MEDLINE=20181126; PubMed=10718198;
RA Nagase T., Kikuno R., Ishikawa K., Hirose M., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XVI.
RT The complete sequences of 150 new cDNA clones from brain which code
RT for large proteins in vitro."
RL DNA Res. 7:65-73(2000).
RN [2]
RP SEQUENCE OF 5-1005 FROM N.A.
RA Jenkins S.G., D'Andrea R.J., Gamble J.R., Vadas M.A.;
RT "Characterization of human TAO1."
RT Submitted (Jul-2001) to the EMBL/Genbank/DBJ databases.
CC 1- SIMILARITY: BELONGS TO THE EMBL/Genbank/DBJ databases.
DR EMBL: AB037782; BA92559.1; -.
DR EMBL: AY049015; AAL12217.1; -.
DR HSSP: P24941; 1B38.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD000001; Euk_pkinase; 1.
DR SMART: SM00220; S_TKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS0011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
FT NON_TER
SQ SEQUENCE 1005 AA; 116540 MW; A83BD4E53569BCB5 CRC64;
```

Query Match 92.0%; Score 1314; DB 4; Length 1005;

Best local Similarity 89.7%; Pred. No. 1.4e-110;

Matches 243; Conservative 17; Mismatches 11; Indels 0; Gaps 0;

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QY 1 VALLFFKDEPEKLFSDLRREIGHSGFAGVYFARDVRNSEVAIAIKMSYSGKSNKMODII 60
Db 19 IALLFFKDEPEKLFSDLRREIGHSGFAGVYFARDVRNSEVAIAIKMSYSGKSNKMODII 78
QY 61 KEVRFLOKLRHPPTIOYRGCYLREHTAMLYMEYCLGSASDLELVHKKPDLQEVETIAAVTHG 120
Db 79 KEVRFLOKLRHPPTIOYRGCYLREHTAMLYMEYCLGSASDLELVHKKPDLQEVETIAAVTHG 138
QY 121 ALQGLAYLHSHNMIRHDVAKAGNILLSEPGVLKIGDFGSASIMAPANSFVGTPTWMAPEVI 180
Db 139 ALQGLAYLHSHNMIRHDVAKAGNILLSEPGVLKIGDFGSASIMAPANSFVGTPTWMAPEVI 198
QY 181 LAMDEQGYDGKVDVWSLGTICIELAEKRPPLFNMNMSALYHTAQNESPALQSGHSEYF 240
Db 199 LAMDEQGYDGKVDVWSLGTICIELAEKRPPLFNMNMSALYHTAQNESPALQSGHSEYF 258
QY 241 RNFVDSCLKIPDRPTSEVLKHKRFVLRER 271
Db 259 RNFVDSCLKIPDRPTSEVLKHKRFVLRER 289
```

```
RESULT 6
O9H2K7 PRELIMINARY: PRT: 1001 AA.
ID 09H2K7
AC 09H2K7:
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, last sequence update)
DE 01-JUN-2002 (TREMblrel. 21, last annotation update)
DE STE20-like kinase (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RX SEQUENCE FROM N.A.
[1]
RA Yustein J.T., Robinson D., Kung H.-T.;
RT "Characterization of a Subfamily of Human STE20-like kinases that
RT Selectively Activate p38 Through MKK3 and are Regulated via a PP2A-
RT dependent Mechanism."
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF263312; AAC38502.1; -.
DR HSSP: P24941; 1B38.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR Pfam: PF00069; pkinase; 1.
DR ProDom: PD000001; Euk_pkinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR SMART: SM00219; TYRKC; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW Kinase.
FT NON_TER
SQ SEQUENCE 1001 AA; 115957 MW; 7F0E534D3E7E159E CRC64;

Query Match 91.5%; Score 1306; DB 4; Length 1001;
Best Local Similarity 89.3%; Pred. No. 7,6e-110;
Matches 242; Conservative 17; Mismatches 12; Indels 0; Gaps 0;

OY 1 VAELEFKDDEPEKLFSDLRREIGHSGFAGVVFARDVRSEVVAIKKMSYSGKQSEKMODII 60
DB 15 IAELEFKDEPEKLFSDLRREIGHSGFAGVVFARDVRSEVVAIKKMSYSGKQSEKMODII 74
OY 61 KEVRFLOKLRHPNTIOYRCGYLREHTAMLYMEYCLGSASDLEVHKPKLOEVEIAAIVTNG 120
DB 75 KEKFFLOKLRHPNTIEYKCYLREHTAMLYMEYCLGSASDLEVHKPKLOEVEIAAIVTNG 134
OY 121 ALQGLAYLHSHNMIRHDVAKGNILISEPGLVKGDFGSASINAPANSFVGTPTWMAPEVI 180
DB 135 ALQGLAYLHSHNMIRHDVAKGNILISEPGLVKGDFGSASINAPANSFVGTPTWMAPEVI 194
OY 181 LAMDEQGYGKVDVMSLGTICIELAEKRPPLFNMMNSALYHIAQNSPALQSGHSEYF 240
DB 195 LAMDEQGYGKVDVMSLGTICIELAEKRPPLFNMMNSALYHIAQNSPALQSGHSEYF 254
OY 241 RNFVDSCLQIKPODRPTSEVLLKHFVLRER 271
DB 255 RNSVDSCLQIKPODRPTSEVLLKHFVLRER 285

RESULT 7
O9H2K7 PRELIMINARY: PRT: 898 AA.
ID 09H2K7
AC 09H2K7:
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, last sequence update)
DE 01-MAR-2002 (TREMblrel. 20, last annotation update)
DE STE20-like kinase.
OS JIK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RX SEQUENCE FROM N.A.
[1]
RA Tassi E., Biesova Z., Di Fiore P.P., Guckind J.S., Wong W.T.;
RT "Human JIK, a novel member of the STE20 kinase family that inhibits
RT JNK and is negatively regulated by epidermal growth factor."
RL J. Biol. Chem. 274:33287-33295(1999).
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AF179867; AAFL4559.1; -.
DR HSSP: P24941; 1B38.
DR InterPro: IPR000719; Euk_pkinase.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR001245; Tyr_pkinase.
DR InterPro: IPR000130; Zn_MTpeptidse.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR00109; TYRKINASE.
DR ProDom: PD000001; Euk_pkinase; 1.
DR SMART: SM00220; S_TKC; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
DR PROSITE: PS00142; ZINC_PROTEASE; UNKNOWN_1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 898 AA; 105657 MW; 61F04628713E6025 CRC64;

Query Match 84.8%; Score 1211; DB 4; Length 898;
Best Local Similarity 81.5%; Pred. No. 2,8e-101;
Matches 221; Conservative 28; Mismatches 22; Indels 0; Gaps 0;

OY 1 VAELEFKDDEPEKLFSDLRREIGHSGFAGVVFARDVRSEVVAIKKMSYSGKQSEKMODII 60
DB 11 IAELEFKDDEPEKLFSDLRREIGHSGFAGVVFARDVRSEVVAIKKMSYSGKQSEKMODII 70
OY 61 KEVRFLOKLRHPNTIOYRCGYLREHTAMLYMEYCLGSASDLEVHKPKLOEVEIAAIVTNG 120
DB 71 KEKFFLOKLRHPNTIEYKCYLREHTAMLYMEYCLGSASDLEVHKPKLOEVEIAAIVTNG 130
OY 121 ALQGLAYLHSHNMIRHDVAKGNILISEPGLVKGDFGSASINAPANSFVGTPTWMAPEVI 180
DB 131 ALQGLAYLHSHNMIRHDVAKGNILISEPGLVKGDFGSASINAPANSFVGTPTWMAPEVI 190
OY 181 LAMDEQGYGKVDVMSLGTICIELAEKRPPLFNMMNSALYHIAQNSPALQSGHSEYF 240
DB 191 LAMDEQGYGKVDVMSLGTICIELAEKRPPLFNMMNSALYHIAQNSPALQSGHSEYF 250
OY 241 RNFVDSCLQIKPODRPTSEVLLKHFVLRER 271
DB 251 RNFVDSCLQIKPODRPTSEVLLKHFVLRER 281

RESULT 8
O9H2K7 PRELIMINARY: PRT: 898 AA.
ID 09H2K7
AC 09H2K7:
DT 01-MAR-2001 (TREMblrel. 16, Created)
DT 01-MAR-2001 (TREMblrel. 16, last sequence update)
DE 01-JUN-2002 (TREMblrel. 21, last annotation update)
DE Serine kinase (STE20-like kinase).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
RX SEQUENCE FROM N.A.
[1]
RA Zhang W., Chen T., Wan T., He L., Li N., Yuan Z., Cao X.;
RT "Cloning of DPK, a novel dendritic cell-derived protein kinase
RT activating the ERK1/ERK2 and JNK/SAPK pathways."
RL Biochem. Biophys. Res. Commun. 274:872-879(2000).
RN [2]
RN SEQUENCE FROM N.A.
```

RC TISSUE-PLACENTA;  
RA Strausberg R.;  
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF131518; AAC09131.1; -  
DR EMBL: BC002756; AAH02756.1; -  
DR HSSP: P24941; 1B38.  
DR InterPro: IPR000719; Euk\_pkinase.  
DR InterPro: IPR002290; Ser\_thr\_pkinase.  
DR InterPro: IPR001245; Tyr\_pkinase.  
DR InterPro: IPR000130; Zn\_MTPptase.  
DR Pfam: PF00069; pkinase; 1.  
DR PRINTS: PR00109; TYRKINASE.  
DR ProDom: PD000001; Euk\_pkinase; 1.  
DR SMART: SM00220; S\_TKC; 1.  
DR SMART: SM00219; TYRKC; 1.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
DR PROSITE: PS00142; ZINC\_PROTEASE; UNKNOWN.1.  
DR ATP-binding; Kinase; Transferase.  
KW ATP-binding; Kinase; Transferase.  
SQ SEQUENCE 898 AA; 105405 MW; AE7E30745B09763C CRC64;

## Query Match

Best Local Similarity 84.8%; Score 1211; DB 4; Length 898;  
Matches 221; Conservative 28; Mismatches 22; Indels 0; Gaps 0;

QY 1 VAELEFDPDEKFLSDREIGHSGFGAVYFARVNRSEVVAIKKMSYSGKSNKMODII 60  
DB 11 IADLFKDPDEELFVGLHEHGSGFGAVYFATNHTSEVVAIKKMSYSGKOTHEKMODII 70  
QY 61 KEVRFLOKLHPNTIYRGCYLREHTAMLVMEYCLGSASDLEVHKKPLQVEEIAATHG 120  
DB 71 KEVRFLOKLHPNTIEKGCYLRKHTAMLVMEYCLGSASDLEVHKKPLQVEEIAATHG 130  
QY 121 ALQGLAVLHSHNMIHRDKAGNILLSPGLYKLGDFGSASIMAPNSFVGTPTWMAPEVI 180  
DB 131 ALHGLAVLHSHALIHRIKAGNILLTEPGQVKLADFGSASMAPNSFVGTPTWMAPEVI 190  
QY 181 LADEGOYDGKVDVWSIGITCIELAEKRPPLFNNMNSALYHTAONESPALOGSHNSEYF 240  
DB 191 LADEGOYDGKVDVWSIGITCIELAEKRPPLFNNMNSALYHTAONESPALOGSHNSEYF 250  
QY 241 RNFVDSCLQKIPDRPTSEVLLKHFVLRER 271  
DB 251 RRFVDYCLQKIPQERPTSSELLRHDFVRDR 281

## RESULT 9

Q919E0 PRELIMINARY; PRT; 898 AA.  
ID Q919E0;  
AC Q919E0;  
DT 01-OCT-2000 (TREMblrel. 15, Created)  
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)  
DT 01-MAR-2002 (TREMblrel. 20, last annotation update)  
DE KFC (Fragment).  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE-20162342; PubMed-10698516;  
RA Yustein J.T., Li D., Robinson D., Kung H.J.;  
RT "KFC, a Ste20-like Kinase with mitogenic potential and capability to  
activate the SAPK/JNK pathway.";  
RL Oncogene 19:710-718(2000).  
DR EMBL: AF263314; AAF73045.1; -  
DR HSSP: P24941; 1B38.  
DR InterPro: IPR000719; Euk\_pkinase.  
DR InterPro: IPR002290; Ser\_thr\_pkinase.  
DR InterPro: IPR000130; Zn\_MTPptase.  
DR Pfam: PF00069; pkinase; 1.

DR ProDom: PD000001; Euk\_pkinase; 1.  
DR SMART: SM00220; S\_TKC; 1.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: PS00142; ZINC\_PROTEASE; UNKNOWN.1.  
DR NON\_TER 898  
FT NON\_TER 898  
SQ SEQUENCE 898 AA; 105289 MW; 46E265937F218AA8 CRC64;

## Query Match

Best Local Similarity 84.7%; Score 1210; DB 13; Length 898;  
Matches 222; Conservative 27; Mismatches 22; Indels 0; Gaps 0;

QY 1 VAELEFDPDEKFLSDREIGHSGFGAVYFARVNRSEVVAIKKMSYSGKSNKMODII 60  
DB 11 IADLFKDPDEELFVGLHEHGSGFGAVYFATNHTSEVVAIKKMSYSGKOTHEKMODII 70  
QY 61 KEVRFLOKLHPNTIYRGCYLREHTAMLVMEYCLGSASDLEVHKKPLQVEEIAATHG 120  
DB 71 KEVRFLOKLHPNTIEKGCYLRKHTAMLVMEYCLGSASDLEVHKKPLQVEEIAATHG 130  
QY 121 ALQGLAVLHSHNMIHRDKAGNILLSPGLYKLGDFGSASIMAPNSFVGTPTWMAPEVI 180  
DB 131 ALQGLAVLHSHCKIHRIKAGNILLTEPGQVKLADFGSASIVSPANSFVGTPTWMAPEVI 190  
QY 181 LADEGOYDGKVDVWSIGITCIELAEKRPPLFNNMNSALYHTAONESPALOGSHNSEYF 240  
DB 191 LADEGOYDGKVDVWSIGITCIELAQRPPLFNNMNSALYHTAONESPALOGSHNSEYF 250  
QY 241 RNFVDSCLQKIPDRPTSEVLLKHFVLRER 271  
DB 251 RGFVDYCLQKIPQERPTSADLLRHDFVRDR 281

## RESULT 10

Q9NZM9 PRELIMINARY; PRT; 898 AA.  
ID Q9NZM9;  
AC Q9NZM9;  
DT 01-OCT-2000 (TREMblrel. 15, Created)  
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)  
DT 01-MAR-2002 (TREMblrel. 20, last annotation update)  
DE Serine/threonine kinase.  
GN KDS.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Carter T.G., Benton B., Fruhling D., Monks C.R.F., Windmiller D.,  
RA Kupfer A., Manfredi J., Johnson G.L., Pleiman C.M.;  
RT "KDS and TAO1, two related proteins with kinase domain homology to  
STE20, differentially relocate in mitogen stimulated T lymphocytes.";  
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.  
DR EMBL: AF181985; AAF25817.1; -  
DR HSSP: P24941; 1B38.  
DR InterPro: IPR000719; Euk\_pkinase.  
DR InterPro: IPR002290; Ser\_thr\_pkinase.  
DR InterPro: IPR001245; Tyr\_pkinase.  
DR InterPro: IPR000130; Zn\_MTPptase.  
DR Pfam: PF00069; pkinase; 1.  
DR PRINTS: PR00109; TYRKINASE.  
DR ProDom: PD000001; Euk\_pkinase; 1.  
DR SMART: SM00220; S\_TKC; 1.  
DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; 1.  
DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
DR PROSITE: PS00142; ZINC\_PROTEASE; UNKNOWN.1.  
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.  
SQ SEQUENCE 898 AA; 105432 MW; 9738BD5DFA12AC9 CRC64;

Query Match 84.6%; Score 1208; DB 4; Length 898;  
Best Local Similarity 81.2%; Pred. No. 5.3e-101;

Cy	121	ALQGIATYHSHNMTHRDYKAGNILLSPGLVYLGDPSASIAMPAASFVGTPYMAAPEVI	180
Dd	131	ALHGITYLHSHALLHRDIKAGNILLTEPPGVKLADFSASMAPPANSFVGTPYMAAPEVI	190
Cy	181	LAMDEGGDYGDVVDWYSGLITCIELAEKKPPLFNMMANSAlyHTIAQNESPALSGHMSSEVF	240
Dd	191	LAMDEGGDYGDVVDIWSLGITCTIELAEKKPPLFNMMANSAlyHTIAQNDSPTLOSNEWTDSGF	250
Cy	241	RNFVDSCLQKITPDPRPTSSEVLTKRPFVRER	271
Dd	251	RNFVDCLOKITPDPRPTSSELLRRDHFVRDR	281

RESULT 12  
O9VMG8 PRELIMINARY; PRT: 1039 AA.

AC	O9VMG8:	
DT	01-MAY-2000	(TREMBLrel. 13, Created)
DT	01-MAY-2000	(TREMBLrel. 13, last sequence update)
DT	01-MAR-2002	(TREMBLrel. 20, last annotation update)
DE	CG14217	protein.

OC *Eusarcophora*, *Metazoa*; *Arthropoda*; *Tracheata*; *Insecta*;  
OC *Pterygota*; *Neoptera*; *Endopterygota*; *Diptera*; *Brachycera*; *Muscomorpha*;  
OC *Ephydroidea*; *Drosophilidae*; *Drosophila*.  
OX NCBI\_TaxID=7227;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=BERKELEY;  
RX MEDLINE=20196006; PubMed=10731132;  
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,  
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,  
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Milos G.L.G.,  
RA Abri'l J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
RA Bailew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
RA Beeson K.I., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,  
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,  
RA Cherry J.M., Cavale S., Dahlke C., Davenport L.B., Davies P.,  
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
RA Dodson K., Doup L.E., Donnes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
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